## STIC-Biotech/ChemLib

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Swope, Sheridan

Sent:

Thursday, March 25, 2004 1:02 PM

To: Subject: STIC-Biotech/ChemLib 09/771,161

For 09/771,161, pls search:

SID 2: Full-length and oligo search (≥20NTs) against the NT and AA data bases.

SID 93: Full-length and oligo search (≥20AAs) against the NT and AA data bases.

THANKS SO VERY MUCH TO THE GREAT STAFF OF STIC!!!!

Sheridan Swope, Ph.D.
Patent Examiner, AU 1652
Recombinant Enzymes
571-272-0943 (voice)
E03A70 Remsen Bld (Office)
E03C70 Remsen Bld (Mailbox)



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Searcher
Phone:
Location:
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TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other

VENDOR/COST (wh	ere applic.)
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Sequence 184, App
Sequence 28, Appl
Sequence 1015, Ap
Sequence 1, Appli
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TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILLE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: U5/09/71,161A
CURRENT FILING DATE: 2001-01-26
FRIOR APPLICATION NUMBER: 09/724,676
FRIOR FILING DATE: 2000-11-28
FRIOR FILING DATE: 2000-06-15
FRIOR FILING DATE: 2000-06-12
FRIOR FILING DATE: 2000-04-12
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US-10-118-984-5
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US-10-014-269-21
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US-10-914-506-21
US-09-941-879B-10
US-09-931-071-11
US-09-771-161A-93
US-09-771-161A-184
US-09-862-027-28
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ORGANISM: Homo sapiens
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| cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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Patent No. US20020110811A1
GENERAL INFORMATION:
FAPPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REPRENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: U3/74,676
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PATENTING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SEQ ID NO 184
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TITLE OF INVENTION: No. US20020142428Alel Kinases and Uses Therefore Tries of INVENTION: No. US20020142428Alel Kinases and Uses Therefore Tries of INVENTION: No. US20020142428Alel Kinases and Uses Therefore Tries are the tries of USA 1862,027

CURRENT FILING DATE: 2001-05-21

PRIOR APPLICATION NUMBER: US 09/345,473

PRIOR PILING DATE: 1999-06-30

NUMBER OF SEQ ID NOS: 82

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 28

LENGTH: 540

TYPE: PRI
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Patent No. US20020052308A1
GENERAL INFORMATION:
APPLICANT: ROSON et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT APPLICATION NUMBER: PCT/US00/05882
PRIOR APPLICATION NUMBER: PCT/US00/05882
                                                 540
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                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
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 ORGANISM: Homo sapiens
                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-09-925-301-1015
, ORGANISM: Hom
US-09-981-397A-14
                                   Alignment Scores:
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US-09-981-397A-14

US-09-981-397A-14

Sequence 14, Application US/09981397A

Publication No: US20030082519A1

Sequence 14, Application US/09981397A

Publication No: US20030082519A1

Sequence 14, Application US-09519A1

APPLICANT: Acxima Pharmaceuticals AG

APPLICANT: Schubart, Danial

APPLICANT: Stein-Gerlach, Matthias

TITLE OF INVENTION: Inhibition

FILE REFREENCE: Axx. 00-11 uS

CURRENT APPLICATION WINBER: US/09/981,397A

CURRENT PILING DATE: 2000-10-16

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn version 3.1

LENGTH: 540

TYPE: PRT
                                     394
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PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SECTWARE: Patentin Ver. 2.0
SEQ ID NO 1015
LENGTH: 544
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Best Local Similarity:
Query Match:
DB:
                                                             TYPE: PRT
ORGANISM: Homo
US-09-925-301-1015
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US-09-748-537-1
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Sequence 1, Application US/09748537; Patent No. US20020061833A1; GENERAL INFORMATION:

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APPLICANT: Chao, Moses V.

APPLICANT: Chao, Moses V.

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILE AND USES THERE
FILE REFERENCE: 07334-316601
CURRENT APPLICATION NUMBER: US/09/748,537

CURRENT FILING DATE: 2000-12-26

PRIOR PAPLICATION NUMBER: US 09/099,041

PRIOR PAPLICATION NUMBER: US 09/019,942

PRIOR APPLICATION NUMBER: US 09/019,94
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Fatent No. US20020061845A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARI
FILE REFERENCE: 07334-124001
CURRENT APPLICATION NUMBER: US/09/728,721
CURRENT FILING DATE: 1999-06-29
FRIOR FILING DATE: 1999-06-28
FRIOR PELING DATE: 1998-12-08
FRIOR FILING DATE: 1998-106-17
FRIOR FILING DATE: 1998-06-17
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STREET: 225 Franklin Street
STREET: 225 Franklin Street
STATE: MA
COUNTRY: USA
COUNTRY: USA
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: SEASES for Windows 95
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/10/133,780
FILING DATE: 26-Apr-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/019,942
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 71
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                    TYPE: PRT
CORGANISM: Homo sapiens
US-09-728-721-2
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Percent Similarity:
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                                                                               SEQ ID NO 2
LENGTH: 540
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Sequence 2, Application US/10105931
Sequence 3, Application US/20020150987A1
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-076001
CURRENT APPLICATION NUMBER: US/10/105,931
CURRENT FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 09/099,041
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
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Matches:
Conservative:
Mismatches:
Indels:
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
RRGISTRATION UNMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/068001
TELECOMMUNICATION INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acid
TYPE: amino acid
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                     TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
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Sequence 2, Application US/10295981

Sequence 2, Application US/10295981

Sequence 2, Application No. US20030120055A1

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

FILE REFERENCE: 07334-124001

CURRENT APPLICATION NUMBER: US/10/295,981

CURRENT PILING DATE: 1999-06-28

PRIOR APPLICATION NUMBER: US 09/245,281

PRIOR PILING DATE: 1998-02-05

PRIOR PILING DATE: 1998-02-06

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

SOFTWARE: FastSEQ for Windows Version 4.0

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US-10-295-981-2
                      Percent Similarity:
Best Local Similarity:
Query Match:
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| DS-1011B-984-2
| Sequence 2, Application US/1011B984
| Publication No. US20020197693A1
| GENERAL INPORMATION:
| APPLICANT: Bertin, John
| TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
| TITLE OF INVENTION: NOVEL MOLESS THEREOF
| FILE REFERENCE: 07334/11B001
| CURRENT APPLICATION NUMBER: US/10/118,984
| CURRENT FILING DATE: 2002-04-09
| PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
| PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08
| PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08
| PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
| SOFTWARE: FastSEQ for Windows Version 4.0
| SSOFTWARE: FASTSEQ FOR WINDOWS VERSION NOWERS OF SACOND OF TANGEN CANDOWS OF TANGEN 
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                                             TYPE: PRT
ORGANISM: Homo sapiens
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CORGANISM: Homo sapiens
US-10-118-984-2
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LENGTH: 540
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21 ThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLys 40
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1 GlnProGly11eAlaGlnGlnTrp11eGlnSerLysArgGluAsp11eValAsnGlnMet
                                                             GACACTACTGACATCCAAGGAGAAGAATTTGCCAAAGTTATAGTACAAAATTGAAAGAT
                                                                                                                                                                                                                                               RESULT 13
US-10-105-931-6
; Sequence 6, Application US/10105931
; Sequence 6, Application No. US20020150987A1
; Publication No. US20020150987A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERRENCE: 07334-076001
; CURRENT FPLIANG DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/099,041
; PRIOR PILING DATE: 1998-06-17
; PRIOR PILING DATE: 1998-06-17
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOOFTWARE: RESEREE OF WINDOWS Version 4.0
; SEQ ID NO 6
; LENGTH: 109
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CORGANISM: Homo sapiens
US-10-105-931-6
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Best Local Similarity:
Query Match:
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; Sequence 6, Application US/09728721
; Retent No. USZ0020061845A1
; GENERAL INFORMATION:
; APPLICANT: BERTIN, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; CURRENT APPLICATION NUMBER: US/09/728,721
CURRENT FILING DATE: 1999-06-28
; PRIOR PILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR PILING DATE: 1998-12-08
; PRIOR PILING DATE: 1998-06-17
; RIUNG BAPELICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; WUMBER OF SEQ ID NOS: 71
; SEQ ID NO 6.5
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                                                                              CCTGGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAAATGACA 751
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ORGANISM: Homo sapiens
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Percent Similarity:
Best Local Similarity:
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Pred. No.:
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US-09-728-721-6
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completed: March 29, 2004, 14:40:27
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Publication No. US20030120055A1

GENERAL INFORMATION:

APPLICANT: Bertin, John MONEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE

TITLE OF INVENTION: US/10/295,981

CURRENT APPLICATION NUMBER: US/10/295,981

CURRENT FILING DATE: 1999-06-28

PRIOR PRILING DATE: 1999-06-28
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squence 6, Application US/10118984

publication No. US20020197693A1

GENERAL INFORMATION:

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY

TITLE OF INVENTION: NOVEL MOLES THEREOF

FILE REFERENCE: 0734/118001

CURRENT PILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281

PRIOR PILING DATE: EARLIER FILING DATE: 1999-02-05

PRIOR PILING DATE: EARLIER FILING DATE: 1998-12-08

PRIOR PILING DATE: EARLIER FILING DATE: 1998-06-17

PRIOR PILING DATE: EARLIER FILING DATE: 1998-06-17

PRIOR PLING DATE: EARLIER FILING DATE: 1998-06-06

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PASSED FOR Windows Version 4.0

SEQ ID NOS: 44

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ORGANISM: Homo sapiens
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
PRIOR FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: US 09/207,359
PRIOR PILING DATE: 1998-12-08
PRIOR PILING DATE: 1998-12-08
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PASISEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 109
                                                                                                                                                                                                                                                                                                                                           5.18e-103
109.00
100.00%
100.00%
20.53%
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US-10-295-981-6
                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
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Sequence 31541, A Sequence 4651, Ap Sequence 10, Appl Sequence 12, Appl Sequence 174, App Sequence 174, App Sequence 215, Appl Sequence 216, Appl Sequence 229, Appl Sequence 23, Appl Sequence 24, Appl Sequence 24,

Sequence

Sequence 10202, A Sequence 108092, Sequence 66230, Sequence 66231, A Sequence 66231, A Sequence 46771, Sequence 188799, Sequence 251225, Sequence 251225,

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Sequence Sequence

Title: Perfect score:

Sequence:

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Run on:

Scoring table:

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Searched:

Database :

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TGTAGGTAATTGTTAGATTTCGAGGATGAAGCTCTGAGACACTGAGAGAAGGTAACCAAT 120
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LOCATION: (1)..(1669)
OTHER INFORMATION: "n" can be any nucleotide 'a', 'c' , 'g' or 't'
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9 US-09-748-537-12

12 US-10-282-122A-35784

9 US-09-748-537-9

9 US-09-741-668-174

9 US-09-912-020-215

9 US-09-912-020-215

10 US-09-812-846-166

10 US-09-919-039-229

10 US-10-312-841-2
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US-10-027-632-108093
US-10-027-632-66230
US-10-027-632-66231
US-10-027-632-46770
US-10-027-632-46771
US-10-027-632-188799
US-10-027-632-251226
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US-10-027-632-249981
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TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-01-128
PRIOR PELING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
SOFTWARE: PATCHIN VINBER: 135619
PRIOR FILING DATE: 2000-04-12
SOFTWARE: PATCHIN VERSION 3.0
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llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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ORGANISM: Homo sapiens
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Matches 1669;
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Sequence 173, App
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Sequence 544, App
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Sequence 2, Appl
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                                                                                                                                                                                           April 1, 2004, 06:30:56; Search time 649 Seconds (without alignments) 9574.273 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_MEW_PUB.seq:*
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18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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                             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-925-301-173
US-09-941-397A-13
US-09-748-537-2
US-09-748-537-2
US-09-748-537-2
US-10-133-780-2
3 US-10-135-984-1
4 US-10-295-981-1
4 US-10-295-981-1
5 US-10-105-931-3
3 US-10-105-931-3
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4 US-10-295-981-3
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Maximum DB seq length: 2000000000
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333 AGTTACAGAGTGTTTCAAGTGCCATTCACCTATGTGACAAGAAAATGGAATTATCTC 392  1204 AGTTACAGAGTGTTTCAAGTGCCATTCACCTATGTGACAAGAAAATGGAATTATCTC 1263  393 TGAACATACCTGTAAATCATGGTCCACAGAGGAATCATGTGGAAATATGTCC 1263  1264 TGAACATACCTGTAAATCATGGTCCACAGAGGAATCATGTGGATCCTCTCAGGTCCATG 452  1264 TGAACATACTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGGTCCATG 1323  453 AAAATAGTGGTTCTCCTGAAACTTCAAGGTCCTGCCAGGACAATGATTTT 512  1324 AAAATAGTGGTTCTCCTGAAACTTCAAGGTCCTGCCTCCAGGACAATGATTTT 1383  513 TATCTAGAAAAGCTCAAGACTTATTATGAAGCTGCATCACTGTCCTGGAAATCACA 1443  513 GTTGGGATAGCTCCAAGACTTATTATGAAGCTGCATCATGTCCTCTGGAAATCACA 1443  573 GTTGGGATAGCACCAATTTTTATGAAGGCTGCATTCTGTGATCACAAGACCACTC 532  11414 GTTGGGAYACCACCATTTTTGAAGGCTGCATTCTTGTGAATCACAAGACCACTC 1503	Db 2284 ACAGAATCCCTGCCCTAAAATCCCCTACAAAAGGGTTATTAAA 2343  Qy 1473 ACTCCATTATTAGGATTACATTTATATTATTATGAATTCCCTTTAAAAATGATT 1532  Db 2244 ACTCCATTATTAGGATTACATTTTATATTATTATGAATTCCCTTTAAAATGATAT 2403  Qy 1533 TTCAAAGGTAAACAATACAATTTATATTTATTATATATAT
633 CATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAGC 692	RESULT 3 US-09-981-397A-13 US-09-981-397A-13 Sequence 13, Application US/09981397A Sequence 13, Application WS/09981397A Sequence 13, Application No. US20030082519A1 SEMBRAL INFORMATION: APPLICANT: APPLICANT: Habenberger, Peter APPLICANT: Bevec, Dorian TITLE OF INVENTION: Callular Kinases Involved in Cytomegalovirus Infection and their TITLE OF INVENTION: Inhibition FILE REPERENCE: AXM-004.1 US
ACTACTGACTTCTTAGATACCACACACACACACACACACA	CURRENT APPLICATION NUMBER: US/09/981,397A CURRENT FILING DATE: 2002-06-28 CURRENT FILING DATE: 2000-10-16 PRIOR PAPPLICATION NUMBER: 60/240,750 PRIOR FILING DATE: 2000-10-16 NUMBER OF SEQ ID NOS: 22 SEQ ID NO 13 LENGTH: 2501 FYPE: DNA CORGANISM: Homo sapiens US-09-981,397A-13
ATTRCTTCAAAATAAAAGCATGTAAGTGACTGTTTTTCAAGAAGAAATGTGTTTCATAA 105	Query Match 48.7%; Score 812; DB 10; Length 2501; Best Local Similarity 99.9%; Pred. No. 0; Matches 862; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy 333 AGTTACAGAGTGTTTCAAGTGCCATTCACCTATGTGACAAGAAAATGGAATTATCTC 392 Db 1162 AGTTACAGAGTGTTTCAAGTGCCATTCACCTATGTGACAAGAAAAATGGAATTATCTC 1221 Qy 393 TGAAAAACTAACTGGTCCAACAGAAGGAAATCTCTCAGGGAATTATCTC 1221
20, 20, 12, 12, 12, 12, 12, 12, 12, 12, 12, 12	Db   1222   IGHACATACTGGTAAATGATGATCATGTGTGTGTGTGTGTGTG
1293 GTATGATGATTTCTGATGGAGCCATTTTTGACGTTCTTCATGGATTATTTGTT 1352	Oy 573 GTTGGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCACTC 632

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TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE OF THE REPERENCE: 07334-124001
CURRENT APPLICATION NUMBER: 08/09/720
FRIOR PRIOR PAPLICATION NUMBER: 09/3340,620
FRIOR PRIOR PLILING DATE: 1999-06-28
FRIOR APPLICATION NUMBER: 09/09/041
FRIOR PLILING DATE: 1998-12-08
FRIOR PRILING DATE: 1998-06-17
FRIOR PLILING DATE: 1998-06-17
FRIOR PLILING DATE: 1998-06-17
FRIOR PLILING DATE: 1998-06-17
FRIOR PLILING DATE: 1998-06-06
NUMBER OF SEQ ID NOS: 71
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1931
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                                                                                                                                                          GTTGGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCACTC
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Patent No. US20020061845A1
GENERAL INFORMATION:
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JS-09-728-721-1
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FEATURE:
NAME/KEY: CDS
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US-09-728-721-1
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Sequence 2, Application US/09748537

Patent No. US2002061833A1

GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILE AND USES THERE
FILE REFERENCE: 0734-316001

CURRENT FILING DATE: 1080-06-17

PRIOR APPLICATION NUMBER: US/09/748,537

CURRENT FILING DATE: 1999-06-17

PRIOR PLING DATE: 1999-06-17

PRIOR PLING DATE: 1999-02-06

NUMBER OF SEQ ID NOS: 14

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENTH: 1931
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Best Local Similarity 99.9%;
Matches 732; Conservative
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ORGANISM: Homo sapiens
US-09-748-537-2
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US-09-748-537-2
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1151 AGTTACAGAGTGTTTCAAGTGCCATTCACCTATGTGACAAGAAGAAAATGGAATTATCTC 1210
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                                                                                                                                                               APPLICATION NUMBER: US/09/019,942
FILING DATE: 06-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-6070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 13;
               MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/133,780
FILING DATE: 26-Apr-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 682; DB
Pred. No. 0;
0; Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1931 base pairs
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STRANDEDNESS: single
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99.9%;
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SEQUENCE CHARACTERISTICS:
 COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
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Best Local Similarity 99.9
Matches 732; Conservative
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TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
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ADDRESSEE: Fish & Richardson P.C.
Score 682; |
Pred. No. 0;
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CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
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40.9%;
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US-10-133-780-2
Query Match
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Sequence 1, Application US/10118984

Publication No. US2002019769341

GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: AND USES THEREOF

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: 07334/118001

CURRENT APPLICATION NUMBER: US/10/118,984

CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281

PRIOR PILING DATE: EARLIER FILING DATE: 1999-02-05

PRIOR PILING DATE: EARLIER FILING DATE: 1999-12-08

PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-05

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-06

NUMBER OF SEQ ID NOS: 44

LENGTHARE FASESE FOR WINDOWS VERSION 4.0

SEQ ID NO 1

LENGTH: 1931
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Best Local Similarity 99.99
Matches 732; Conservative
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; LOCATION: (214)...(1833)
US-10-118-984-1
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ORGANISM: Homo sapiens
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US-10-118-984-1
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                                      AACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAA 1810
                                                                                      ATTTACTTCAAAATAAAAGCATGTAAGTGACTGTTTTTCAAGAAAATGTGTTTTCATAA 1052
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TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROPEL PAMILY AND USES THEREOF
FILE REFERENCE: 07334-076001
CURRENT APPLICATION NUMBER: US/10/105,931
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: 09/099,041
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 09/019,942
PRIOR APPLICATION NUMBER: 09/019,942
PRIOR APPLICATION NUMBER: 09/019,942
PRIOR PRING DATE: 1998-06-17
SEQ ID NO SEQ ID NOS: 37
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llarity 99.9%;
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; LOCATION: (214)...(1833)
US-10-105-931-1
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ORGANISM: Homo sapiens
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RESULT 10
US-09-728-721-3
Squence 3 Application US/09728721
Factor No. US20020061845A1
GENERAL INFORMATION:
APPLICANT Bertin, John
TITLE OF INVERTION:
CURRENT APPLICATION NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREC
FILE REPERENCE: 07334-124001
CURRENT PILING DATE: 1990-06-28
FRIOR APPLICATION NUMBER: US 09/340,620
FRIOR APPLICATION NUMBER: US 09/207,359
FRIOR FILING DATE: 1998-06-28
FRIOR PELING DATE: 1998-06-17
FRIOR PELING DATE: 1998-06-06-17
FRIOR PELING DATE: 1998-06-06-17
FRIOR PELING DATE: 1998-06-07
FRIOR PELING DATE: 1998-06-06-07
FRIOR PELING DATE: 1998-07-06-07
FRIOR PELING DATE: 1998-07-07
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; Sequence 1, Application US/10295981
; Publication No. US20030120055A1
GENREAL INFORMATION:
APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; TILE REFRENCE: 0734-124001
; CURRENT APPLICATION NUMBER: US/09/340,620
; PRIOR APPLICATION NUMBER: US/09/340,620
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-06-18
; PRIOR FILING DATE: 1998-06-10
; PRIOR FILING DATE: 1998-06-10
; PRIOR FILING DATE: 1998-06-10
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 711
; SEQ ID NOS: 711
; SEQ ID NOS: 711
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Best Local Similarity 99.9%;
Matches 732; Conservative
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NAME/KEY: CDS
LOCATION: (214)...(1833)
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ORGANISM: Homo sapiens
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US-10-295-981-1
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                                                                      Length 1620;
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| Sequence 3, Application US/10105931
| Publication No. US20020150987A1
| GENERAL INFORMATION:
| APPLICANT: Bertin, John
| TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
| TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
| FILLE REPERENCE: 0734-07601
| CURRENT APPLICATION NUMBER: US/10/105,931
| CURRENT FILING DATE: 2002-03-25
| PRIOR APPLICATION NUMBER: 09/099,041
| PRIOR PILING DATE: 1998-06-17
| PRIOR FILING DATE: 1998-06-17
| PRIOR FILING DATE: 1998-02-06
                                                                                               1; Indels
                                                                 Score 632; DB 9; I
Pred. No. 1.1e-298;
0; Mismatches 1;
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            TYPE: DNA; ORGANISM: Homo sapiens
US-09-728-721-3
LENGTH: 1620
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US-10-105-931-3
                                                                   Query Match
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US-10-118-984-3

Squence 3, Application US/10118984

Sequence 3, Application US/20197633A1

GENERAL INFORMATION:

APPLICATION NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY

TITLE OF INVENTION: AND USES THEREOF

TITLE OF INVENTION: AND USES THEREOF

TITLE OF LERERANCE: 07334/118001

CURRENT APPLICATION NUMBER: US/10/118,984

CURRENT FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281
                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                         Length 1620;
                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                         Score 632; DB 13;
Pred. No. 1.1e-298;
0; Mismatches 1;
                      Version 4.0
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                                                                                                                                                                                         Query Match
Best Local Similarity 99.9%;
Matches 682; Conservative
SEQ ID NOS: 37
FastSEQ for Windows
                                                                                            TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                            US-10-105-931-3
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37.9%;
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Best Local Similarity 99.9
Matches 682; Conservative
                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-981-3
                                                                                                                                                                                                                                     LENGTH: 1620
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PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/207,359
PRIOR FILING DATE: BARLIER FILING DATE: 1998-12-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/099,041
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/019,942
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PASLSEQ for Windows Version 4.0
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                                                                                                                                                                                              Length 1620;
                                                                                                                                                                                                                       Indels
                                                                                                                                                                                              Score 632; DB 13;
Pred. No. 1.1e-298;
                                                                                                                                                                                                                       0; Mismatches
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Publication No. US20030120055A1
GENERAL INFORMATION:
                                                                                                                                                                                              37.9%;
                                                                                                                                                                                              Query Match 37.5
Best Local Similarity 99.5
Matches 682; Conservative
                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                 LENGTH: 1620
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US-10-295-981-3
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USES
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES;
FILE REPERENCE: 07334-124001
CURRENT APPLICATION NUMBER: US/10/295,981
CURRENT FILING DATE: 1999-06-28
FRIOR APPLICATION NUMBER: US 09/245,281
FRIOR APPLICATION NUMBER: US 09/245,281
FRIOR APPLICATION NUMBER: US 09/245,281
FRIOR APPLICATION NUMBER: US 09/209,041
FRIOR APPLICATION NUMBER: US 09/209,041
FRIOR APPLICATION NUMBER: US 09/099,041
FRIOR APPLICATION NUMBER: US 09/019,942
FRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 71
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Pred. No. 1.1e-298;
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1598 ATTTACTTCAAAATAAAAGCATG 1620

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Patent No. US20020110832A1

GRBERAL INFORMATION:
APPLICANT: Pyle, Ruth
APPLICANT: Yu, Jiangchun
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
CURRENT APPLICATION NUMBER: US/09/919,580
CURRENT FILING DATE: 2001-07-30
CURRENT FILING DATE: 2001-07-30

NUMBER OF SEQ ID NOS: 934

SEQ ID NO 544
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Pred. No. 5.5e-167;
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Best Local Similarity
Matches 363; Conserv
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100.0%; Pred. No. 5.9e-97;
tive 0; Mismatches 0;
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 243
CTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 100.
Matches 220; Conservative
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(c) 1993 - 2004 Compugen Ltd.
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US-09-245-341-3
US-09-245-37-10
US-09-246-33-10
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APPLICANT: Donna T. Ward
APPLICANT: Lex M. COWSERT
TITLE OF INVENTION: ANTISENSE MODULATION OF RIP2 EXPRESSION
FILE REFERENCE: RTS-0233
CURRENT APPLICATION NUMBER: US/09/920,663
CURRENT FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 3
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US-09-920-663-42
US-09-920-663-44
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US-09-920-663-46
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US-09-557-884-1
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Pred. No. 0;
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Patent No. 6426221
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Best Local Similarity 99.9
Matches 862; Conservative
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; LOCATION: (225)...(1847)
US-09-920-663-3
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
TITLE OF INVENTION: DOMAIN POLYPEPTIDES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
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MEDIUM TYPE: Diskette
COMPUTER: IDEN COMPATIBLE
COMPUTER: IDEN COMPATIBLE
COMPUTER: SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENY APPLICATION DATA:
FILLING DATE: 06-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REPERENCE/DOCKET NUMBER: 07334/068001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTAATTAATACAAGTAAAAAGTT 1195
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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ZIP: 0213
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Sequence 2, Application US/09069023A

GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Innez, Gabriel
APPLICANT: Nunez, Gabriel
APPLICANT: Noseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
CURRENT APPLICATION NUMBER: US/09/069,023A
CURRENT FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 2502
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48.7%; Score 812; DE
Best Local Similarity 99.9%; Pred. No. 0;
Matches 862; Conservative 0; Mismatches
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CRGANISM: Homo sapiens
US-09-069-023-2
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Matches 732; Conservative
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US-09-099-041A-1
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ORGANISM: Homo sapiens
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                                                                                                                                                                  LENGTH: 1931
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Pred. No. 1.2e-309;
0; Mismatches 1;
TELEPHONE: 617/542-5070
TELEFAX: 200154
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1931 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                Query Match
Best Local Similarity 99.9%;
Matches 732; Conservative
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                                                                                                           TOPOLOGY: linear MOLECULE TYPE: cDNA
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US-09-019-942-2
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Sequence 1, Application US/09099041A Patent No. 6340576

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TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL MOLECULES OF THEREOF
TITLE OF INVENTION: NOVEL MOLECULES OF THEREOF
TITLE OF INVENTION: 07334-07601
CURRENT FELLING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 09/019,942
PRIOR APPLICATION NUMBER: 09/019,942
PRIOR APPLICATION NUMBER: 09/019,942
PRIOR APPLICATION NUMBER: 09/019,942
PRIOR SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1; Indels 40.9%; Score 682; DB 4; I 99.9%; Pred. No. 1.2e-309; tive 0; Mismatches 1; 1053 AAGGATATTTATA 1065 à 8

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1691 CTACTGACATCCAAGGAGAAGAATTTGCCAAAGTTATAGTACAAAAATTGAAAGATAACA 1750
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Pred. No: 1.2e-309;
0; Mismatches 1;
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SOFTWARE: FRSESSO for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/470,271
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REGISTRATION NUMBER: 35,283
REFRENCE/DOCKET NUMBER: 07334/068001
TELECOMMUICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-8906
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APPLICATION NUMBER: 09/019,942
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09470271
Patent No. 6410689
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Best Local Similarity 99.9%;
Matches 732; Conservative
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                                                                                                                                                                                                                                                                                                                                                1931 base pairs
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APPLICANT: Bertin, John
TITLE OF INVENTION: GENES
TITLE OF INVENTION: DOMAI
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richa
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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ZIP: 02110-2804
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                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOLES
FILE REFERENCE: 07334/118001
CURRENT APPLICATION NUMBER: US/09/245,281
CURRENT PELICATION NUMBER: US 09/207,359
EARLIER PELICATION NUMBER: US 09/099,041
EARLIER PILING DATE: 1998-12-08
EARLIER FILING DATE: 1998-06-17
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Pred. No. 1.2e-309;
0; Mismatches 1; Indels
                                                                                                                                                                        ; Sequence 1, Application US/09245281
; Patent No. 6369196
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US-09-245-281-1
  ORGANISM: Homo sapiens
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                                                                                                                RESULT 5
US-09-245-281-1
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APPLICANT: BETLIN, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
CURRENT APPLICATION NUMBER: US/09/340,620A
CURRENT FILING DATE: 1999-06-28
FRIOR FILING DATE: 1999-02-05
FRIOR PALING DATE: 1999-02-05
FRIOR PAPLICATION NUMBER: US 09/207,359
FRIOR PAPLICATION NUMBER: US 09/099,041
FRIOR PELING DATE: 1998-06-17
FRIOR PELING DATE: 1998-06-17
NUMBER OF SEQ ID NOS: 71
                                             AAAATAGTGGTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACATGATTTTT 1330
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US-09-340-620A-1
'Sequence 1, Application US/09340620A,
'Patent No. 6482933
'GENERAL INFORMATION:
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Pred. No. 1.2e-309;
0; Mismatches 1; Indels (
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Patent No. 6469140
GENERAL INFORMATION:
TITLE OF INVERTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVERTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-11200 I
CURRENT APPLICATION NUMBER: US/09/207,359B
CURRENT FILING DATE: 1998-12-08
PRIOR PRIOR APPLICATION NUMBER: US 09/019,041
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 99.9
Matches 732; Conservative
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; NAME/KEY: CDS
; LOCATION: (214)...
US-09-207-359B-1
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US-09-207-359B-1
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                                                                                                                               Score 682; DB 4; Length 1931;
Pred. No. 1.2e-309;
0; Mismatches 1; Indels
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1 LENGTH: 1931
                                                                                                                                 Query Match
Best Local Similarity 99.9%;
Matches 732; Conservative
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                                                                     ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-09-340-620A-1
                                            TYPE: DNA ORGANISM: Homo sapiens
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US-09-865-364-1
; Sequence 1, Application US/09865364
; Patent No. 6613521
; GENERAL INFORMATION:
; APPLICANT: Bertin, John

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TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
FILE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REPERENCE: 07334-112001
CURRENT APPLICATION NUMBER: US/09/865,364
CURRENT FILING DATE: 1090-105-25
PRIOR PLILING DATE: 1998-12-08
PRIOR PLILING DATE: 1998-12-08
PRIOR PLILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR PLILING DATE: 1998-06-17
PRIOR PLILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 47
SCOID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
40.9%; Score 682; DB 4; I
Best Local Similarity 99.9%; Pred. No. 1.2e-309;
Matches 732; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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                    993 ATTTACTTCAAAATAAAAGCATGTAAGTGACTGTTTTTCAAGAAGAAATGTGTTTCATAA
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AACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAA
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APPLICANT: Bertin, John
TITLE OF INVENTION:
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: 0734-076001
CURRENT APPLICATION NUMBER: 08/09/099,041A
CURRENT APPLICATION NUMBER: 09/019,942
PRIOR PILING DATE: 1998-06-17
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
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99.9%; Pred. No. 3e-286;
live 0; Mismatches 1
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Matches 682; Conservative
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; ORGANISM: Homo sapiens
US-09-099-041A-3
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US-09-099-041A-3
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Pred. No. 1.2e-309;
                                                                                                                                                                                                        APPLICANT: Bertin, John
APPLICANT: Chao, Moses V.
TITLE OF INVENTION: NOVEL MOLECULES OF THE CAR.
FILE REFERENCE: 07334-316001
CURRENT APPLICATION NUMBER: US/09/748,537
CURRENT APPLICATION NUMBER: US 09/099,041
PRIOR FILING DATE: 1998-06-17
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FASTERQ for Windows Version 4.0
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                                                                                                                                                     Sequence 2, Application US/09748537
Patent No. 6680167
GENERAL INFORMATION:
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                                       Query Match
Best Local Similarity 99.9
Matches 732; Conservative
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, ORGANISM: Homo sapiens
US-09-748-537-2
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                                        ACTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAAGTCAGACAATTACTAGACA
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TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REPERENCE: 07334-112001
CURRENT APPLICATION NUMBER: US/09/207,359B
FRIOR APPLICATION NUMBER: US 09/099,041
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
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Best Local Similarity 99.9%; Pred. No. 3e-286;
Matches 682; Conservative 0; Mismatches 1
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1620
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GENERAL INFORMATION:
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Pred. No. 3e-286;
0; Mismatches 1; Indels
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APPLICANT: Bertin, John
TITLE OF INVENTION: ANOVEL MOLECULES OF THE C;
TITLE OF INVENTION: AND USES THEREOF
FILE REPERENCE: 07334/11801
CURRENT APPLICATION NUMBER: US/09/245,281
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: US 09/207,359
EARLIER APPLICATION NUMBER: US 09/09,041
EARLIER APPLICATION NUMBER: US 09/099,041
EARLIER PILING DATE: 1998-06-17
EARLIER PILING DATE: 1998-06-17
SARLIER FILING DATE: 1998-06-17
SARLIER PILING DATE: 1998-06-06
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1620
                                                                                                                                                                                                                       1598 ATTTACTTCAAATAAAAGCATG 1620
                                                                                                                                                                                     993 ATTTACTTCAAAATAAAGCATG 1015
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; Patent No. 6369196
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Best Local Similarity 99.9%;
Matches 682; Conservative
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; ORGANISM: Homo sapiens
US-09-245-281-3
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US-09-245-281-3
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37.9%; Score 632; DB 4;
Best Local Similarity 99.9%; Pred. No. 3e-286;
Matches 682; Conservative 0; Mismatches 1.
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CORGANISM: Homo sapiens
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US-09-865-364-3
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Patent No. 6482933
GENERAL INCORMATION:

JAPPLICARNI: Bettin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
FILE REFERENCE: 0734-12401

CURRENT APPLICATION NUMBER: US 09/245,281

PRIOR APPLICATION NUMBER: US 09/245,281

PRIOR APPLICATION NUMBER: US 09/207,359

PRIOR FILING DATE: 1998-12-08

PRIOR FILING DATE: 1998-12-08

PRIOR PRIOR APPLICATION NUMBER: US 09/099,041

PRIOR PRILING DATE: 1998-06-17

PRIOR PRILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

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PRIOR FILING DATE: 1998-06-17

SEQ ID NOS: 71

SOFTWARE: FastESQ for Windows Version 4.0
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CORGANISM: Homo sapiens
US-09-340-620A-3
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Best Local Similarity
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GenCore version 5.1.6  Copyright (c) 1993 - 2004 Compugen Ltd.  leic search, using sw model  April 1, 2004, 06:17:41; Search time 4639 Seconds  (without alignments) 10743 690 Million cell undates/sec	ctgatgtgtae	ecys, 1199109020 residue isfying chosen parameters: 000000000 first 45 summaries	EST:* em_estba:* em_esthum:* em_estin:* em_estov:* em_estpl:* em_btc:* em_	13: 9D_est1:* 14: 9D_est5:* 15: em_estfun:* 16: em_estfun:* 17: em_gss_lnu:* 19: em_gss_lnu:* 19: em_gss_lnu:* 20: em_gss_lnu:* 21: em_gss_lnu:* 22: em_gss_lnu:* 23: em_gss_lnu:* 24: em_gss_lnu:* 25: em_gss_lnu:* 26: em_gss_lnu:* 27: em_gss_lnu:* 28: 9D_gss_l:* 29: 9D_gss_l:* 20: 9D_gss_l:*
Co OM nucleic - nucleic Run on: Apri	Title: US Perfect score: 16 Sequence: 1 Scoring table: OI Searched: 27	e : mber of DB seq DB seq cessing	Database : 11 11 11 11 11 11 11 11 11 11 11 11 1	Pred. No. 16 Score Man. 165 S 3 3 577 4 4 665 S 3

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Location/Qualifiers
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                                                                                               /cell_type="HELA_CELLS COT 25-NORMALIZED"
/cell_line="HELA"
/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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Faraday Avenue Genoscope sequence ID : CSODK011AE09NP1
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                                                                                                                                                                                                                                      Score 835; D
Pred. No. 0;
                                           organism="Homo sapiens"
                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK011Y117"
         location/Qualifiers
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Best Local Similarity
Matches 985; Conserv
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/ Isbue__vpe="...nonincosarcoma Grade II"
// dev stage="Adult" |
// lab_host="Adult" |
// lab_host="Adult" |
// lab_host="Adult" |
// cone_lib="NoI_cGAP Chi"
// note="Organ: Icft Pelvis; Vector: pT7T3-Pac (Pharmacia)
with a modified polylinker; Site_I: EcoR I; Site_2: Not I;
NOI_cGAP Chi is a cDNA library containing the following
tissue(s): Chondrosarcoma Grade II. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
                                                                                                                           1493
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UI-H-EZO-bau-f-07-0-UI.S1 NCI CGAP_Ch1 Homo sapiens cDNA clone
UI-H-EZO-bau-f-07-0-UI 3', mRNA sequence.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        obtained
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ORTHOAD ALD ALGORITHM OF THE STATE OF TOWA CODA LIDEARY PREPARATION: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution
                                             213
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 709)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
272 ATTTATGAAGTATATACCCTTTACCCACCAGAGACAGTACAGAATCCCTGCCCTAAAAT
                                                                                                                                                                                                      212 CCCAGGCTTAATTGCCCTACAAAGGTTATTAATTTAAAACTCCATTATTAGGATTACAT
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The following repetitive elements were found in this cDNA
sequence: 1-64, AT rich#Low_complexity (matched compliment)
Seq primer: M13 FORWARD
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (dT)18 tail. The sequence tag for this library is TGATCACGCT.
TGATGASUBE-grade-2-chondrosarcoma-TAG LIB-UL-H-EZO
TAG_SEQ-ATCTAATATG"
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/db_xref="texaon:9606"
/clone="UJ-H-E20-bau-f-07-0-UJ"
/tissue_type="Chondrosarcoma Grade II"
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CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 432 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stops: 460.
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           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
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Contact: Robert Strausberg,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 738)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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602411943F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4540787 5', mRNA sequence.
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(Dases 1 to 883)

NIH-MGC http://mgc.nci.nih.gov/
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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   DB 12;
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39.8%; Score 665; DE 100.0%; Pred. No. 0; ive 0; Mismatches
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Best Local Similarity 100.0
Matches 665; Conservative
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
POLYA-Yes.
                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 734)
NCI-CAAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 AGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAGCCTGGTATAGC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 TGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACACTACTGACAT 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                        /tissue_type="embryonal carcinoma, cell line"
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/clone_lib="NIH_MGC_Blage
/clone_lib="NIH_MGC_Blage
/clone_lib="NIH_MGC_Blage
/clone_lib="NIH_MGC_Blage
/clone_lib="NIH_MGC_Blage
/clone_lib is a NIH_MGC_Library."
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10471 row: e column: 12
High quality sequence stop: 767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCATGAAAATAGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCATGAAAATAGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAATAAAAGCATGTAAGTGACTGTTTTTTCAAGAAGAAATGTGTTTTCATAA 650
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                                                                                                                                                                                                                                                                                                                                                                                         Length 883;
                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        38.9%; Score 650; DB 12;
100.0%; Pred. No. 8e-308;
iive 0; Mismatches 0;
                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                         /mol_type="mRNA"
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/clone="IMAGE:4540787"
                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 650; Conservative
                                                                                                                                               1. .883
                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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1081 bp mRNA linear EST 20-FEB-2002
_6561869 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5547645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /_issue_type="melanotic melanoma"
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/clone_lib="NH MGC 72"
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Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life
Technologies."
                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates; Catarrhini, Hominidae, Homo.

1 (bases 1 to 1081)

NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12255 row: e column: 22
High quality sequence stop: 662.
Location/Qualifiers
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/organism="Homo sapiens"
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/clone="IMAGE:5547645"
                                                                                                        BM557041.1 GI:18798748
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Homo sapiens
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BM557041
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BM973770 656 bp mRNA linear EST 20-FEB-2003 UI-CF-EC1-ach-1-07-0-UI-SI UI-CF-EC1 Homo sapiens cDNA clone UI-CF-EC1-ach-1-07-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    211 ACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAAA 152
                                                                                                                                                                                                                                                                                                                                                                                                         TGGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAAATGACAGA 753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                391 AGCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                   271 TACTGACATCCAAGGAGAAGTTTGCCAAAGTTATAGTACAAAATTGAAAGGATAACAA
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                                                                                                                                                                             631 ATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCCTGGAAATCACAG
                                                                                                                                                                                                                          TTGGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCACTCC
                                                                                                                                                                                                                                                    634 ATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAGCC
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                                                                                       0
                                        Length 667;
                                                                                     Indels
                                          Score 613; DB 13; I Pred. No. 1.3e-289;
                          36.7%; Scor.
100.0%; Pred. No. 1...
... 0; Mismatches
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McCray Lab
University of Iowa
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                                                             Local Similarity 100.
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//dev stage="Additt"
//dev stage="Additt"
//lab_host="DH10B (Life Technologies)"
//clone lib="MCI CGAP_Ch2"
//note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
//note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
//note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
//note="Organ: Left Pelvis; Site 1: EcoR I; Site 2: Not I;
//note="Organ: Left Pelvis; Site 1: EcoR I; Site 2: Not I;
//note="Organ: Left Pelvis; Site 1: EcoR I; Site 2: Not I;
//note="Organ: Left Pelvis; Site 1: EcoR I;
//note="Organ: Left Pelvis; Site 1: The library
//note constructed according to Bonaldo, Lemon and Soares,
//denome Research, 6:791-806, 1996. First strand cDNA
//note synthesis was primed with an oligo-dT primer containing a
//not I site. Double stranded cDNA was ligated to an EcoR I
//note synthesis of first-strand cDNA contains a library tag
//note synthesis of first-strand cDNA contains a library tag
//note synthesis of first-strand cDNA contains a library tag
//note synthesis of first-strand cDNA contains a library tag
//darcaccorr
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Seq primer: M13 FORWARD

POLYAPAYS.
                                                                                                                                                                                                    ATATATTAATACGGCTTCCTGTCCCATTTTTAACCTCAGCCTTCCCTACTGTCACCAA 1630
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept.
                       TACAAAGGGTTATTAATTTTAAAACTCCATTATTAGGATTACATTTTAAAGGTTTTATTAT
                                                                481 GAATTCCCTTTAAAATGATATTTCAAAGGTAAAACAATACAATATAAAGAAAAAATAA
                                                                                                                                                                                                                                                 541 ATATATTAATACCGGCTTCCTGTCCCCATTTTTAACCTCAGCCTTCCCTACTGTCACAA
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/tissue_type="Chondrosarcoma Grade II"
                                                                                                                                                                                                                                                                                              1666
                                                                                                                                                                                                                                                                                                                      601 CAACCAAGCTAAATAAAGTCAACAGCCTGATGTGT 636
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TAG_LIB=UI-H-EZ1
TAG_SEQ=ATCTAATATG"
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/organism="Homo sapiens"
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Inpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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/db_xref="taxon:9606"
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BQ773811.1 GI:21982287
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92

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267 TIGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACACTACTGACA 208
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/db_xref="taxon:9606"
/clone="UI-CF-FN0-aem-o-20-0-UI"
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/organism="Homo sapiens"
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//lab_host="Mailt and Fetal"
//lab_host="DH10B (Life Technologies) (T1 phage resistant)"
//lab_host="DH10B (Life Technologies) (T1 phage resistant)"
//clone lib="Ull-GF-EG1"
//note="Organ: Lung: Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
Ul-CF-EG1 is a normalized cDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986, 1986
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Tel: 319 356 4866
Fax: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resegen.com) or from Open Biosystems
(www.openbiosystems.com).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGGACTATGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCACCATTTCTGGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCACTCCATGCTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (dT)18 tail. The sequence tag for this library is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 36.5%; Score 609; DB 12; L
Best Local Similarity 100.0%; Pred. No. 1.2e-287;
Matches 609; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="U1-CF-EC1-ach-1-07-0-U1"
/tissue_type="Lung"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAG_LIB=UI-CF-EC1
TAG_SEQ=AAGTGCTTAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                               Seg primer: M13 FORWARD POLYA=Yes.
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Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com)
The following repetitive elements were found in this CDNA
sequence: 1-24, >AT_richHLow_complexity (matched compliment)
Seq primer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CB851847 115 bp mRNA linear EST 22-APR-2003 UI-CF-FNO-aem-o-20-0-UI.51 UI-CF-FNO Homo sapiens cDNA clone UI-CF-FNO-aem-o-20-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue type="Minan Lung Epithelial cells"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone lib="UT-CF-FNO"
/note="Organ: Lung; vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; U1-CF-FNO is a subtracted cDNA library derived from two normalized Human lung epithelial cell libraries (EN1 and DU1) The library was subtracted according to according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact:
                                                                                                                                                                                                                                                                                                                                             1002 AAAATAAAAGCATGTAAGTGACTGTTTTTCAAGAAGAATGTGTTTCATAAAAGGATATT 1061
                                                                                                                                                                      942 GICTICAGCCITACCCGGAAATACTIGIGGTITCTAGAICACCAICTITAAATTTACTIC 1001
                                                                                                                                                                                                                                      147 GTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCCATCTTTAAATTTACTTC 88
                                                                                                                                                                                                                                                                                                                                                                                                                                   28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (basea) 1 to 715)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                 207 TCCAAGGAGAAGAATTTGCCAAAGTTATAGTACAAAAATTGAAAAGATAAACAAAATGG
                                                                                                                                                                                                                                                                                                                                                                                           TCCAAGGAGAAGAATTTGCCAAAGTTATAGTACAAAAATTGAAAGATAACAAATGG
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/ Organism="Homo sapiens"
// mol_type="mRNA"
// mol_type="mRNA"
// db xere="acxon:9606"
// tissue_type="Huma Chondrosarcoma Cell Line"
// tissue_type="Huma Chondrosarcoma Cell Line"
// dev stage="Adult"
// lab_bost="DH10B (Life Technologies)"
// clone_lib="NVI CGAP FH0"
// note="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR 1; Site 2: Not 1;
// note="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR 1; Site 2: Not 1;
// CGAP FH0 is a CDNA library containing the following tissue(s): Human Grade 1 Chondrosarcoma Cell Line The library was constructed according to Bonaldo, Lennon and Soares, Genome Reactoh, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded CDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tas AGAATCCGGC. The cell line was provided by Dr James Martin from University of Iowa
**Total Trans **Contains Contains Contains Contains Contains Contains Contains Contains Series and the (dT)18 tail. The sequence tag for this library is AGAATCCGGC. The cell line was provided by Dr James Martin from University of Iowa
**Total Trans **Contains Contains Contain
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAG TISSUE=Human Chondrosarcoma Cell Line CS8 - Grade 1
Chondrosarcoma
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                                                                                                        from Dr. M. Bento Soares, bento-soaresoulows.edu
The following repetitive elements were found in this cDNA
Sequence: 1-22, >AT_rich#Low_complexity (matched compliment)
Seq primer: M13 FORWARD
POLYA=Yes.
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Pred. No. 9.4e-283;
0; Mismatches 1;
                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAG_LIB=UI-H-FH0
TAG_SEQ=AGAATCCGGC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 35.9%;
Best Local Similarity 99.8%;
Matches 649; Conservative
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UI-H-FHO-bcd-1-20-0-UI.S1 NCI CGAP FHO Homo sapiens cDNA clone
UI-H-FHO-bcd-1-20-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1002 AAAATAAAAGCATGTAAGTGACTGTTTTTCAAGAAGAAATGTGTTTCATAAAAGGATATT 1061
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
bento-soares@uiowa.edu
                         TAG SEQ=None found"
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REFERENCE AUTHORS TITLE

JOURNAL COMMENT

ACCESSION VERSION KEYWORDS

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746 305 806 245

485 626 425 686 866

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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llni.gov/bbrp/image.html
Insert Length: 673 Std Error: 0.00

Seq primer: -400P from Gibcro.

High quality sequence stop: 459.
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(Dases 1 to 592)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                         424 CCACTCCATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCCAGAACGTC
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//db xref="mRNA"
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//db xref="mRNA"
//db xref="lu-H-FT2-bjj-h-03-0-UI"
//tissue type="Aveolar Macrophage"
//dev stage="Aveolar Macrophage"
//done lib="NOI CGAP FT2"
//doce="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: BcoR I; Site 2: Not I;
//doce="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: BcoR I; Site 2: Not I;
//doce="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 2: Not I;
//doce="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 2: Not I;
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//doce="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 2: Not I;
//doce="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 2: Not I;
//doce="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 2: Not I;
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UI-H-FTZ-bjj-h-03-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CONA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
Seg primer: M13 FORWARD
POLYA=Yes.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                  185 GTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAAATTTACTTC
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TAG_SEQ=GGCCATGCCG"
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Pred. No. 9.3e-283;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index
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CD365404/c
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SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 624)
                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index University (1997)
                     sapiens (human)
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Matches 591; Conservative
                                      Homo sapiens
                     Homo
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                                                                                                          AUTHORS
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                                                                                                                                                  /clone_libe="NCI_CGAP_Pr28"
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
caction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          953 TACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAAATTTACTTCAAAATAAAAGC 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                    473 ACTITCAAGGICCCIGCCAGCICCTCAAGACAAIGAITITITIAICIAGAAAAGCICCAAGAC 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 AAGCCTACAAGGACCTCAAAAGTCAGACATTACTAGACACTACTGACATCCAAGGAGAA 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           592 ACTICAAGGICCCIGCCAGCICCTCAAGACAATGATTTTTTAICTAGAAAAGCTCAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 CTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGGACTATGAACTTGTTAGTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      532 IGITATITIATGAAGCIGCATCACIGICCIGGAAATCACAGTIGGGATAGCACCATITCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCACTCCATGCTCTTCAGCAATAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             653 AATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAGCCTGGTATAGCCCCAGCAGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                               35.5%; Score 592; DB 9; Length 592; 100.0%; Pred. No. 2.7e-279; ive 0; Mismatches 0; Indels
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Location/Qualifiers
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                                                                                                       sex="male
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 592; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     533
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CD368863/c
LOCUS
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/tissue type="Avendra" /
/tissue type="Avendra" /
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/lab_host="Datalla" /
/lab_host="Datalla" /
/clone lib="NCI CGAP FTI" /
/clone lib="NCI lib="Ilb="NCI lib="NCI l
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
    Tissue Procurement: Dr. Gary W. Hunninghake, U of I
    CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
    CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
    DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
    Clone Distribution: Distribution information can be found at
    http://genome.uiowa.edu/distribution/cgap.html
    Seq primer: M13 FORWARD
    POUVA-Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  783 TTCTGTCCAGGGACTTGATCATGAAAGAGGACTATGAACTTGTTAGTACCAAGCCTACAA
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|db_xref="taxon:9606"
|clone="UI-FT1-bjx-o-04-0-UI"
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CD368863 624 bp mRNA linear EST 29-MAY-2003 UI-H-FT1-bjx-o-04-0-UI.81 NCI CGAP\_FT1 Homo sapiens cDNA clone UI-H-FT1-bjx-o-04-0-UI 3', mRNA sequence.
CD368863 1 GI:31152953

DEFINITION ACCESSION VERSION

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Gaps

969 529 756 469 816 409

349

876

289 966 229

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ACTICAAAATAAAAGCAIGTAAGIGACTGTITITCAAGAAGAAAIGIGTTICATAAAAGG 1056
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AGENCOURT B191703 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6257019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTTCAAAATAAAAGCATGTAAGTGACTGTTTTTCAAGAAGAAATGTGTTTCATAAAAGG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 ATATTTATATCTCTGTTGCTTTGACTTTTTTATATAAAATCCGTGAGTATTAAAGCTTT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 ATTGAAGGTTCTTTGGGTAAATATTAGTCTCCCTCCATGACACTGCAGTATTTTTTAA 49
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (base 1 to 938)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
first-strand cDNA contains a library tag sequence that i located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGATCATTGC. TAG_TISSUE=Lung TAG_TISSUE=Lung TAG_ESEQ=AGATCATTGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACACTAC
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                                                                                                                                                                                                      34.2%; Score 571; DB 12; L
100.0%; Pred. No. 5.5e-269;
iive 0; Mismatches 0;
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Best Local Similarity 100.
Matches 571; Conservative
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BQ670832
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/clone="Indaxon..goog"
/tissue_type="Metastatic Chondrosarcoma"
/dev stage="Adult"
/lab host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP_DH1"
/clone_lib="NCI CGAP_DH1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_l: EcoR I; Site_2: Not I;
NCI CGAP_DH1 is a normalized cDNA library containing the following tissue(s): VS-8 Cell line from Metastatic Chondrosarcoma in Lung. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-df primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-pac vector. The oligonucleotide used to prime the synthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BQ000991 628 bp mRNA linear EST 26-MAR-2002
UI-H-DH1-awt-c-10-0-UI.s1 NCI_CGAP_DH1 Homo sapiens cDNA clone
IMAGE:5823297 3', mRNA sequence.
                                                                                                                                                          1022
                                                                                                                                                                                                                                                      CIGITITICAAGAAGAAAIGIGITICATAAAAGGATATITATATCICIGITGCITIGACT 1082
                                                                                                                                                                                                                                                                                                                                                    TTTTTTATATAAAATCCGTGAGTATTAAAGCTTTATTGAAGGTTCTTTGGGTAAATATTA 1142
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.B. Consortium/LLML at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
sequence: 1-60, >AT rich#Low_complexity (matched compliment)
BOUNA=Yes.
                                                                                                             265
                                                              962
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                                                                                                                                                                                                                                                                                                     145
              GGACCTCAAAAGTCAGACAATTACTAGACACTACTGACATCCAAGGAGAAGAATTTGCCA 325
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NCI-CAAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                      324 AAGTTATAGTACAAAAATTGAAAGATAACAAACAAATGGGTCTTCAGCCTTACCCGGAAA
                                                                                                                                                       TACTTGTGGTTTCTAGATCACCATCTTTAAATTTACTTCAAAATAAAAGCATGTAAGTGA
                                                                                                                                                                                                                                                                                           204 CTGTTTTTCAAGAAATGTGTTTCATAAAGGATATTTATATATCTCTGTTGCTTTGACT
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                                                                                                                                                                                                    264 TACTTGTGGTTTCTAGATCACCATCTTTAAATTTACTTCAAAATAAAAGCATGTAAGTGA
                                                           AAGTTATAGTACAAAAATTGAAAGATAACAAACAAATGGGTCTTCAGCCTTACCCGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCTCCCTCCATGACACTGCAGTATTTTTTTAATTAATACAAGTAAAAG 1193
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/mol_type="mRNA"
/db_xref="taxon:9606"
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BQ000991.1 GI:19725891
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Unpublished (1997)
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SOURCE
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/tissue_type="epidermoid carcinoma, cell line"
/lab host="DH10B (phage-resistant)"
/clone_lib="NNHH_MGC_102"
/note="Organ: salivary gland, Vector: pOTB7, Site_1: XhoI;
Site_2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/XhoI sites using the
following 5' adaptor: GGGACGAG(0). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMA10 row: k column: 04
High quality sequence stop: 659.

Location/Qualifiers
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33.3%; Score 556; DB 13; Length 938;
Best Local Similarity 100.0%; Pred. No. 1.2e-261;
Matches 556; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                          /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:6257019"
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APPLICANT: Inohara, Naohiro
APPLICANT: Naohiro
APPLICANT: Roselt, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
CURRENT APPLICATION NUMBER: US/09/069,023A
CURRENT FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PALENTIN Ver. 2.0
SEQ ID NO 5
ELENGTH: 284
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US-09-207-159B-6
US-09-09-041A-6
US-09-09-041A-6
US-09-340-620A-6
US-09-245-281-5
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-G-/cgn2 1/USPT0-5pool p/US09771161/runat 29032004_124858_14368/app_query.fasta_1.1863
-De-/cgn2 1/USPT0-5pool p/US09771161/runat 29032004_124858_14368/app_query.fasta_1.1863
-DB=16881ed Patente AA -OFMT=fastan -SUFFIX=01120n2p.rai -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-ALIGN=15 -MODE=LCOAL -OUTPWT=pto -NORM=ear -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09771161 @CGN 1 1 27 @runat 29032004 124858_14368
-LOCPU=S -NOW MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLÖCK=100
-LONGLGG -DEV TIMEOUT=12 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=60
-LONGLGG -DEV TIMEOUT=17 -YGAPOP=60 -YGAPEXT=60 -DELOPE -DELEXT=7
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                      GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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APPLICANT: Inohara, Nachiro
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ORGANISM: Homo sapiens
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Best Local Similarity:
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                                                                                         Sequence 4, Application US/09069023A

Sequence 4, Application US/09069023A

Beneral No. 6348573

GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Inchara, Nachiro
APPLICANT: Nomez, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS
CURRENT APPLICATION NUMBER: US/09/069,023A
CURRENT FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 478
                                                                   GCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGGAC 814
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US-09-069-023-4
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; Sequence 27, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Inchara, Nachiro
; APPLICANT: Inchara, Nachiro
; APPLICANT: Inchara, Nachiro
; APPLICANT: Inchara, Nachiro
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REPERRINCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NOS: 38
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; TYPE: PRT
; ORGANISM: Homo s.
US-09-069-023-27
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US-09-069-023-27
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TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr
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ORGANISM: Homo sapiens
US-09-069-023-1
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US-09-069-023-1
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US-09-069-023-6

i Sequence 6, Application US/09069023A

j Patent No. 6348573

j GENERAL INFORMATION:
    APPLICANT: Nunez, Gabriel
    APPLICANT: Nunez, Machina, Nachina, TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
    TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
    TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
    TITLE REFERENCE: UM-03333
    CURRENT FILING DATE: 1998-04-27
    CURRENT FILING DATE: 1998-04-27
    NUMBER OF SEQ ID NOS: 38
    SOFTWARE: PATENTIN Ver. 2.0

seQ ID NO 6
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      -09-771-161A-2 (1-1669) x US-09-345-473E-28 (1-540)
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US-09-069-023-6
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Pred. No.:
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                                                 AACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGGTCCATGAA 454
                                                              TGGGATAGCACCATTICTGGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCACTCCA 634
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Patent No. 6558903
GENERAL INFORMATION:
FAPLICANT: Hodge, Martin
TITLE OF INVENTION: No. 6558903e1 Kinases and Uses Thereof
FILE REFERENCE: 35800/183781
CURRENT APPLICATION NUMBER: US/09/345,473E
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSEQ for Windows Version 4.0
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Matches:
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Mismatches:
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LENGTH: 540
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019/942
FILING DATE: 06-FEB-1998
PRIOR APPLICATION DATA:
PRICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Meikleichn ne
           Conservative:
Mismatches:
                                                                         US-09-771-161A-2 (1-1669) x US-09-069-023-6 (1-167)
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Patent No. 6033855
GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: GENES ENCODING CASPASE
TITLE OF INVENTION: DOMAIN POLYPEPTIDES
OCRRESPONDENCES: 4
CORRESPONDENCE Fish & Richardson P.C.
STREET: 225 Franklin Street
  Matches:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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Best Local Similarity:
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COUNTRY: U
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TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 0734-076001
CURRENT APPLICATION NUMBER: US/09/099,041A
CURRENT FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASELSEQ for Windows Version 4.0
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128
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Matches:
Conservative:
Mismatches:
Indels:
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35,283
ER: 07334/068001
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                REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-8906
                                                                        TELEFAX: 617/542-8906
TELEX: 200154
INPORMATION.FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENTH: 540 amino acids
TYPE: amino acid
TOPOLOGY: linear
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100.00%
100.00%
24.11%
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    REGISTRATION NUMBER:
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US-09-099-041A-2
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Best Local Similarity:
Query Match:
DB:
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LENGTH: 540
TYPE: PRT
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US-09-099-041A-2
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TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
TITLE OF INVENTION: DOMAIN POLYPEPTIDES
NUMBER OF SEQUENCES: 4
CORRESPONDENES: ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: MA
COUNTRY: Boston
STATE: MA
COMPUTE: MA
COMPUTER READABLE FORM:
MEDLIM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Fast-SEQ for Windows Version 2.0b
SOFTWARE: Tam CAPICATION DATA:
APPLICATION NUMBER: US/09/470,271
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/019,942
FILING DATE:
RELING DATE:
APPLICATION NUMBER: 09/019,942
FILING DATE:
RELING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Amita L.
REGISCHRATON NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/068001
TELEFRONE: 617/542-5070
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Patent No. 6410689
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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amino acid
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Pred. No.:
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Patent No. 6369196

GENERAL INFORMATION:

APPLICANT: BETTIN O'S DAIL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: 07334/118001

CURRENT APPLICATION NUMBER: US/09/245,281

CURRENT FILING DATE: 1999-02-05

EARLIER FILING DATE: 1998-12-08

EARLIER PELLORATION NUMBER: US 09/207,359

EARLIER PELLORATION NUMBER: US 09/099,041

EARLIER FILING DATE: 1998-06-17

EARLIER FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 44

NUMBER OF SEQ ID NOS: 44
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US-09-245-281-2
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TITLE OF INVENTION. NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREC.
TITLE OF INVENTION. NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREC.
TITLE OF INVENTION. NOWER. US/09/340,620A
CURRENT APPLICATION NUMBER: US 09/245,281
PRIOR APPLICATION NUMBER: US 09/245,281
PRIOR PILING DATE: 1999-02-05
PRIOR FILING DATE: 1999-02-05
PRIOR FILING DATE: 1998-12-08
PRIOR FILING DATE: 1998-02-06
PRIOR PLING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR PILING DATE: 1998-02-06
PRIOR PLING DATE: 1998-02-06
SPRIOR PLING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 71
SEQ ID NO 2
ILBNGTH: 540
TYPE: PRI
CORGANISM: Homo sapiens
US-09-340-620A-2
                                                            473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
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US-09-340-620A-2
Sequence 2, Application US/09340620A
Patent No. 6482933
GENERAL INFORMATION:
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Patent No. 6469140

GENERAL INFORMATION:
APPLICANT: Bertin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 0734-112001
CURRENT APPLICATION NUMBER: US/09/207,359B
CURRENT FILING DATE: 1998-12-08
PRIOR PILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR FILING DATE: 1998-06-17
SPRIOR FILING DATE: 1998-06-17
SPRIOR FILING DATE: 1998-06-17
SPRIOR FILING DATE: 1998-06-17
SOFFWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 540
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US-09-207-359B-2
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RESULT 15

US-09-748-537-1

Sequence 1, Application US/09748537

Patent No. 6680167

GENERAL INFORMATION:

APPLICANT: Bertin, John

APPLICANT: Chao, Moses V.

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILE AND USES THEREC CURRENT APPLICATION NUMBER: US/09/748,537

CURRENT APPLICATION NUMBER: US 09/099,041

PRIOR PRILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: US 09/099,041

PRIOR APPLICATION NUMBER: US 09/019,942

NUMBER OF EXO ID NOS: 14

SOFTWARE: FastSEQ for Windows Version 4.0

TYPE: PRI
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US-09-748-537-1
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                                                                    ThrThrAsp11eGlnGlyGluGluPheAlaLysVall1eValGlnLysLeuLysAspAsn 512
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US-09-865-364-2

Sequence 2, Application US/09865364

Patent No. 6613510

GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

FILE REFERENCE: 07334-112001

CURRENT APPLICATION NUMBER: US/09/865,364

CURRENT FILING DATE: 1998-1-2-5

PRIOR APPLICATION NUMBER: US 09/099,041

PRIOR FILING DATE: 1998-1-08

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-0-2-06

NUMBER OF SEQ ID NOS: 47

SEQ ID NO 2

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US-09-865-364-2
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This sequence is a fragment of the human RICK (RIP-like interacting CLARP kinase) protein of the invention. RICK acts as a positive regulator of kinase) protein of the invention. RICK acts as a positive regulator of during CD95 signalling. The invention provides methods for identifying apoptosis signalling pathway inhibitors and activators, and methods and compositions for screening compounds which will modulate the interactions of the various compositions identified: RICK, and the CIDE family of activators (CIDE-A, CIDE-B and DREP-I). RICK, and the CIDE family of activators (CIDE-A, CIDE-B and DREP-I). RICK is useful in screening assays for agents, useful in the diagnosis, prognosis or treatment of disease associated with excess cell growth and dysregulation of apoptosis. Complexes containing RICK and CLARP can be used in drug screening assays to identify inhibitor molecules blocking CD95-mediated apoptosis. Overexpression of ARC in an in vitro cell system can be used to therapy treatment of disease with increased cell death in muscle tissue therapy treatment of disease with increased cell death in muscle tissue and cardiac disorders. Therapputic compositions of CIDEs can be used to treat e-g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia, ischaemic injury, and toxin-induced liver disease. AntiRICK antibodies can be used as reagents for the preparation or affinity chromatography
                                                                                                                                                                                                                                                                                                                                                                RICK; human, RIP-like interacting CLARP kinase; apoptosis regulator; ARC; caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway; CIDE-A; DREP-1, diagnosis, cell growth; apoptosis dysregulation; gene therapy; cardiac disorder; neurodegenerative disorder; AIDS; aplastic anaemia; ischaemic injury; toxin-induced liver disease.
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Adb81362
Abus6272
Aao22110
Aao22109
Abus6271
Abj04754
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Aao22107
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                                      ABG31075
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AA022109
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Copyright (c) 1993 - 2004 Compugen Ltd.
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caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway; CIDE-A; CIDE-B, PDEP-1; diagnosis; cell growth; apoptosis dysregulation; gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS; aplastic anaemia; ischaemic injury; toxin-induced liver disease.

human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;

Human RICK protein sequence residues 54-531.

(first entry)

21-MAR-2000

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measuring RICK levels. A specific inhibitor
              of an essential step in the blochemistry of apoptosis is needed. RICK interaction with intracellular factors such as CLARP and FADD appears to be essential for apoptosis, inhibitors of RICK binding to intracellular apoptosis factors are potential drug candidates. Note: This sequence was created using information given in the specification
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ALT This sequence is a fragment of the human RICK (RIP-like interacting CLARP kinase) protein of the invention. RICK acts as a positive regulator of apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10 during CD95 signalling apoptosis induced by caspase-8 and caspase-10 apoptosis signalling. The invention provides methods for identifying apoptosis signalling pathway inhibitors and activators, and methods and compositions for screening compounds which will modulate the interactions of the various compositions identified: ARC, RICK, and the CIDE family of activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening assays for agents, useful in the diagnosis, prognosis or treatment of disease associated with excess cell growth and dysregulation of apoptosis. Complexes containing RICK and CLARP can be used in drug screening assays to identify inhibitor molecules blocking CD95-mediated apoptosis. Overspression of ARC in an in vitro cell system can be used to therapy treatment of disease with increased cell dath in muscle tissue can cardiac disorders. Therapeutic compositions of CIDEs can be used to treat e.g. cancer, AIDS, neurodegenrative disorders, aplastic anaemia, ischaemic injury, and toxin-induced liver disease. AntiRICK antibodies can be used as reagents for the preparation or affinity chromatography media, and for diagnostically measuring RICK levels. A specific inhibitor of an essential step in the biochemistry of apoptosis is needed. RICK interaction with intracellular factors such as CLARP and PADD appears to the essential for apoptosis, inhibitors of RICK binding to intracellular apoptosis factors are potential drug candidates. Note: This sequence was compared using information given in the specification 

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GGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAAATGACAGAA 754

GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu

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TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr

TATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAAGTCAGACAATTACTAGACACT

AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp

GCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGGAC

Compositions for identifying apoptosis signaling pathway inhibitors

useful for treating diseases

Claim 6; Page; 93pp; English

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Koseki

Inohara N,

Nunez G,

WPI; 2000-072163/06

99WO-US009183

27-APR-1999; 27-APR-1998;

WO9955134-A2.

04-NOV-1999.

98US-00069023

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**ACTGACATCCAAGGAGAAGTTTTGCCAAAGTTATAGTACAAAAATTGAAAGATAACAAA** 

GINMETGLYLEUGINPROTYTPROGIUILELEUVALVALSERARGSERPROSERLEUASR

TTACTTCAAAATAAAAGCATG 1015

258 995 278

AAY59405 standard; protein; 478

AAY59405

RESULT 2
AAY59405
ID AAY5
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AC AAY5
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CAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAAAT

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                       Conservative:
Mismatches:
Indels:
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Matches:
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(1-478)US-09-771-161A-2 (1-1669) x AAY59405

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TTACAGAGTGTTTCAAGTGCCATTCACCTATGTGACAAGAAGAAAATGGAATTATCTCTG 394
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Koseki T;

Inohara N,

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This sequence is the invention. The RICK protein acts as a positive regulator of the invention. The RICK protein acts as a positive regulator of apoptosis potentiating apoptosis induced by caspase-8 and caspase-10 aurig CDS signalling. The invention provides methods for indentifying apoptosis signalling pathway inhibitors and activators, and methods and compositions for screening compounds which will modulate the interactions of the various compositions identified: RRC, RICK, and the CIDE family of activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening assays for agents, useful in the diagnosis, prognosis or treatment of disease associated with excess cell growth and dysregulation of capptosis. Complexes containing RICK and CLARP can be used in drug screening assays to identify inhibitor molecules blocking CD95-mediated of apoptosis. Overexpression of ARC in an in vitro cell system can be used to identify inhibitors of the enzymatic activity of caspase-8.

Condentification of ARC-like inhibitory compounds may be useful for gene thrapy treatment of disease with increased cell death in muscole tissue and cardiac disorders. Therapeutic compositions of CIDEs can be used to treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia, confined as reagents for the preparation or affinity chromatography media, and for diagnostically measuring RICK levels. A specific inhibitor center and essential for apoptosis, inhibitors of RICK binding to intracellular correct are potential drug candidates
                                                                   Compositions for identifying apoptosis signaling pathway inhibitors useful for treating diseases.
                                                                                                                                          sequence is the human RICK (RIP-like interacting CLARP kinase)
                                                                                                              Claim 1; Fig 7a; 93pp; English
                          WPI; 2000-072163/06.
N-PSDB; AAZ48762.
 Nunez G,
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                                                                                                                                                                                                                        New Bl protein regulates cell death and cell survival pathways - derivatives, DNA and antibodies, also regulate intracellular inflammation ; for treating AIDS, cancer.
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ANY68769-95 and AAY68797-99 represent human phosphorylation effectors (PHSP), designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not given in the specification). The sequences were isolated from cDNA libraries prepared from various human tissues. The PHSP proteins are useful for the diagnosis, treatment and prevention of proliferative disorders, immune disorders and neuronal disorders. The PHSP proteins form pharmaceutical compositions which useful for treating or preventing disorders associated with decreased PHSP expression/activity. PHSP antagonists are useful for treating or preventing disorders associated with increased PHSP expression/activity.
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RIP; Nck-Interacting kinase; MKK3; SRPK-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation.
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T, Koga
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                                                                                                                                                                                                            Human; full length cDNA; cDNA synthesis; oligo-capping
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Nagai K, Kojima S, Otsuki
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Wakamatsu A, Sugiyama T, Nagai
LeuLeuGlnAsnLysSerMet
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               The present invention relates to a new method for identifying compounds for treating and/or preventing cytomegalovirus (CMV) infection and/or related diseases. The method of the invention comprises contacting a test compound with at least one of the cellular kinases RICK, RIP, Nck-Interacting kinase, MKK3 and SRPK-2 and detecting any change in kinase activity. The method of the invention can be used to treat and/or prevent CMV infections and related diseases. Oligonucleotides that can detect the specified kinases can also be used for diagnosis of infection. The present amino acid sequence represents the human cellular kinase RICK protein of the invention, as described above
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g diseases
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                                                                                                                                     Human; receptor interacting protein; RIP2; antisense; gene therapy
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encoding human receptor interacting protein (RIP)2,
associated with RIP2 expression.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                      interacting protein
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227.00
100.00%
100.00%
42.75%
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AAE27882 standard; protein;
                                                                     (first entry)
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Best Local Similarity:
Query Match:
DB:
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                                                                                                        receptor
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                                                                                                                                                                                                                                                                                                                                                      (ISIS-) ISIS
                                                                                                                                                                          Homo sapiens
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Pred. No.:
                                                                     27-DEC-2002
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                                                                       GCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGGAC
                                                                                       ACTGACATCCAAGGAGAAGAATTTGCCAAAGTTATAGTACAAAAATTGAAAGATAACAAA
                                                                                             TATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACACT
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cancer associated protein sequence SEQ ID NO:1015. 544 AA AAB43570 standard; protein; 08-FEB-2001 (first entry) AAB43570; 

Human; cancer associated gene; cancer antigen; detection, cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiathritic; antiarthritic; antiviral; antidiamatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antissoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoletic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.

Homo sapiens

WO200055350-A1

08-MAR-2000; 2000WO-US005882 21-SEP-2000.

SCI INC (HUMA-) HUMAN GENOME

99US-0124270P

12-MAR-1999;

CA, Ruben SM; Rosen

2000-587533/55. N-PSDB; AAC77779

acids comprising sequences encoding peptides diagnosing e.g. cancer. Novel isolated nucleic useful for treating or

11; Page 1595-1597; 2352pp; English. Claim

AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the

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include: cytostatic; proliferative; vulnerary; immunomodulator; antiabetic; antiathwatic; antiphyoid; antiphematic; antiarthritic; antiabetic; antiathwatic; antiphyoid; antiphyoid; antiphyoid; antiphyoid; ardiant; thrombolytic; coagulant; corrective; ardiant; thrombolytic; coagulant; corrective; antiphyoid; antiphoriatic and antiangiogenic. The motropic; vasotropic; antiphoriatic and antiangiogenic. The polymucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. CC Polymucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of correction, modulate haemostatic or thrombolytic activity, modulate (disorders, allergic reactions; graft versus host disease and organ colection, modulate haemostatic or thrombolytic activity, modulate (disorders) and infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to the present sequences used in the exemplification of the control of the contr
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                                                                                                                                                                                                                                                                      anti-HIV; antiallergic; antiinflammatory; antianaemic; antiparkinsonian; mootropic; anticonvulsant; antiarteriosclerotic; antiasthmatic; immunosuppressive; antiathyroid; cytostatic; hepatotropic; dermatological; antidabetic; nephrotropic; antigout; thyromimetic; neuroprotective; osteopathic; antiarthritic; antiparasitic; antihelminthic; antipacterive; opteopathic; antibacterive; antibacterive; intropathic; opthalmological, antihelmentic; hemostatic; antibacterial; virucide; protozoacide; fungicide; kinase; phosphatase; KPP; cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis; cancer; developmental; mental retardation; neurological; Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's; diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan; helminthic infection; transgenic; gene therapy; human; enzyme.
                  537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human kinases and phosphatases and polynucleotides, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
Tang YT;
Yao MG, Yue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Duggan BM;
AE, Griffin JA;
Lee EA, Lee SY;
Pen DB, Arvizu CS;
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                                                TTACTTCAAAATAAAAGCATG 1015
                                                                                                                                              ADC99079 standard; protein; 510 AA
                                                                 Human KPP protein - SEQ ID 32
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02-NOV-2001; 2001US-0343910P.
13-NOV-2001; 2001US-033998P.
16-NOV-2001; 2001US-0334248P.
30-NOV-2001; 2001US-0334288P.
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                                                                                                                                                                                                           01-JAN-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                               544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTATAGTACAAAAATTGAAAGATAACAAACAAATGGGTCTTCAGCCTTACCCGGAAATA 964
polynucleotides encoding KPP may be useful for creating transgenic animals to model human disease, as well as during gene therapy procedures. The current sequence is that of the human KPP protein of the
                                                                                                                                                                                                                                                                                                                                                                                          AAGCTGCATCACTGTCCTGGAAATCACAGTTGGGATAGCACCATTTCTGGATCTCAAAGG
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Mismatches:
Indels:
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                                                                                                                     Length:
Matches:
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197.00
100.00%
100.00%
37.10%
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Best Local Similarity:
Query Match:
DB:
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                                                                          Sequence 510
                                                                                                    Alignment Scores:
Pred. No.:
Score:
                                              invention.
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874

814

120 934 140

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CARD-3; caspase recruitment domain, CARD-4; regulation, detection; caspase activation; detection; screening; therapy; diagnosis; disease; apoptotic cell death; Fas/APO-1 receptor complex; TNF receptor complex; cancer; follicular lymphoma; carcinoma; p53 mutation; viral infection; hormone-dependent tumour; autoimmune disorder; Alzheimer's disease; systemic lupus erythematosis; immune-mediated glomerulonephritis; stroke; Parkinson's disease; amyorcophic lateral sclerosis; retinitis pigmentosa; spinal muscular dystrophy; cerebellar degeneration; anaemia; drug; myelodysplastic syndrome; myocardial infarction; cell proliferation; cell differentiation; cell survival; CARD-41; CARD-42; CARD-42;
                                                                                                                                                                                                                                                                                                                                                    141 GlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsn 160
                                                                                                                                                                                                                                                                                                                           CAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTAAAT 994
61 GlylleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 80
                                                                                         81 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp
                                                                                                                                                                              101 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr
                                                                                                                                                                                                                                                               GCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGGAC
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432. .540
/note= "predicted CARD domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY31140 standard; protein; 540 AA
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98US-00099041.
98US-00207359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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17-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence is a tragment or the number NLCK (NTP-INFE INCEPTION CLARKY Kinase) protein of the invention. RICK acts as a positive regulator of apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10 during CD95 signalling. The invention provides methods for identifying apoptosis signalling pathway inhibitors and activators, and methods and compositions for screening compounds which will modulate the interactions of the various compositions identified: ARC, RICK, and the CIDE family of activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening caspas for agents, useful in the diagnosis, prognosis or treatment of disease associated with excess cell growth and dysrequlation of apoptosis. Complexes containing RICK and CLARP can be used in drug screening assays to identify inhibitor molecules blocking CD95-mediated apoptosis. Ownerexpression of ARC in an in vitro cell system can be used to therapy treatment of disease with increased cell death in muscle tissue and candiac disorders. Therapeutic ocmpositions of CIDEs can be used to treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anemia, ischaemic injury, and toxin-induced liver disease. AntiRICK antibodies can be used as reagents for the preparation or affinity chromatography media, and for diagnostically measuring RICK levels. A specific inhibitor of an essential step in the biochemistry of apoptosis is needed. RICK interaction with intreacellular factors such as CLARP and FADD appears to be essential for apoptosis, inhibitors of RICK levels. This sequence was a reagent of propersion in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence is a fragment of the human RICK (RIP-like interacting CLARP
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                                                                                                                                                                                                                                                                                                                                                  Compositions for identifying apoptosis signaling pathway inhibitors
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Matches:
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                                                                                                                                                                                                                                                               Koseki T;
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167.00
100.00%
100.00%
31.45%
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Page; 93pp; English.
                                                                                                                               27-APR-1999; · 99WO-US009183
                                                                                                                                                                            98US-00069023
                                                                                                                                                                                                                                                                                                                                                                          useful for treating diseases
                                                                                                                                                                                                                  (UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                                                               Nunez G, Inohara N,
                                                                                                                                                                                                                                                                                                       WPI; 2000-072163/06
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Best Local Similarity:
    Homo sapiens
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                                                                                                                                                                            27-APR-1998;
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Pred. No.:
                                                                                       04-NOV-1999.
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AAB20079

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This invention describes the isolation of novel numan cappase recruitment domain, CARD-3 and CARD-4 polynuclectides and proteins and a partial murine CARD-1 protein and genes. The genes and proteins of the invention care involved in the regulation of caspase activation. The caspase recruitment domain (CARD) polynuclectides, polypeptides, homologues and recruitment domain (CARD) polynuclectic methods of treatment. The medicine and therapeutic and prophylactic methods of treatment. The medicine and therapeutic and prophylactic methods of treatment. The caspase certivity of the prophylactic methods may be used to diagnose and treat patients which are suffering from a disorder associated with abnormal level or rate of apoptotic cell death, abnormal activity of the Fas/APO-1 receptor complex, abnormal activity of the TMF receptor complex, or abnormal activity of a caspase. Complex associated with mutations in p53 and hormone-ceptor complex, associated with mutations in p53 and hormone-ceptor complex, immune-mediated glomerulonephritis), viral infections, capthemer's disease, parkinson's disease, amyorcophic lateral sclerosis, retinitis pigmentosa, spinal muscular dystrophy, cerebellar degeneration, anaemia, myelodysplastic syndrome, myocardial infarction, and stroke. CARD-3 protein interacts with other cellular proteins, and so can be used for requiration of cellular proliferation and differentiation and cell curvival. The CARD proteins may also be used to for screen drugs or compounds which modulate their activity. The CARD-4 gene can express a long transcript that encodes CARD-4S or two CARD-4 spince variants, a short transcript that encodes CARD-4S or two CARD-4 spince variants, as short transcript that encodes CARD-4S or two CARD-4 spince variants, as short transcript that encodes CARD-4S or two CARD-4 spince variants, as short transcript that encodes CARD-4S and second publications and cellular proteins as about the method of the
                                                                                                                                                                              invention describes the isolation of novel human caspase recruitment
regulation of cellular proliferation and differentiation and cell
                                                                                                           Example 2; Fig 2; 181pp; English
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Sequence 540 AA;

7	מכתמכנונכ	3				
Alignment Scores: Pred. No.: Score: Percent Similarity Best Local Similar Query Match: DB:	nt Sco D.: Simil. Sal Si	Alignment Scores: Pred. No.: Score: Percent Similarity: Query Match:	1.47e-129 128.00 100.00\$ 100.00\$ 24.11\$	Length: Matches: Conservative: Mismatches: Indels:	540 1128 0 0 0	
US-09-771-161A-2	71-161	A-2 (1-1669)	x AAY31140	(1-540)		
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ò	692	_	GCCCAGCAGTGGATC	CAGAGCAAAAGGGAAC		21
qq	433					22
ò	752	_	CTTAACCAGTCGCTA	GATGCCCTTCTGTCC	GAAGCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATGAAAGAG 811	11
qu	453	_				72
ò	812	GACTATGAA	CTTGTTAGTA	CCAAGCCTACAAGGACCTCAA	CAAAAGTCAGACAATTACTAGAC 871	7.7
qa	473	AspTyrGluLeuVal	LeuValSerThrLys			2
ò	872		ACTACTGACATCCAAGGAGAATTTGCCAAAGTTATA		STACAAAATTGAAAGATAAC 931	31
DÞ	493					12
È	932		GGTCTTCAGCCTTAC	CCGGAAATACTTGTGC	AAACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGGTTTCTAGATCACCATCTTTA 991	91
qq	513		GlybeuGlnProTyr	ProGlulleLeuValv		32
ò	992	AATTTACT	CAAAATAAAAGCATG	1015		
Ор	533			540		

RESULT 13

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The present sequence is that of human caspase recruitment domain 3 (CARD-3), an intracellular protein predicted to be involved in regulating caspase activation. The sequence is predicted from an isolated CDNA clone (see AAF30001). Methods of diagnoshing and treating patients suffering from a disorder associated with an abnormal level or rate of apoptotic cell death, abnormal activity of the Fas/APO-1 receptor complex, abnormal activity of the twoorn necrosis factor receptor complex or abnormal activity of a caspase involve administering a compound that modulates the expression or activity of CARD-3, CARD-4, CARD-5 or CARD-6 e.g. using gene therapy methods. Such disorders include cancer, viral infection, autoimmune disorders, neurological diseases, haematological disorders, inflammatory disorders and immune disorders. CARD-3, CARD-4, CARD-3, CARD-4, CARD-5 or CARD-6 and 6 proteins can be used to regulate cell prodiferation, cell survival and cell growth. They can also be used to screen drugs or compounds that coll growth. They can also be used to screen drugs or compounds that modulate their activity or expression and to treat disorders associated with insufficient or excessive production of CARD-3, -4, -5 or -6 protein, or production of an aberrant protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isolated intracellular proteins predicted to be involved in regulating cappase activation are used for diagnosis and treatment of e.g. cancer, viral infections, autoimmune diseases, neurological diseases and hematological disorders.
                                                                                                                                      CARD-3; caspase recruitment domain; human; cancer; infection; autoimmune disease, neurological disease; haematological disease; immune disease; inflammation; antitumour; antiseptic; immunomodulator; antiinflammatory; apoptosis; diagnosis; gene therapy.
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Matches:
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/note= "kinase domain"
                                                                                                                                                                                                                                                                                                                 401. .431
/note= "linker domain"
432. .540
                                                                                                                                                                                                                                                              Location/Qualifiers
AAB20079 standard; protein; 540 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MILL-) MILLENNIUM PHARM INC.
                                                                   (first entry)
                                                                                                     Human CARD-3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-061973/07.
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 540 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     WO200100826-A2
                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JUN-1999;
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                                                                     23-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                         04-JAN-2001.
                                  AAB20079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bertin J;
                                                                                                                                                                                                                                                                                Domain
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Example 2; Fig 2; 139pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; caspase recruitment domain; CARD-3; CARD-4; LRR; leucine rich repeat; LPS; lipopolysaccharide; NF-kB; nuclear factor-kappa B; cancer; viral infection; autoimmune disorder; aystemic lupus evythematosus; immune-mediated glomerulonephritis; arthritis; immune disorder; multiple sclerosis; Hashimoto's thyroiditis; atopic condition; asthma; allergy; psoriasis; contact dermatitis; gastrointestinal allergy; insulin-dependent diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARD-
                                                                                                                                                  CCTGGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAAATGACA
                                                                                                                                                                                                                                   GAAGCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying modulators of long form of caspase recruitment domain, (4L useful for treating cancer, infections, and immune disorders, by contacting test compound with CARD-4L and determining effect of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bacterial infection, tuberculosis, lepromatous leprosy, cell signalling disorder, tissue disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bertin J, Philpott D, Sansonetti P, Girardin S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human caspase recruitment domain protein CARD-3.
                          US-09-771-161A-2 (1-1669) x AAB20079 (1-540)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG31075 standard; protein; 540 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-DEC-2000; 2000US-0258724P.
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N-PSDB; ABK89280.
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purypeptide with a by councating the peak compound and determining the effect of the test compound on the activity of the determining the effect of the test compound which binds to the LRR polypeptide to identify a compound which binds to the LRR (leucine rich repeat) domain of CARD-4. Also included is a method of calcine rich repeat) domain of CARD-4. Also included is a method of dentifying a candidate compound for modulating LPS (lipopolysaccharide).

CC identifying a candidate compound for modulating LPS (lipopolysaccharide) and cell expressing a polypeptide comprising the LRR domain of CARD-4 and contraction, where altered NF-kB activation polypeptide in the presence of the test compound compared to the binding in the absence of the test compound indicates that the test compound is a candidate compound for modulating LPS-mediated activation of NF-kB. Modulators identified by (MI) are useful for treating a disorder characterised by aberrant CARD-4 creating LPS-mediated activation of NF-kB. Modulators identified by confliction, an uncleic acid. Compounds that modulate the activity of CARD-4 care useful to treat or diagnose disorders such as cancer, viral care useful to treat or diagnose disorders such as cancer, viral care useful to treat or diagnose disorders such as cancer, viral care useful activations, Hashimoto's thyroiditis, atopic conditions such as multiple sclerosis, Hashimoto's thyroiditis, atopic conditions such as largies, insulin-dependent diabetes, bacterial infections, including tuberculosis, and lepromatous leprosy, disorders of cell signalling and disorders of cell signalling and classifier and represents human CARD-3 archerial inceptions.
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The invention relates to identifying (M1) a compound which modulates a human or murine caspase recruitment domain (CARD)-4L (long form) polypeptide with a by contacting the polypeptide with a test compound and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAAGTCAGACAATTACTAGAC
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Best Local Similarity:
Query Match:
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cerebroprotective, antiparkinsonian; antisclerotic; ophthalmological; nootropic; antianaemic; Caspase Recruitment Domain; CARD; CARD-4L; p53; cancer; CARD-4S; follicular lymphoma; carcinoma; autoimmune disorder; hormone-dependent tumour; breast cancer; prostate cancer; ovarian cancer; systemic lupus; herpes virus; poxvirus; adenovirus; neurological disease; anaemia; neutropenia; myelodysplastic syndrome; human.
                                                        Cytostatic; virucide; immunomodulatory; neuroprotective; antialzheimers;
                                     Protein of human CARD-3 SEQ ID No 2.
                                                                                                                                                                                                                98US-00019942.
98US-00099041.
98US-00207359.
                                                                                                                                                                                              99US-00245281.
                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                       N-PSDB; AAL40752, AAL40753.
                  27-SEP-2002 (first entry)
                                                                                                                                                                                                                                                                                             WPI; 2002-391988/42
                                                                                                                                      Homo sapiens.
                                                                                                                                                        US6369196-B1
                                                                                                                                                                                             05-FEB-1999;
                                                                                                                                                                                                                  06-FEB-1998;
                                                                                                                                                                                                                          17-JUN-1998;
08-DEC-1998;
                                                                                                                                                                           09-APR-2002.
AA022107;
                                                                                                                                                                                                                                                                            Bertin J;
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Isolated Caspase Recruitment Domain (CARD) polypeptides (CARD-4L and CARD-4S) useful for diagnosing and treating e.g. Parkinson's and Alzheimer's disease, cancers and viral infections.

Example 2; Fig 2; 116pp; English.

The invention relates to novel isolated Caspase Recruitment Domain (CARD) polypeptides, CARD-41 and CARD-45. The CARD proteins of the invention may be used to treat disorders associated with decreased CARD expression by supplementing the patient's own production of CARD. Disorders associated with the expression and activity of CARD include Cancers (particularly follicular lymphomas, carcinomas associated with mutations in p53, and covarian cancer), autoimmune disorders (such as systemic lupus erythematosus, immune-mediated glomerulonephritis), viral infections erythematosus, immune-mediated glomerulonephritis), viral infections or such as there is an adenoviruses, neurological diseases (such as Alzeimer's disease, Parkinson's disease, amylotrophic lateral sclerosis (ALS) retinitis pigmentosa, spinal muscular atrophy, and various forms of cerebellar degeneration), annemia associated with chronic disease, aplastic anaemia, chronic neutropenia, and the myelodysplastic syndromes. This sequence represents a human CARD protein relating to the invention

Sequence 540 AA;

	540	28				
	Length: 5		nservative: 0	Mismatches: 0	Indels: 0	Gaps: 0
	1.47e-129 Le	-		100.00% Mi	24.118 In	. Ga
Alignment Scores:				Best Local Similarity: 1	•	DB:

US-09-771-161A-2 (1-1669) x AAO22107 (1-540)

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632 CCATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAG 691		413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
CCATGCTCTT		ProCysSerS
632		413
ò	i	g

692 CCTGGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAAATGACA 751

qq	433		452
ολ	752	GAAGCCTGCCTTAACCAGTGCCTAGATGCCCTTCTGTCCAGGGACTTGATGAAAGAG	811
Д	453		472
δλ	812	GACTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGAC	871
원	473	AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp	492
, č	872	ACTACTGACATCCAAGGAGAAGAATTTGCCAAAGTTATAGTACAAAAATTGAAAGATAAC	931
qa	493	ThrThrAspIleGlnGlyGluGluPheAlaLysVallleValGlnLysLeuLysAspAsn	512
ζō	932	AAACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTA	991
qa	513		532
λ	992	AATTTACTTCAAAATAAAAGCATG 1015	
QC	533	AsnLeuLeuGlnAsnLysSerMet 540	
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version 5.1.6 - 2004 Compugen Ltd.

GenCore Copyright (c) 1993

nucleic search, using frame\_plus\_p2n model

OM protein -

Run on:

US-09-771-161A-93

Perfect score:

Seguence:

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AAZ46138-Z46168 encode human phosphorylation effectors (PHSP), designated PHSP1-PHSP3. (the protein sequence for PHSP2 is not given in the specification). The sequences were isolated from cDNA libraries prepared from various human tissues. The PHSP proteins are useful for the diagnosis, treatment and prevention of proliferative disorders, immune disorders and neuronal disorders. The PHSP proteins form pharmaceutical compositions which useful for treating or preventing disorders associated with decreased PHSP expression/activity. PHSP antagonists are useful for treating or preventing disorders associated with increased PHSP
Abx75870 Human CaB
Aaz09246 Human CAR
Aaf20001 Human CAR
Abk89280 Human CDN
Aa140752 CDNA of h
Abx75869 Human CDN
Adb61363 Human cab
Ach33353 Human end
Aa140753 DNA of hu
Acd86414 Human col
Aa4893010 Human col
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H, Azimzai Y;
                                                                                                                                                                                                                                                                                                                                                                            cDNA sequence encoding a human phosphorylation effector PHSP-6.
                                                                                                                                                                                                                                                                                                                                                                                                        Human; phosphorylation effector; PHSP; proliferative disorder; immune disorder; neuronal disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YT, Corley NC, Guegler KJ,
Au-Young J, Gorgone GA, Yue
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/*tag= a
/product= "phósphorylation effector"
                                                                                                                                                                                                                ALIGNMENTS
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   ABX75870
AAZ09246
AAF30001
ABK89280
AAL40752
ABX75869
                                                                                                                ACH33353
AAL40753
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                                                                                                                                                                                                                                                                              AAZ46143 standard; cDNA; 2024 BP.
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98US-0155239P.
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Patterson C, Bandman O, Av
Reddy R, Lu DAM, Shih LL;
                                                                                                                                                                                                                                                                                                                                            (first entry)
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12-JAN-1999;
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-MODEL=frame+ p2n.model -DEV=x1h
-Q05EL=frame+ p2n.model -DEV=x1h
-Q05/Cgn2_1/USPTO_spool/US09771161/runat_29032004_124850_19848/app_query.fasta_1.391
-Q05/Cgn2_1/USPTO_spool/US09771161/runat_29032004_124850_19848/app_query.fasta_1.391
-DB=N Geneseq_29Jan04 -QFMT=fastap -SUFFTX=01120p2n.rng -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -STRAT=1 -END=-1 -MATRIX=01150
-TRANS=human40.cdi -LIST=45 -DOCALIGN=x00 - HR SCORE=quality - THR_MIN=20
-MAXLEN=2000000000 -USER=US09771161_@CGN 1 1_470_@runat_29032004_124850_19848
-NCFUS=5 -NO MAAP -LARGEQUERY -NGE_SCORES=0 -WAIT_-DSPBLOCK=100
-LONGLOG -DEV_TIMEOTT=120 -WANT_TIMEOTT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELEXT=7
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Aax0558 Human B1
Abx51169 CDNA enco
Aad4172 Human rec
Aaz4862 Human RIC
Aaz7779 Human Can
Adc99131 Human KPP
                                                                                                              April 1, 2004, 10:15:17; Search time 471 Seconds (without alignments) 2092.531 Million cell updates/sec
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1 MYSLQLQSVSSAIHLCDKKK.....PBILVVSRSPBLNLLQNKSM 232
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SUMMARIES

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Query Match Length DB

Score

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geneseqn1980s:\*
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geneseqn2000s:\*
geneseqn2001as:\*

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Database :

geneseqn2001bs:\* geneseqn2002s:\* geneseqn2003as:\*

geneseqn2003bs:\*geneseqn2003cs:\* geneseqn2004s:\* AAZ46143 AAX02554 AAX02558 ABK51169 AAD45172 AAZ48762 AAC77779

2033 2098 2501 2501 2502 2709 1959

97.8 97.8 97.8 97.8

72222 72222 7222 7222 7222 7221

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Potal number of hits satisfying chosen parameters:

20

Word size:

Searched:

Post-processing: Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

3373863 segs, 2124099041 residues

0 60.0 , Xgapext 60.0 0 60.0 , Ygapext 60.0 0 6.0 , Fgapext 7.0 6.0 , Delext 7.0

Xgapop 6 Ygapop 6 Fgapop Delop

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Scoring table:

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218 AACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCATGAA 1277
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Query Match:
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 Homo sapiens
                        EP1130094-A2.
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           U; 0 Other;
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Matches:
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           612 A; 445
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612 A; 447 C; 438 G; 536 T; 0 U; 0 Other;

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Length:
Matches:
Conservative:
Mismatches:
Indels:

1.13e-218 227.00 100.00\$ 100.00\$ 97.84\$

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1458 TGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAGCCT 1517

106 CysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125

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Human; full length cDNA; cDNA synthesis; oligo-capping;

Human full-length cDNA, SEQ ID NO: 3453

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synthesizing full length cDNA clones and their use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated be and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the thin the printed specification, but was obtained in CD-ROM format directly from BPO.
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T, Koga
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Otsuki 1
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Nagai K, Kojima
                                                        08-JUL-1999; 99JP-00194486.
11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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07-JUL-2000; 2000EP-00114089
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Wakamatsu A, Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                              830 Primers useful for s in genetic manipulation.
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P-PSDB; AAM93621.
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1259 AACATACCTGTAAATCATGGTCCACAAGAAATCATGTGGTGGATCCTCTCAGCTCCATGAA 1318
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RIP, Nck-Interacting kinase, MKK3; SRPK-2; gene; 88.
                                                                                                                                                                  TrpAspSerThr1leSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrPro
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               Length:
Matches:
Conservative:
Mismatches:
                                                                                   Indels:
                                                                                                                                    US-09-771-161A-93 (1-232) x AAX02558 (1-2098)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes the isolation of a novel human B1 protein which can interact with, intracellular mediators or modulators of inflammation, cell death and/or cell survival pathways, directly or indirectly. Cells can be modulated or mediated in inflammation, cell death or cell survival pathways or another intracellular signalling activity using B1. Conditions such as AIDS and cancer can be treated using B1. Antibodies, oligonucleotides and ribozymes can also be used to regulate the above
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New B1 protein regulates cell death and cell survival pathways -derivatives, DNA and antibodies, also regulate intracellular inflammation; for treating AIDS, cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 otein; intracellular mediator; modulator; inflammation; cell death; survival pathway; intracellular signalling; AIDS; cancer; human; ss
GCCTGCCTTAAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGGGC
                                                                                                                                                                                                                                                                                        CAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAAAT
                                                                                                                                    TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr
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                                                                                                                                                                                                     ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys
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                                                                 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp
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97IL-00121199.
97IL-00121746.
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P-PSDB; AAW92795.
                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
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30-JUN-1997;
11-SEP-1997;
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Seguence 2098 BP; 649 A; 452 C; 449 G; 539 T; 0 U; 9 Other;

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1524 GGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAAACAAATGACAAA 1583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antisense oligonucleotide that targets regions of a nucleic acid encoding human receptor interacting protein (RIP)2, for treating diseases associated with RIP2 expression.
    126 GlyileAlaGlnGlnTrpileGlnSerLysArgGluAspileValAsnGlnMetThrGlu 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor interacting protein; RIP2; antisense; gene therapy; gene;
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                                                                                                            1584 GCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGGAC
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                                                                                                                                                                                                                                               ThraspileGinGlyGluGluPhealaLysValileValGlnLysLeuLysAspAsnLys
                                                                                  146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp
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/product= "Human RIP2 protein"
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225. .1847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-673017/72.
P-PSDB; AAE27882.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1224 AACATACCTGTAAATCATGGTCCACAAGAGAATCATGTGGATCCTCTCAGCTCCATGAA 1283
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                                                                                                                                                                                                                                                                                                                                                                                                          Identifying agents for treatment or prevention of cytomegalovirus infection, comprises contacting test compound with cellular kinase detecting change in cellular kinase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2501 BP; 768 A; 535 C; 499 G; 699 T; 0 U; 0 Other;
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/*tag= a
/product= "Human cellular kinase RICK"
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Indels:
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Location/Qualifiers
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC; caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway; CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation; gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;
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                                                                                                                    LeuGlnSerValSerSerAlaıleHisLeuCysAspLysLysLysMetGluLeuSerLeu
                                                                                                                                                              26 AsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHisGlu
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          Alignment Scores:
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This sequence encodes the numan kick (kir-like interacting Liker kinase), protein of the invention. The RICK protein acts as a positive regulator of apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10 adving CDS signalling. The invention provides methods for identifying apoptosis signalling pathway inhibitors and activators, and methods and compositions for screening compounds which will modulate the interactions of the various compositions identified; RKC, RKCK, and the CIDE family of activators (CIDE-A, CIDE-B and DRED-I). RICK is useful in screening assays for agents, useful in the diagnosis, prognosis or treatment of disease associated with excess cell growth and dysregulation of cappotosis. Complexes containing RICK and CLARP can be used in drug screening assays to identify inhibitor molecules blocking CD95-mediated apoptosis. Overexpression of ARC in an in vitro cell system can be used to identify inhibitors of the enzymatic activity of caspase-8.

Closing assays to identify inhibitory compounds may be useful for gene thrapy treatment of disease with increased cell death in muscle tissue and cardiac disorders. Therapeutic compositions of CIDEs can be used to treat e.g. cancer, AIDS, meurodegenerative disorders, aplastic anaemia, is chaemic injury, and toxin-induced liver disease. AntiRICK antibodies can be used as reagents for the preparation or affinity chromatography media, and for diagnostically measuring RICK levels. A specific inhibitor can be used as reagents for the preparation or affinity chromatography can be used as reagents for the preparation or affinity chromatography can be used as reagents for the preparation or affinity chromatography can be used as reagents for the preparation or affinity chromatography can be used as reagents for the preparation or affinity chromatography continuated liver disease. All can be used as reagents of an essential for apoptosis, and for diagnosic and can be used as reagents of an essential for apoptosis and can be used as recopration with int
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Compositions for identifying apoptosis signaling pathway inhibitors useful for treating diseases.
aplastic anaemia; ischaemic injury; toxin-induced liver disease;
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                                             TCTAGAAAAGCTCAAGAATGTTATTTATGAAGCTGCATCACTGTCCTGGAAATCACAGT
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99US-0124270P 2000WO-US005882

12-MAR-1999;

08-MAR-2000;

(HUMA-) HUMAN GENOME SCI INC

Ruben SM;

Rosen CA,

WPI; 2000-587533/55

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AAC77607 to AAC78448 encode the human cancer associated proteins given in ABB4338 to AAB4439. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidabetic; antiasthmatic; antitalerary; immunomodulator; antidabetic; antipsordective; cardiant; thrombolytic; coagulant; dermatological; neuroprotective; cardiant; thrombolytic; coagulant; coortropic; vasotropic; antipsoriatic and antidangogenic. The polymucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Colymucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune dissorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune rejection, modulate haemostatic or thrombolytic activity, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral inflections. The peptides, mucleotides, and antagonists may be also be used in the exemplification of the content of t
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                                          Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2709 BP; 810 A; 580 C; 540 G; 769 T; 0 U; 10 Other;
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                                                                                                                        Claim 1; Page 751-752; 2352pp; English.
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                                                                                                      GlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsn 225
                                                                                                                                                                                                                                                                                                                                                anti-HIV; antiallergic; antiinflammatory; antianaemic; antiparkinsonian; nootropic; anticonvulsant; antiarteriosclerotic; antiasthmatic; mamunosuppressive; anticonvulsant; antiarteriosclerotic; antiasthmatic; anticonvulsant; anticonvolus; dermatological; antidout; thyromimetic; neuroprotective; osteopathic; antiarthritic; antipout; thyromimetic; neuroprotective; osteopathic; antiarthritic; antiparasitic; antibacterial; virucide; protozoacide; fungicide; Annase; phosphatase; KPP; cell proliferative disorder; antherosclerosis; chrhosis; hepatitis; cancer; developmental; mental retardation; neurological; hepatitis; Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's; diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan; helminthic infection; transgenic; gene therapy; human; ss; gene.
                                                     205
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Yao MG, Yue H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human kinases and phosphatases and polynucleotides, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis, cancer or hepatitis.
            1686 TATGAACTTGTTAGTACCAGCCTACAAGGCCTCAAAAGTCAGACAATTACTAGACACT
                                                  ThrAspileGinGlyGlugluPheAlaLysValileValGinLysLeulysAspAsnLys
TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bandman O, Baughn MR, Becha SD, Borowsky ML, Duggan BM; Emerling BM, Forsythe IJ, Gandhi AR, Gorvad AE, Griffin JA; Guruzajan R, Hafalia AJA, Khan FA, Lal PG, Lee EA, Lee SY; Lindquist EA, Lu DAM, Lu Y, Marquis JP, Nguyen DB, Arvizu CS; Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Tang YT; Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Yao MG, Y
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13-NOV-2001; 2001US-0333098P.
16-NOV-2001; 2001US-0332424P.
30-NOV-2001; 2001US-0334288P.
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P-PSDB; ADC99079.
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The invention relates to a novel isolated polypeptide which is a human kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides, pagonists and antagonists are useful for diagnosing, treating or preventing cell proliferative disorders such as atherosclerosis, cirrhosis, hepatitis and cancer, developmental disorders e.g. mental Parkinson's disease, autoimmune and inflammatory disorders such as crohn's disease and diabetes mellitus and finally, viral, bacterial, fungal, parasitic, protozoan or helminchic infections. Furthermore, the polynucleotides encoding KPP may be useful for creating transgenic animals to model human disease, as well as during gene therapy procedures. The current sequence is that of the human KPP cDNA of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1220 CTGCCAGCTCCTCAAGACAATGATTTTTTTTTTTTTGTAGAAAGCTCAAGACTGTTATTTTATG
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CARD-41; CARD-45; CARD-47; CARD-42; apoptosis; cancer; AIDS; autoimmune disorder; systemic lugue erythematosue; viral infection; immune related glomerulonephritis; acquired immunodeficiency syndrome; neurological disease; Alzheimer's disease; Parkinson's disease; mayotrophic lateral sclerosis; retinitis pigmentosa; spinal muscular atrophy; cerebellar degeneration; haematological disease; anaemia; neutropaenia; myelodysplastic syndrome; myocardial infarction;
                         recruitment domain; CARD; CARD-3; CARD-4;
        Human Caspase recruitment domain protein 3, open reading frame.
                         caspase
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stroke; chromosome 7.

Homo sapiens

US6469140-B1

22-OCT-2002.

98US-00207359 08-DEC-1998; 98US-00019942. 98US-00099041. 06-FEB-1998; 17-JUN-1998;

(MILL-) MILLENNIUM PHARM INC

Bertin J;

WPI; 2003-147109/14. P-PSDB; ABU56269 Novel isolated human caspase recruitment domain (CARD)-4Y or CARD-4Z polypeptide, or murine CARD-4L polypeptide, useful in screening assays, detection assays, predictive medicine, and in therapeutic applications.

Disclosure; Col 71-74; 99pp; English

The invention relates to an isolated polypeptide, comprising at least 25 contiguous amino acids of a human caspase recruitment domain (CARD)-4Y, human CARD-4Z or murine CARD-4L (all splice variants of CARD)-4, polypeptide. Also included is an isolated fusion protein, comprising the CARD polypeptide is useful in screening assays, polypeptide covalently linked by a peptide bond to a heterologous polypeptide covalently linked by a peptide bond to a heterologous polypeptide covalently linked by a peptide bond to a heterologous polypeptide covalently linked by a peptide bond to a heterologous polypeptide is useful in screening assays, confocution assays (e.g. chromosomal mapping, tissue typing and forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, conforing clinical trials and pharmacogenomics), and in therapeutic and corphylactic treatments (in diseases essociated with apoptotic cell death e.g. cancers autoimmune disorders (e.g. systemic lupus erythematosus and immunodeficiency syndrome), neurological disease (e.g. Alzheimer's disease, parkinson's disease, amyotrophic lateral sclerosis, retinitis pigmentosa, spinal muscular atrophy and cerebellar degeneration), haematological diseases (e.g. anaemia, neutropaemia and myelodysplastic syndromes), myocardial infarction and stroke). The CARD polypeptide is useful as bait protein in a two-hybrid assay or three hybrid assay to identify other proteins, which bind to or interact with other CARD proteins. Also disclosed are CARD-3 proteins and cDNAS. The gene for human CARD-4 is located on chromosome 7. The present sequence is a human CDNA CARD

U; 0 Other; T; 0 G; 423 Seguence 1620 BP; 517 A; 360 C; 320

	1620	226	0	1	7	0
	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
	5.84e-119	128.00	99.12%	99.12%	55.17%	7
Alignment Scores:	Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:

LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25

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US-09-771-161A-93 (1-232) x ABX75870 (1-1620)

1119 1238 1298 1358 1418 1538 .000 AACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCATGAA 1059 1419 CTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACAC 1478 1539 ACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAAA 1598 105 125 145 165 185 205 225 940 TTACAGAGTGTTTCAAGTGCCATTCACCTATGTGACAAGAAAATGGAATTATCTCTG 999 45 65 85 1060 AATAGTGGTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTTTTA SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer TrpAspSerThr11eSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr-Pr 1239 ATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAGCCC uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 1359 AGCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAAGGA 1479 TACTGACATCCAAGGAGAAGTTTTGCCAAAGTTATAGTACAAAAATTGAAAGATAACAA sGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAs AsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHisGlu oCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 1299 TGGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAAATGACAGA rThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLy 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 125 oGlylleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGl pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGl 232 1599 TTTACTTCAAAATAAAAGCATG 225 nLeuLeuGlnAsnLysSerMet 1120 99 98 105 145 165 185 205 56 8 g 8 g 8 - 유 ò g ò g ò g à g ò D ò 셤 ð g ò

AAZ09246 standard; cDNA; 1931

25-OCT-1999 (first entry)

Human CARD-3 cDNA

caspase activation; detection; screening; therapy; diagnosis; disease; apoptotic cell death; Fas/APO-1 receptor complex; TNF receptor complex; acancer; follicular lymphoma; carcinoma; p53 mutation; viral infection; hormone-dependent tumour, autoimmune disorder; Alzheimer's disease; systemic lupus erythematosis; immune-mediated glomerulonephritis; stroke; Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa; spinal muscular dystrophy; cerebellar degeneration; anaemia; drug; myelodysplastic syndrome; myocardial infarction; cell proliferation; cell differentiation; cell survival; CARD-41; CARD-45; CARD-47; CARD-42; CARD-3; caspase recruitment domain; CARD-4; regulation; detection; human; 

sapiens

Location/Qualifiers 214. .1836

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1273 AATAGTGGTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTTTTA 1332
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                                                                                                                                                                                                      1692 TACTGACATCCAAGGAGAAGAATTTGCCAAAGTTATAGAAAAAATTGAAAGATAAAAA
                                                                                                                         TrpAspSerThr11eSerGlySerGlnArgAlaAlaPheCysAspHisLysThr7hr-Pr
                                                                                                                                                                                                                                                                                                   1632 CTATGAACTTGTTAGTACCAAGCCTACAAGACCTCAAAAGTCAGACAATTACTAGACAC
                                                                                   ualaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs
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                                                            SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer
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/*tag= a
/note= "the open reading frame is also specifically
claimed in Claim 1(a)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes the isolation of novel human caspase recruitment domain, CARD-1 protein and genes. The genes and proteins and a partial curine (CARD-14 protein and genes. The genes and proteins of the invention are involved in the regulation of caspase activation. The caspase cretainment domain (CARD) polynuclectides, polypeptides, homologues and antibodies can be used in screening assays, detection assays, predictive medicine and therapeutic and prophylactic methods of treatment. The medicine and therapeutic and prophylactic methods of treatment. The captured may be used to disponse and treat patients which are suffering from a disorder associated with abnormal level or rate of apoptotic cell death, abnormal activity of the TMF receptor complex, or abnormal activity of a caspase. Cativity of the TMF receptor complex, or abnormal activity of a caspase. Diseases that may be treated include cancer (particularly follicular lymphoma, carcinomas associated with mutations in p53 and hormone-captorent tumours), autoimmune disorders (e.g. systemic luque erythematosis, immune-mediated glomerulonephritis), viral infections, captomers in pfamentosa, sprinal muscular dystrophy, cerebellar degeneration, anaemia, myelodysplastic syndrome, myocardial infarction, and stroke.

CARD-3 protein interacts with other cellular proteins, and so can be used for regulation of cellular proliferation and differentiation and erythematosis protein modulate their activity. The CARD-4 gene can express a long transcript that encodes CARD-4s and CARD-4s and CARD-42. This sequence compounds which modulate activity. CARD-47 and CARD-42. This sequence compounds which modulate their activity. The CARD-47 and CARD-42. This sequence compounds which when modulate activity and store an express a long transcript that encodes CARD-47 and CARD-42. This sequence compounds the human CARD-4 splice variants.
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                                                                                                                                                                                                                                                                                                                                                                           Novel CARD-3 and CARD-4 genes and polypeptides used or treating regulation of cellular proliferation and differentiation and cell
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           /*tag= a
/product= "CARD-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Fig 1; 181pp; English
                                                                                                                                                                      98US-00019942.
98US-00099041.
98US-00207359.
                                                                                                                                    99WO-US002544
                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PHARM INC
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128.00
99.12%
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                                                                WO9940102-A1
                                                                                                                                                                        06-FEB-1998;
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                                                                                                                                                            The present sequence is that of cDNA encoding human caspase recruitment domain 3 (CARD-3, see AAB20079). The cDNA was isolated following a database search using known CARD sequences. Plasmid pXE17A containing CARD-3 cDNA is deposited as ATCC 20307. CARD-3 is an intracellular protein predicted to be involved in regulating caspase activation. It is useful as a modulating agent in regulating callular processes include cell growth and cell death. Methods of diagnosing and treating patients suffering from a disorder associated with an abnormal level or rate of apoptotic cell death, abnormal activity of the Fas/APO-1 receptor complex. Complex, abnormal activity of the tumour necrosis factor receptor complex or abnormal activity of the tumour necrosis factor receptor complex or abnormal activity of a caspase involve administering a compound that modulates the expression or activity of CARD-3, CARD-4, CARD-5 or CARD-6 or as small molecule, antisense nucleic acid, ribozyme or polypeptide. Such disorders include cancer, viral infection, autoimmune disorders, neurological diseases, haematological disorders, inflammatory disorders and immune disorders. CARD nucleic acids can be used to express CARD proteins in a host cell e-9. for gene therapy applications, to detect a genetic lesion and to modulate CARD activity
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                                                           Isolated intracellular proteins predicted to be involved in regulating caspase activation are used for diagnosis and treatment of e.g. cancer, viral infections, autoimmune diseases, neurological diseases and hematological disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1931 BP; 613 A; 428 C; 416 G; 474 T; 0 U; 0 Other;
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Matches:
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Mismatches:
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1752 ACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAAA 1811
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                                                                                                                                        205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leucine rich repeat; LPS; lipopolysaccharide; NF-kB; nuclear factor-kappa B; cancer; viral infection; autoimmune disorder; systemic lupus erythematosus; immune-mediated glomerulonephritis; arthritis; immune disorder; multiple sclerosis; Hashimoto's thyroiditis; atopic condition; asthma; allergy; psoriasis; contact dermatitis; gastrointestinal allergy; insulin-dependent diabetes;
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                                        CTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACAC
                                                                                                                                                                                        1692 TACTGACATCCAAGGAGAAGAATTTGCCAAAGTTATAGTACAAAAATTGAAAGATAACAA
pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh
                                                                                                                                        rThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLy
                                                                                                                                                                                                                                                                                 sGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene; caspase recruitment domain; CARD-3; CARD-4; LRR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cDNA encoding caspase recruitment domain protein CARD-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bacterial infection; tuberculosis; lepromatous leprosy; cell signalling disorder; tissue disorder.
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/product= "CARD-3"
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                                                                                                                                                                                                                                                                                                                                                                                                                          nLeuLeuGlnAsnLysSerMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK89280 standard; cDNA; 1931
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                                                                  1632
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165
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dentifying a candidate compound for modulating LPS (lipopolysaccharide)-
mediated activation of nuclear factor-kappa B (NF-kB), by providing a
cell expressing a polypeptide comprising the LRR domain of CARD-4 and
charbouring LPS, exposing the cell to a test compound and measuring NF-kB
activation, where altered NF-kB activation polypeptide in the presence of
the test compound compared to the binding in the absence of the test
compound indicates that the test compound is a candidate compound for
compound indicates that the test compound is a candidate compound for
modulating LPS-mediated activation of NF-kB. Modulators identified by
(MI) are useful for treating a disorder characterised by abserrant CARD-4
c protein or nucleic acid. Compounds that modulate the activity of CARD-41
care useful to treat or diagnose disorders such as cancer, viral
cinfections, autoimmune disorders e.g. systemic lupus erythematosus,
cinmune-mediated glomerulonephritis and arthritis, immune disorders, such
as multiple sclerosis, Habilmoto's thyroiditis, atopic conditions such as
as multiple sclerosis, Habilmoto's thyroiditis, gastrointestinal
casthma, allergy, psoriasis, contact dermatitis, gastrointestinal
cuberculosis, and lepromatous leprosy, disorders of cell signalling and
characters of tissues. The present sequence is the human cDNA encoding
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Seguence 1931 BP: 613 A: 429 C: 416 G: 473 T: 0 U: 0 Other:

œ	Sequence	1931 BP;	613 A; 429 C;	416 G; 473 T; 0	U; 0 Other;	
Aligna Pred. Score: Percer Best I Query	Alignment Scores: Pred. No.: Score: Score: Percent Similarity: Best Local Similari Query Match:	es: arity: nilarity:	6.9e-119 128.00 99.12% 99.12% 55.17%	Length: Matches: Conservative: Mismatches: Indels: Gaps:	1931 226 0 1 2 0	
us-0	US-09-771-161A-93	7	-232) x ABK89280	(1-1931)		
ò	9	LeuGlnSer	LeuGlnSerValSerSerAlall	leHisLeuCysAspLysLysLy	SLysLysMetGluLeuSerLeu	25
g	1153	TTACAGAGI	GTTTCAAGTGCCA	TTCACCTATGTGACAAC	TTACAGAGTGTTTCAAGTGCCATTCACCTATGTGACAAGAAGAAATGGAATTATCTCTG	1212
ò	26	AsnilePro	ValAsnHisGlyP	snlleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnL	GlySerSerGlnLeuHisGlu	45
qq	1213	AACATACCI	GTAAATCATGGTC	CACAAGAGGAATCATGI	AACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGGTCCTCTCTGGGCTCCAGAAAAAAAA	1272
ò	46	AsnSerG1	/SerProGluThrS	erArgSerLeuProAla	snSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu	9
qq	1273	AATAGTGGT	TCTCCTGAAACTT	CAAGGTCCCTGCCAGCT		1332
ò	99	SerArgLys	sAlaGlnAspCysT	YrPheMetLysLeuHis	erArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer	85
q	1333	TCTAGAAA	AGCTCAAGACTGTT	ATTTTATGAAGCTGCAT	TCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCCTGGAAATCACAG	1392
ò	98	TrpAspSer	ThrileSerGlyS	erGlnArgAlaAlaPhe	TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr-Pr	105
q	1393	TGGGATAGG	ACCATTTCTGGAT	CTCAAAGGGCTGCATTC		1451
ò	105	oCysSerSe	erAlalleIleAsn	ProbeuSerThrAlaG	OCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr	125
q	1452	-	CAGCAATAATAAAT	CCACTCTCAACTGCAGG	ATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAGCC	1511
ò	125	ogly11eA]	laGlnGlnTrpIle	GlnSerLysArgGluAs	oGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGl	145
q	1512	TGGTATAGG	CCAGCAGTGGATC	CAGAGCAAAAGGGAAG	TGGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAAATGACAGA	1571
ò	145	uAlaCysLe	euAsnGlnSerLeu	AspAlaLeuLeuSerA	uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs	165
g	1572	AGCCTGCCT	TAACCAGTCGCTA	GATGCCCTTCTGTCCAC	AGCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGGA	1631
ò	165	pTyrGluLe	euValSerThrLys	ProThrArgThrSerLy	TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh	185
Q	1632	_	rtgttagtaccaag	SCTACAAGGACCTCAA	CTATGAACTTGTTAGTACCAAGCCTACAAGACCTCAAAAGTCAGACATTACTAGAACAC	1691
ò	185	rThrAspI]	leGlnGlyGluGlv	PheAlaLysVallleVa	rThraspileGlnGlyGluPheAlaLysVallleValGlnLysLeuLysAspAsnLy	205
qq	1692	TACTGACAT	rccaaggagaaga	TTTGCCAAAGTTATAG	TACTGACATCCAAGGAGAAGAATTTGCCAAAGTTATAGTACAAAATTGAAAGATAACAA	1751
ò	205		lyLeuGlnProTyr	:ProGluIleLeuValVa	sGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAs	225

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The invention relates to novel isolated Caspase Recruitment Domain (CARD)

CC polypeptides, CARD-4L and CARD-4S. The CARD proteins of the invention may

be used to treat disorders associated with decreased CARD expression by

cupplementing the patient's own production of CARD. Disorders associated

with the expression and activity of CARD include cancers (particularly

continuar lymphomas, carcinomas associated with mutations in p53, and

chormone-dependent tumours such as pressit cancer, prostate cancer, and

covarian cancer), autoimmune disorders (such as systemic lupus

covarian cancer), autoimmune disorders (such as systemic lupus

covarian cancer), autoimmune disorders (such as systemic lupus

covarian cancer), autoimmune as of general operations

covarian cancer), autoimmune as of general operations

covarian cancer, immune-mediated glomerulomephritis), viral infections

(such as those caused by herpes viruses, poxviruses, and adenoviruses),

convolocial diseases (such as Alzhaimer's disease, Parkinson's disease,

amylotrophic lateral sclerosis (ALS) retinitis pigmentosa, spinal

muscular atrophy, and various forms of cerebellar degeneration), anaemia

associated with chronic disease, aplastic anaemia, chronic neutropenia,

and the myelodysplastic syndromes. This polynoclebic equence
1752 ACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGGTTTCTAGATCACCATCTTTAAA 1811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated Caspase Recruitment Domain (CARD) polypeptides (CARD-4L and CARD-4S) useful for diagnosing and treating e.g. Parkinson's and Alzheimer's disease, cancers and viral infections.
                                                                                                                                                                                                                                                                                                                                                                                     Cytostatic; virucide; immunomodulatory; neuroprotective; antialzheimers; cerebroprotective; antiparkinsonian; antisclerotic; ophthalmological; nootropic; antianaemic; Caspase Recruitment Domain; CARD; CARD-4L; p53; cancer; CARD-4S; follicular lymphoma; carcinoma; autoimmune disorder; hormone-dependent tumour; breast cancer; prostate cancer; ovarian cancer; systemic lupus; herpes virus; poxvirus; adenovirus; neurological disease; anaemia; neutropenia; myelodysplastic syndrome; human; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       represents the cDNA of a human CARD relating to the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1931 BP; 613 A; 430 C; 416 G; 472 T; 0 U; 0 Other;
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Matches:
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                                                                                                                    1812 TTTACTTCAAAATAAAGCATG 1833
                                                                          225 nLeuLeuGlnAsnLysSerMet 232
                                                                                                                                                                                                                                                                                                                                               cDNA of human CARD-3 SEQ ID No 1.
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                                                                                                                                                                                                             AAL40752 standard; cDNA; 1931 BP
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99.12$
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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08-DEC-1998;
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1273 AATAGTGGTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTTTTA 1332
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              Homo sapiens
                                       US6469140-B1.
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                                                                                                1213 AACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCATGAA 1272
                                                                                                                                                                                                         AATAGTGGTTCTCCTGAAACTTCAAGGTCCCTGCAGCTCCTCAAGACAATGATTTTTTA 1332
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 Mismatches:
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                                                   US-09-771-161A-93 (1-232) x AAL40752 (1-1931)
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The invention relates to an isolated polypeptide, comprising at least 25 contiguous amino acids of a human caspase recruitment domain (CARD)-4Y, human CARD-4Z or murine CARD-4L (all splice variants of CARD-4) contiguous amino acids of a human caspase recruitment domain (CARD)-4Y, polypeptide. Also included is an isolated fusion protein, comprising the CARD polypeptide is useful in screening assays, colypeptide. The CARD polypeptide is useful in screening assays, detection assays (e.g. chromosomal mapping, tissue typing and forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, contioning clinical trials and pharmacogenomics), and in therapeutic and prophylactic treatments (in diseases associated with apoptotic call death crophylactic treatments (in diseases associated with apoptotic call death crophylactic treatments disorders (e.g. systemic lupus erythematosus and immunodeficiency syndrome), neurological disease (e.g. systemic lupus erythematosus immunodeficiency syndrome), neurological disease (e.g. short in a crobhylactic syndromes), mycardial infarction and stroke). The CARD polypeptide is useful as bait protein in a two-hybrid assay or three hybrid assay to identify other proteins, which bind to or interact with other CARD proteins. Also disclosed are CARD-3 proteins and charact with other CARD characters. Annual CARD-3 proteins and characteris and characteris a human can be numan care as a human can be numan care as a human can be numan care as a human can be not caredomed in a human can be numan care as a human care as a human can be not caredomed in the numan caredomed in a human caredomed in the numan caredomed in a human caredomed in the numan caredomed in a human caredomed in the numan caredomed in the numan caredomed in the numan caredomed in the numan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated human caspase recruitment domain (CARD)-4Y or CARD-4Z polypeptide, or murine CARD-4L polypeptide, useful in screening assays, detection assays, predictive medicine, and in therapeutic applications.
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98US-00207359
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Best Local Similarity:
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P-PSDB; ADB81362.

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                                         OGly1leAlaGlnGlnTrp1leGlnSerLysArgGluAsp1leValAsnGlnMetThrG1
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This invention relates to two novel genes CARD-3 and CARD-4 (caspase recruitment domains), which are mediators of apoptosis and are useful in the identification of compounds that modulate apoptosis. Specifically, CARD-3 (also known as RIP2, RICK and CARDIAK) is known to be a mediator. CARD-3 (also known as RIP2, RICK and CARDIAK) is known to be a mediator. CARD-4 (a member of the tumour necrosis factor (TNP) family), and is believed to provide the switch for cell survival and cell death decisions mediated by this p7s neutrophin receptor. Accordingly these genes, and mediated by this p7s neutrophin receptor. Accordingly these genes, and with an increased number of cells surviving and proliferating when apoptosis is inhibited. These include cancer, autolimune disorders e.g. systemic lupus and immune mediated glomerulomephritis, viral infections such as those caused by the herpesvirus, neurological disorders such as retinitis pigmentosa, haematologic diseases including chronic neutropenia, as well as myocardial infarction and strokes. The present invention further describes a novel method for determining whether a test compound alters the binding of CARD-3 to p75, which comprises measuring the binding of a polypeptide containing the CARD domain of CARD-3 to a polypeptide compained, and determining if binding is altered. This polypeptide is the human CARD-3 cDNA sequence of the invention.
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                                      Detecting compounds which alter binding of the caspase recruitment domain (CARD) of CARD-3 polypeptide to the neurotrophin receptor p75 is useful to provide compounds for treating CARD-3 mediated disorders.
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165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185

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Db 1632 CTATGAACTTGTTAGTACCAAGGCCTACAAAGTCAGACAATTACTAGAACTCAGACCACTACAAAGTCAAAAGTCTAGAACTCTAGACCC 1691

Qy 185 TTATAADTIAGING1) YGINGIUPheAlaLySValIleValGinLySLeuLySASpAsnLy 205

Db 1692 TACTGCAACATCCAAGGAAAAATTTGCCAAAGTTATAAAAATTGAAAGATAACAA 1751

Qy 205 SGINMetGlyLeuGinProTyrProGluIleLeuValValSerArgSerProSerLeuAs 225

Db 1752 ACAAATGGGTCTTCAGCCTTACCCGGAATACTTGTGGTTTCTAGATCACCATCTTTAAA 1811

Qy 225 nLeuLeuGinAsnLySSerMet 232

Db 1812 TTACTTCAAAATAAAAGCATG 1833

Search completed: April 1, 2004, 12:58:53

Job time: 485 secs
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us-09-771-161a-2.oli20.rng

	GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
OM nucleic - nu	OM nucleic - nucleic search, using sw model
Run on:	April 1, 2004, 03:06:50 ; Search time 754 Seconds (without alignments) 9403.505 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-771-161A-2 1669 1 acctagtttatacccagatacaacagcctgatgtgtaaaa 1669
Scoring table:	OLIGO NUC Gapop 60.0 , Gapext 60.0
Searched:	3373863 seqs, 2124099041 residues
Word size :	

Post-processing: Listing first 45 summaries

86

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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1: geneseqn1980s:\*
2: geneseqn1990s:\*
3: geneseqn2001s:\*
4: geneseqn2001as:\*
5: geneseqn2001bs:\* geneseqn2003bs:\*geneseqn2003cs:\* geneseqn2003as:\* geneseqn2004s:\* geneseqn2002s:\* 23. 55. 76. 10. Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

-	Description	Aac77779 Human can	Aaz46143 cDNA sequ	Aak94554 Human ful	Abk51169 cDNA enco	Aad45172 Human rec	Aaz48762 Human RIC	Adc99131 Human KPP	Aax02558 Human B1	Aaz09246 Human CAR	Aaf30001 Human CAR	Abk89280 Human cDN	Aal40752 cDNA of h	Abx75869 Human cDN	Adb81363 Human cas	Abx75870 Human Cas	Aal40753 DNA of hu	Ach33353 Human end	Abk55074 Human col	Aak93010 Human cDN	Acd96414 Human col	Abn58531 Human spl	Human	Abn41051 Human spl
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æ	Query Match	64.6	52.7	49.6	48.7	48.7	48.7	47.0	46.9	40.9	40.9	40.9	40.9	40.9	40.9	37.9	34.6	21.7	13.2	10.7	7.8	3.6	3.6	3.6
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ABZ04660 AAT19776 ADB81375	ADB81373 ACA47914 ADB81372 AAX02614	AAX02615 AAA66023 AAH81375	ABK16480 ABV53180 AAH07021	AAH07379 AAC77039 AAH14699 ABK35775	ABL28950 ABL28946 AAZ42043 AAS03899 ABT16854
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## ALIGNMENTS

Human cancer associated gene sequence SEQ ID NO:173. ВР. AAC77779 standard; cDNA; 2709 (first entry) 08-FEB-2001 AAC77779; RESULT 1 AAC77779 

Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidabetic; antiarthritic; antiviral; antinflammatory; antithyroid; antiallergic; antiarthritic; antiviral; dermatological; natithyroid; antiallergic; antibacterial; cardiant; dermatological; natipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoletic cell disorder; attoimmune disorder; allergic craction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening; ss. Homo sapiens.

08-MAR-2000; 2000WO-US005882. (HUMA-) HUMAN GENOME SCI INC. 12-MAR-1999; 99US-0124270P Rosen CA, Ruben SM; WPI; 2000-587533/55. P-PSDB; AAB43570. WO200055350-A1. 21-SEP-2000.

Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer. Claim 1; Page 751-752; 2352pp; English. AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB4239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities

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2103 1292 2163 1352 2223 1412

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/product= "phosphorylation effector"
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include: cytostatic; proliferative; vulnerary; immunomodulator;
antianthmatic; antirheumatic; antiarthritic;
antianthmatic; antithycoid; antiallergic; antibacterial; antiviral;
dermatological; neuroprofective; cardian; thrombolytic; coagulant;
coerropic; vasotropic; antipsoriatic and antiangiogenic. The
polynucleotides and polypeptides can be used for preventing, treating or
ameliorating medical conditions and diagnosing pathological conditions.
Complicating medical conditions and diagnosing pathological conditions.
Complicating medical conditions and diagnosing pathological conditions.
Complicating medical conditions of the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haemacopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in the exemplification of the antibodies.

ANCTORIA ANCTORIA represent sequences used in the exemplification of
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                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.6%;
Matches 1329; Conservative
                                                                                                                                                                                                                                                                      the present invention
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H, Azimzai Y;
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and prevention of proliferative, immune and neuronal disorders.
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Pred. No. 0;
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100.0%; Pred. No. v,
... 0; Mismatches
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98US-0155239P.
98US-0106889P.
98US-0109093P.
98US-0113796P.
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Best Local Similarity 100.
Matches 879; Conservative
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Bandman O,
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   14-OCT-1998;
03-NOV-1998;
19-NOV-1998;
22-DEC-1998;
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Patterson C,
                                                                                                                      12-JAN-1999;
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                                                                                                                                                                                                                               CTITATIGAAGGITCITIGGGIAAATATTAGICTCCCTCCAIGACACTGCAGTAITITIT 1172
                                                                                                                                                                                                                                                   830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      closes. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5' and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA essily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly
                   CTACTGACATCCAAGGAGAAGAATTTGCCAAAGTTATAGTACAAAAATTGAAAGATAACA
                                                                                                               ATTTACTTCAAAATAAAAGCATGTAAGTGACTGTTTTTCAAGAAGAAATGTGTTTCATAA
                                                         AACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; full length cDNA; cDNA synthesis; oligo-capping;
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K, Kojima
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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Wakamatsu A, Sugiyama
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cellular kinase; RICK; ss.

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Identifying agents for treatment or prevention of cytomegalovirus infection, comprises contacting test compound with cellular kinase detecting change in cellular kinase activity.
                                                                                                                                                                         /*tag= a
/product= "Human cellular kinase RICK"
                                                   encoding human cellular kinase RICK protein
                                                                             Human; virucide; cytomegalovirus infection; CMV; RIP; Nck-Interacting kinase; MKK3; SRPK-2; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 20-23; 49pp; English
                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                           16-OCT-2000; 2000US-0240750P
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P-PSDB; AAU80369.
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The present invention relates to a new method for identifying compounds for treating and/or preventing cytomegalovirus (CMV) infection and/or related diseases. The method of the invention comprises contacting a test compound with at least one of the cellular kinases RICK, RIP, Noklinteracting kinase, MKK3 and SRPK-2 and detecting any change in kinase activity. The method of the invention can be used to treat and/or prevent CMV infections and related diseases. Oligonucleotides that can detect the specified kinases can also be used for diagnosis of infection. The present nucleic acid sequence encodes the human cellular kinase RICK
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                                                                                                                                                                                                                                                                                               protein of the invention, as described above
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense oligonucleotide that targets regions of a nucleic acid encoding human receptor interacting protein (RIP)2, for treating diseases associated with RIP2 expression.
                                                                                                                                          The invention relates to antisense compounds targetted to a nucleic acid encoding human receptor interacting protein (RIP)2 to inhibit its expression. Antisense compounds are used for treating diseases associated with RIP2 expression. They are also useful in antisense gene therapy. The present sequence is human RIP2 DNA
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                                                                                                                                                AAGCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGG
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                                                   RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC; caspase-10; CD95 signalling; apoptosis signalling pathway; CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation; gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS; aplastic anaemia; ischaemic injury; toxin-induced liver disease; ss.
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                      Compositions for identifying apoptosis signaling pathway inhibitors
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Sequence 2502 BP; 769 A; 535 C; 499 G; 699 T; 0 U; 0 Other;
                                        DB 3;
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anti-HIV; antiallergic; antiinflammatory; antianaemic; antiparkinsonian; mootropic; anticonvulsant; antiarteriosclerotic; antiasthmatic; immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological; antidabetic; nephrotropic; antigout; thyromimetic; neuroprotective; osteopathic; nephrotropic; antidout; thyromimetic; neuroprotective; osteopathic; antiarthritic; antiparasitic; antihelminthic; antiparatic; uropathic; ophthalmological, antirheumatic; namostatic; antibacterial; virucide; protozoacide; fungicide; kinase; phosphatase; kPP; cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis; cancer; developmental; mental retardation; neurological; Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's; diabates mellitus; viral; bacterial; fungal; parasitic; protozoan; helminthic infection; transgenic; gene therapy; human; ss; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel isolated polypeptide which is a human kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides, pagonists and antagonists are useful for diagnosing, treating or preventing cell proliferative disorders such as atherosclerosis, cirrhosis, hepatitis and cancer, developmental disorders e.g. mental retardation, neurological disorders including Alzheimer's disease and Parkinson's disease, autoimmune and inflammatory disorders such as Crohn's disease and diabetes mellitus and finally, viral, bacterial, fungal, paramitic, protozoan or helminthic infections. Furthermore, the polynucleotides encoding KPP may be useful for creating transgenic animals to model human disease, as well as during gene therapy procedures. The current sequence is that of the human KPP CDNA of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human kinases and phosphatases and polynucleotides, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis, cancer or hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bandman O, Baughn MR, Becha SD, Borowsky ML, Duggan BM; Emerling BM, Forsythe IJ, Gandhi AR, Gorvad AE, Griffin JA; Gururajan R, Hafalia AJA, Khan FA, Lal PG, Lee EA, Lee SY; Lindquist EA, Lu DAM, Lu Y, Marquis DP, Nguyen DB, Arvizu CS; Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Tang YT; Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Yao MG,
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02-NOV-2001; 2001US-0343910P.
13-NOV-2001; 2001US-03398P.
16-NOV-2001; 2001US-0334248P.
30-NOV-2001; 2001US-0334288P.
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                                                                 KPP CDNA - SEQ ID 84
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P-PSDB; ADC99079.
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CCCTGCCAGCTCCTCAAGACAATGATTTTTTATCTAGAAAAGCTCAAGACTGTTATTTTA
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Tang YT; Yao MG, Yue H;

1697

Homo sapiens WO9855507-A2 Gaps ., 0 DB 9; Length 1959; 0; Indels . Match
Local Similarity 100.0%; Pred. No. 0;
les 785; Conservative 0; Mismatches

Query Match

Best Loca Matches

423 AGGAATCATGTGGATCCTCTCAGCTCCATGAAAATAGTGGTTCTCCTGAAACTTCAAGGT 482

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                   CTACTGACATCCAAGGAGAAGAATTTGCCAAAGTTATAGTACAAAAATTGAAAGATAACA 1796
                                                                                          AACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAA 1856
                                                                                                                                                                                                                             CARD-3; caspase recruitment domain; CARD-4; regulation; detection; caspase activation; derection; screening; therapy; diagnosis; disease; apoptotic call death; Fas/APO-1 receptor complex; TWF receptor complex; cancer; follicular lymphoma; carcinoma; p53 mutation; viral infection; hormone-dependent tumour; autoimmune disorder; Alzhaimer* disease; systemic lupus erythematosis; immune-mediated glomerulonephritis; stroke; Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa; spinal muscular dystrophy; cerebellar degeneration; anaemia; drug; myelodysplastic syndrome; myocazdial infarction; call proliferation; cell differentiation; cell survival; CARD-41; CARD-45; CARD-47; CARD-42;
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                                                                                                                                                                                                             Novel CARD-3 and CARD-4 genes and polypeptides used or treating regulation of cellular proliferation and differentiation and cell
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/product= "CARD-3"
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08-DEC-1998;
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                                                                                                                                                                                                                                                                                  New B1 protein regulates cell death and cell survival pathways -derivatives, DNA and antibodies, also regulate intracellular inflammation ; for treating AIDS, cancer.
                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes the isolation of a novel human B1 protein which can interact with, intracellular mediators or modulators of inflammation, cell death and/or cell survival pathways, directly or indirectly. Cells can be modulated or mediated in inflammation, cell death or cell survival pathways or another intracellular signalling activity using B1. Conditions such as A1DS and cancer can be treated using B1. Antibodies, oligonucleotides and ribozymes can also be used to regulate the above
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Pred. No. 0;
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100.0%; Pred. No. v,
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783; Conservative
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cc domain, CARD-3 and CARD-4 polynuclectides and proteins and a partial murine CARD-11 protein and genes. The genes and proteins of the invention crecuitment domain (CARD) polynuclectides, polypeptides, homologues and recruitment domain (CARD) polynuclectides, polypeptides, homologues and antibodies can be used in screening assays, detection assays, predictive methods may be used to diagnose and treat patients which are suffering from a disorder associated with abnormal level or rate of apoptotic cell catch, abnormal activity of the Fas/APO-1 receptor complex, abnormal cativity of the TMF receptor complex, abnormal activity of the TMF receptor complex, abnormal activity of the TMF receptor complex, or abnormal activity of a caspase. Complex associated with mutations in p53 and hormone-cativity of the TMF receptor complex, or subnormal activity of a caspase. Complement tumours), autoinmune disorders (e.g. systemic lupus captions, immune-mediated with mutations in p53 and hormone-captinitis pigmentosa, spinal muscular dystrophy, cerebellar degeneration, angelodysplastic syndrome, myocardial infarction, and stroke. Capp. 3 protein interacts with other cellular proteins, and so can be used for requiring pigmentosa, spinal muscular dystrophy, cerebellar degeneration, angendysplastic syndrome, myocardial infarction, and stroke. Compounds which modulate their activity. The CARD-4 gene can express a long transcript that encodes CARD-41, as short transcript that encodes CARD-45 and CARD-47 and CARD-47. This sequence compounds the human CARD-4 spince variants, and the transcript that encodes captor and the method of the invention
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Sequence 1931 BP; 613 A; 429 C; 416 G; 473 T; 0 U; 0 Other;

1270 1330 CATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAGC 1510 1571 AAGCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGG 1630 ö 151 AGTTACAGAGTGTTTCAAGTGCCATTCACCTATGTGACAAGAAAAATGGAATTATCTC 1210 1631 ACTATGAACTIGITAGIACCAAGCCIACAAGGACCICAAAAGICAGACAATIACIAGACA 1690 1691 CTACTGACATCCAAGGAGAAGTTTGCCAAAGTTATAGTACAAAATTGAAAGATAACA 1750 632 812 872 932 392 452 512 572 692 CTGGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAAATGACAG 752 992 1211 TGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCATG AAAATAGTGGTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGTTTTT 513 TATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCCTGGAAATCACA 1331 TATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCCTGGAAATCACA CTACTGACATCCAAGGAGAAGAATTTGCCAAAGTTATAGTACAAAAATTGAAAGATAACA AACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAA TGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCGTCTCTCAGCTCCATG GTTGGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCACTC 633 CATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAAACGTCTGCAGC AAGCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGG ACTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACA AGTTACAGAGTGTTTCAAGTGCCATTCACCTATGTGACAAGAAGAAATGGAATTATCTC AAAATAGTGGTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTTT Gaps . Score 682; DB 2; Length 1931; Pred. No. 0; 1; Indels 0; Mismatches 40.98; 186.66 Query Match Best Local Similarity 99.9° Matches 732, Conservative 753 813 873 1271 1451 333 393 453 573 693 ଚ 요 Ω g ઠે 유 Š d ઠે 엄 ò g δ g ò ద 8 원 ઠે ò

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AAF30001 standard; cDNA; 1931 BP. AAF3000

AAF30001;

(first entry) 23-APR-2001

Human CARD-3 cDNA

CARD-3; caspase recruitment domain; human; cancer; infection; autoimmune disease; neurological disease; hammarioladical disease; inflammarion; antitumour; antiseptic; immunomodulator; antinflammatory; apoptosis; diagnosis; gene therapy; ss.

Homo sapiens.

Location/Qualifiers

WO200100826-A2

04-JAN-2001.

28-JUN-2000; 2000WO-US017691.

99US-00340620. 28-JUN-1999;

(MILL-) MILLENNIUM PHARM INC.

Bertin J;

WPI; 2001-061973/07. P-PSDB; AAB20079 Isolated intracellular proteins predicted to be involved in regulating caspase activation are used for diagnosis and treatment of e.g. cancer, viral infections, autoimmune diseases, neurological diseases and hematological disorders.

Claim 1(a); Fig 1; 208pp; English.

The present sequence is that of cDNA encoding human caspase recruitment domain. 3 (CARD-3, see AAB20079). The cDNA was isolated following a database search using known CARD sequences. Plasmid pXE17A containing CARD-3 cDNA is deposited as ATCC 203037. CARD-3 is an intracellular protein predicted to be involved in regulating caspase activation. It is useful as a modulating agent in regulating cellular processes include cell growth and cell death, Methods of diagnosing and treating patients culfering from a disorder associated with an abnormal level or rate of apoptotic cell death, abnormal activity of the tumour necrosis factor receptor complex, abnormal activity of the tumour necrosis factor receptor complex. Abnormal activity of the tumour necrosis factor receptor complex as mall molecule, antisense nucleic acid, ribozyme or polypeptide. Such disorders include cancer, viral infection, autoimmune disorders. Candiamatory disorders and immune disorders. CARD mucleic acids can be used to express CARD proteins in a host cell e.g. for gene therapy applications, to detect a

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The invention relates to identifying (MI) a compound which modulates a human or murine caspase recruitement domain (CARD) 4D (long form) human or murine caspase recruitement domain (CARD) 4D (long form) polypeptide with a test compound and determining the effect of the test compound on the activity of the polypeptide to identify a compound which modulates the polypeptide. The method may be adapted for identifying a compound which binds to the LRR (leucine rich repeat) domain of CARD-4. Also included is a method of identifying a candidate compound for modulating LPS (lipopolygaccharide) mediated activation of nuclear factor-kappa B (NF-kB), by providing a cell expressing a polypeptide comprising the LRR domain of CARD-4 and harbouring LPS, exposing the cell to a test compound and measuring NF-kB activation, where altered NF-kB activation polypeptide in the presence of the test compound compared to the binding in the absence of the test compound indicates that the test compound is a candidate compound for modulating LPS-mediated activation of NF-kB. Modulators identified by (MI) are useful for treating a disorder characterised by aberrant CARD-4. Expression of the test of the test of the compounds that modulate the activity of CARD-4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  are useful to treat or diagnose disorders such as cancer, viral infections, autofinmune disorders e.g. systemic lupus erythemaclosus, immune-mediated glomerulonephritis and arthritis, immune disorders, such as multiple sclerosis, Hashimoto's thyroiditis, atopic conditions such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         333 AGTTACAGAGTGTTTCAAGTGCCATTCACCTATGTGACAAGAAGAAATGGAATTATCTC 392
nuclear factor-kappa B; cancer; viral infection; autoimmune disorder; systemic lupus erythematosus; immune-mediated glomerulonephritis; arthritis; immune disorder; multiple sclerosis; Hashimoto's thyroiditis; atopic condition; asthma; allergy; psoriasis; contact dermatitis; gastrointestinal allergy; insulin-dependent diabetes; bacterial infection; tuberculosis; lepromatous leprosy; cell signalling disorder; tissue disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   asthma, allergy, psoriasis, contact dermatitis, gastrointestinal allergies, insulin-dependent diabetes, bacterial infections, including tuberculosis, and lepromatous leprosy, disorders of cell signalling and disorders of tissues. The present sequence is the human cDNA encoding
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Human; 98; gene; caspase recruitment domain; CARD-3; CARD-4; LRR; leucine rich repeat; LPS; lipopolysaccharide; NF-KB;

Human cDNA encoding caspase recruitment domain protein CARD-3

(first entry)

21-OCT-2002

ABK89280

98US-00099041. 98US-00207359.

99US-00245281 98US-00019942

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The invention relates to novel isolated Caspase Recruitment Domain (CARD) polypeptides, CARD-4L and CARD-4S. The CARD proteins of the invention may be used to treat disorders associated with decreased CARD expression by supplementing the patient's own production of CARD. Disorders associated with the expression and activity of CARD include cancers (particularly folloular lymphomas, carcinomas associated with mutations in p53, and hormone-dependent tumours such as brossic cancer, prostate cancer, and ovarian cancer), autoimmune-mediated glomerulonephritis), viral infections erythematosus, immune-mediated glomerulonephritis), viral infections cutch as those caused by herspes viruses, poxylruses, and ademoviruses), neurological diseases (such as Alzheimer's disease, Parkinson's disease, amylotrophic lateral sclerosis (ALS) retinitis pigmentosa, spinal muscular atrophy, and various forms of cerebellar degeneration), anaemia associated with chronic disease, aplastic anaemia, chronic neutropenia, and the myelodysplastic syndromes. This polynucleotide sequence represents the CDNA of a human CARD relating to the invention
                                                                                                                                                                                                                              Isolated Caspase Recruitment Domain (CARD) polypeptides (CARD-4L and CARD-4S) useful for diagnosing and treating e.g. Parkinson's and Alzheimer's disease, cancers and vixal infections.
                                                                                                                                                                                                N-PSDB; AAO22107, AAO22108, AAO22109, AAO22110.
                                                                                                                                                                                                                                                                                                  Example 2; Fig 1; 116pp; English.
                                                                                                               (MILL-) MILLENNIUM PHARM INC.
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cerebroprotective, antiparkinsonian, antisclerotic; ophthalmological; nootropic; antianaemic; Caspase Recruitment Domain; CARD; CARD-4L; p53; cancer; CARD-4S; follicular lymphoma; carcinoma; autoimmune disorder; hormone-dependent tumour; breast cancer; prostate cancer; ovarian cancer; systemic lupus; herpes virus; poxvirus; adenovirus; neurological disease; anaemia; neutropenia; myelodysplastic syndrome; human; gene; ss.
                                                                                                                                         Cytostatic; virucide; immunomodulatory; neuroprotective; antialzheimers;
                                                                                                      cDNA of human CARD-3 SEQ ID No 1.
                                                                     (first entry)
                                                                     27-SEP-2002
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US6369196-B1

09-APR-2002.

BP

AAL40752 standard; cDNA; 1931

RESULT 12 AAL40752

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Sequence 1931 BP; 613 A; 430 C; 416 G; 472 T; 0 U; 0 Other;
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                               40.9%; Score 682;
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.571 AAGCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGG 1630
                                                                                                                                                                                                                                                                                                                                                                                                                 Human; ss; gene; caspase recruitment domain; CARD, CARD-3; CARD-4; CARD-4L; CARD-4S; CARD-4Y; CARD-4Z; apoptosis; cancer; AIDS; autoimmune disorder; systemic lupus erythematosus; viral infection; immune related glomerulonephritis; acquired immunodeficiency syndrome; neurological disease; Alzheimer's disease; Parkinson's disease; mayotrophic lateral sclerosis; retinitis pigmentosa; spinal muscular atrophy; cerebellar degeneration; haematological disease; anaemia; neutropaenia; myelodysplastic syndrome; myocardial infarction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated polypeptide, comprising at least 25 contiguous amino acids of a human caspase recruitment domain (CARD)-4Y, human CARD-4Z or murine CARD-4L (all splice variants of CARD-4) polypeptide. Also included is an isolated fusion protein, comprising the CARD polypeptide covalently linked by a peptide bond to a heterologous polypeptide. The CARD polypeptide is useful in screening assays,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated human caspase recruitment domain (CARD)-4Y or CARD-4Z polypeptide, or murine CARD-4L polypeptide, useful in screening assays, detection assays, predictive medicine, and in therapeutic applications.
                        ACTATGAACTIGITAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACA
                                                 ACTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACA
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                                                                                                                            AACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAA
                                                                                                                                                                                                                                                                                                                                                                                            Human cDNA encoding Caspase recruitment domain protein, CARD-3.
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biology), predictive medicine (e.g. diagnostic assays, prognostic assays, biology), predictive medicine (e.g. diagnostic assays, prophylactic treatments (in diseases associated with apoptotic cell death e.g. cancers, autoimmune diseases essociated with apoptotic cell death c.g. cancers, autoimmune diseases e.g. systemic lupus erythematosus and immuneaficiency syndrome), neurological disease (e.g. Alzheimer's clisease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis pigmentosa, spinal muscular atrophy and cerebellar degeneration), c.g. haematological diseases (e.g. anaemia, neutropeania and myelodysplastic syndromes), myocardial infarction and stroke). Three hybrid assay to identify other protein in a two-hybrid assay or three hybrid assay to identify other proteins, which bind to or interact with other CARD contents. Also disclosed are CARD-3 proteins and cDNAS. The gene for human CARD-4 is located on chromosome 7. The present sequence is a human CARD cDNA.
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Pred. No. 0;
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Matches 732; Conservative
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0; Mismatches Pred. No. 0;

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812

1690

932

872

1052

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polynucleotide is the human CARD-3 cDNA sequence of the invention.
1871 AAGGATATTTATA 1883
                                                                           214. .1836
/*tag= a
                               (first entry)
                                                                                                                                         WPI; 2003-657125/62
P-PSDB; ADB81362.
                                                                                                                                  Bertin J, Chao MV;
                                                                                                                        (BERT/) BERTIN J. (CHAO/) CHAO M V.
                                                                                         US2002061833-A1
                                                                                                              06-FEB-1998;
                                                                 sapiens
                              04-DEC-2003
                                                                                                23-MAY-2002
                        ADB81363;
                                                                 Homo
          RESULT 14
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1691 CTACTGACATCCAAGGAGGAGTTTTGCCAAGTTATAGTACAAAAATTGAAAGATAACA 1750
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                                                                                                                                                                                                                                                          1211 TGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCATG
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                                                                                         AGTTACAGAGTGTTTCAAGTGCCATTCACCTATGTGACAAGAAGAAAATGGAATTATCTC
                                                                                                                                                                                                               393 TGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCATG
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Best Local Similarity 99.9
Matches 732; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to two novel genes CARD-3 and CARD-4 (caspase recruitment domains), which are mediators of apoptosis and are useful in the identification of compounds that modulate apoptosis. Specifically, CARD-3 (also known as RTP2, RICK and CARDLAK) is known to be a mediator of p75 (a member of the tumour necrosis factor (TNF) family), and is believed to provide the switch for cell survival and cell death decisions mediated by this p75 neutrophin receptor. Accordingly these genes, and the proteins encoded thereof, are linked to certain disorders associated with an increased number of cells surviving and proliferating when a popoposis is inhibited. These include cancer, autoimmune disorders e.g. systemic lupus and immune mediated glomerulonephritis, viral infections such as those caused by the herpesvirus, neurological disorders such as those caused by the herpesvirus, neurological disorders such as retinitis pigmentosa, hemmatologic diseases including chronic neutropenia, as well as myocardial infarction and strokes. The present invention further describes a novel method for determining whether a test compound alters the binding of a polypeptide containing the CARD domain of CARD-3 to a polypeptide comparishing the death domain of p75 in the presence and a polypeptide companial, and determining if binding is altered. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting compounds which alter binding of the caspase recruitment domain (CARD) of CARD-3 polypeptide to the neurotrophin receptor p75 is useful to provide compounds for treating CARD-3 mediated disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                  p75; tumour necrosis factor; TNF; neutrophin receptor; cancer; autoimmune disorder; systemic lupus; immune mediated glomerulonephritis; viral infection; neurological; retinitis pigmentosa; haematological; chronic neutropenia; myocardial infarction; stroke; RIP; RICK; CARDIAK.
                                                                                                                                                                                                                                                                                                                                                                                         gene; CARD-3; CARD-4; caspase recruitment domain; apoptosis;
                                                                                                                                                                                                                                                                                                                              Human caspase recruitement domain 3 (CARD-3) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/product= "CARD-3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 2; 40pp; English
                                                                                                                                                 ADB81363 standard; cDNA; 1931 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-DEC-2000; 2000US-00748537
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Human; ss; gene; caspase recruitment domain; CARD-3; CARD-4; CARD-4L; CARD-4S; CARD-4Y; CARD-4Z; apoptosis; cancer; AIDS; autoimmune disorder; systemic lupus erythematosus; viral infection; immune related glomerulonephritis; acquired immunodeficiency syndrome; neurological disease; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa; spinal muscular atrophy; cerebellar degeneration; haematological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Caspase recruitment domain protein 3, open reading frame.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
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1053 AAGGATATTTATA 1065
                                                                                                       AAGGATATTTATA 1883
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XX
AC ABX7
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AC ABX7
XX
DE HUME
XX
KW HUME
KW AULE
K
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DB 9; Length 1931;

Score 682;

Query Match

Sequence 1931 BP; 613 A; 430 C; 416 G; 472 T; 0 U; 0 Other;

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The invention relates to an isolated polypeptide, comprising at least 25 contiguous amino acids of a human caspase recruitment domain (CARD)-4Y, human CARD-4Z or muthine CARD-4L (all splice variants of CARD)-4Y, polypeptide. Also included is an isolated fusion protein, comprising the CARD polypeptide is useful in screening assays, polypeptide. The CARD polypeptide is useful in screening assays, detection assays (e.g. chromosomal mapping, tissue typing and forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenomics), and in therapeutic and prophylactic treatments (in disease associated with apoptotic call death e.g. cancers, autoimmune disorders (e.g. systemic lupus erythematosus and immunodeficiency syndrome), neurological disease (e.g. Alzheimer's disease, anyotrophic lateral sclerosis, retinitis pigmentosa, spinal muscular atrophy and cereballar degeneration), haematological disease, envolupida assay or three hybrid assay to sharp protein in a two-hybrid assay or three hybrid assay to redenins, which bind to or interact with other CARD proteins, and care the proteins a human can human can buman can be considered by the present sequence is a human can buman can be considered by the present sequence is a human can be considered by the present sequence is a human can be considered by the present sequence is a human can be considered by the present sequence is a human can be considered by the present sequence is a human can be considered by the present sequence is a human can be considered by the present sequence is a human can be considered by the present sequence is a human can be considered by the present sequence is a human can be considered by the present sequence is a human can be considered by the present sequence is a human can be considered by the present sequence is a human can be considered by the present sequence is a human can be considered by the present sequence is a human can be considered by the present sequence is a human can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated human caspase recruitment domain (CARD)-4Y or CARD-4Z polypeptide, or murine CARD-4L polypeptide, useful in screening assays, detection assays, predictive medicine, and in therapeutic applications.
anaemia; neutropaenia; myelodysplastic syndrome; myocardial infarction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGAACATACCTGTAAATCATGGTCCACAAGAAGGAATCATGTGGATCCTCTCAGCTCCATG
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99.9%; Pred. No. 4.4e-291;
iive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                            98US-00019942
98US-00099041
                                                                                                                                                                                                                             98US-00207359
                                                                                                                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                            stroke; chromosome 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-147109/14.
P-PSDB; ABU56269.
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Matches 682; Conserve
                                                                              Homo sapiens
                                                                                                                             US6469140-B1
                                                                                                                                                                                                                             38-DEC-1998;
                                                                                                                                                                                                                                                                            06-FEB-1998;
17-JUN-1998;
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Description	AY358814 Homo	AG004003	9 AFII7829 Homo Bapi	B0231608	BD12	AK075213	AR221453	AX429236	AF027706	AR19431	A62111 35 AD106658		AC139421 1	AF064824	.5 AY335645	AR183234 Sequence	ARZUS634 Sequenc	AK216112	AR256252 Semienc	AR391599 Sequenc	AX082199 Sequence	BD123998	АF078530 Ношо вар	AR183235	ARZ05635		AR391600	AX082201	BD123999	AK380139 Sequenc		D122033	AF487539 Mus	9 AL807379 Mous	AJ341343 H	A AL109815 Plasm	AC119395 Mus m	12 Continuation	AC102277 Mus	7 AC132407 Mus muscu	
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AY358814 2521 bp mRNA linear PRI 03-OCT-2003 Homo sapiens clone DNA43305 RIPK2 (UNQ277) mRNA, complete cds. AY358814

RESULT 1 AY358814 LOCUS

AY358814.1 GI:37182745 FLI CDNA. Homo sapiens (human) DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS

Eukary Organia, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(Dark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E.,

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Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Leavis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoonfeld, J., Semplairi, S., Simmon, L., Singh, J., Smith, V., Stinson, J., Vagte, A., Vandlen, R., Watanabe, C., Wieand, D., Woods, K., Kie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, K., The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INBLLHRKTEYPDVAMPLRFRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNBFHY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1368
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Clark,H.F.
Direct Submission
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
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2 (bases 1 to 2521)
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1532

SOURCE ORGANISM

KEYWORDS

REFERENCE AUTHORS TITLE AUTHORS TITLE JOURNAL

JOURNAL REFERENCE REFERENCE AUTHORS TITLE JOURNAL AUTHORS TITLE

REFERENCE

JOURNAL

COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IADFGLSKWRMMSLSQSRSSKSAPEGGTIIYMPPENYEPGQKSRASIKHDIYSYAVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thote="gerine/Threonine kinase RICK; match to protein AF027706 (PID:93123887); and mRNA AF027706 (NID:93123886);
                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(7872. 8044,12642. 12795,15154. 15309,19584. 1977
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note="CpG island (%GC=69.1, o/e=0.80, #CpGs=93)"

1872. .40218

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      evidence=not_experimental
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16460. 1600.
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22863. .21
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23575. 2357
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198. .649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                         submitted (15-JAN-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
3 (bases 1 to 116650)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Genetics, Washington
Park Avenue, St. Louis, Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone CTA-437115 is from a release of the human BAC library CTB-HS-A. The library contains cloned DNA from human sperm. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). The clone is available from Research Genetics, Inc. (http://www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is CTA-237G1. The actual start of
this clone is at base position 1 of CTA-437L15; actual end is at
                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This chromosome 8 clone was provided by Dr. Patrick Concannon (patcon@vmmc.org) at the Virginia Mason Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                            1 (bases 1 to 116650)
Ozersky, P., Holmes, A. and Broy, M.
The sequence of Homo sapiens BAC clone CTA-437L15
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone contains STS HS275YF1 (NID:g1051703)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: H_RG437L15
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/chromosome="8"
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1. .116650
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                                                                                                                                                                                                                                                                                                                                                                                            Submitted (27-JUN-1998)
University, 4444 Forest
4 (bases 1 to 116650)
                                                                                                                                                                                                      (bases 1 to 116650)
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                     sapiens (human)
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                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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                                              sapiens
                                                                                                                                                                                                                                 Vaterston, R.
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source

FEATURES

н .	repeat_region 2626826500 /rnf family=#MRP1 tvne"	Db 40117 AAATTGAAAGATAACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCT 40176
н	2661127000 /rpt_family="L1"	
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н	repeat_region 33380. 33437 /rot_familv="MIR"	Db 40477 ATAACAGTGCCTTAAGGTATGATGTATTTCTGATGGAAGCCATTTTCACATTCATGTTCT 40536
н	repeat_region 3443334514 /rot family=!WER2 tvne"	Qy 1337 ICAIGGAITAITHGITACTHGICTAAGAIGCAATHTIGAITHTATGAAGHATAACCCTTT 1396
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ы	repeat_region 3.486 3.486 3.487 4.48	Qy 1517 CCTTTAAAAATGATATTTCAAAGGTAAAACAATACAATA
H	/_tpramil_r	Db 40717 CCTTTAAAATGATATTTCAAAGGTAAAAACAATACAATA
н	385	Qy 1577 PASTACCGGCTTCCTGTCCCCATTTTTAACCTCAGCCTTCCCTACTGTCACCAACAACAA 1636
н	repeat_region 41954. 42006 /rpt family=112"	Db 40777 TAATACCGGCTTCCTGTCCCCATTTTTAACCTCAGCCTTCCCTACTGTCACCACAACCA 40836
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Quer Best Matc	Query Match 59.3%; Score 990; DB 9; Length 116650; Best Local Similarity 100.0%; Pred. No. 0; Matches 990; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	AF117829 320187 bp DNA linear P
ò	CTGCAGCCTGGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGAAG	s chromosome 8 multiple
걸		ACCESSION AF117829 VERSION AF117829.2 GI:38153762
ر م	737 GTGAACCAAATGACAGAAGCCTGCCTTAACCAGTGGCTAGATGCCCTTCTGTCCAGGGAC 796	nic. Homo sapiens (human) Homo sapiens Enkarvota: Marazoa: Chordata: Craniata: Vertebrata:
i è	このでは、このでは、このでは、このでは、このでは、このでは、このでは、このでは、	Manmalia, Merazoa, Libiates, Camaran, Vercessara, Laceroscom, Manmalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
중 음 중		
ò 4	857 AGACAAITACTAGACATCTAAGGAGAAGAATTTGCCAAAGTTATAGTACAA 916	REFERENCE 2 (bases 1 to 320187)  WITHORS Platzer, M. and Varon, R.
3 &	ABATTGAAAGATAACAAACAATGGGTCTTCAGCCTTACCCGGAAATACTGTGCTTTCT	E F

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4309. .64312
'note="deleted in clone: SCb-282k6 , SCb-228C20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44479. .44606
/note="asingle stranded/single chemistry region"
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                                                                                                                                                                                                                                                                                     .. .19—
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                                                                                                                                                                                                                                                                                                                                     9564. .9663
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19692. .19708
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27998. .28050
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8051. .28095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="C substituted in clone: SCb-228C20"
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note="AC substituted in clone: RGP-64M4"
replace="GT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="A substituted in clone: SCb-282k6"
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212762. 320187
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                                                                                                                                                                                                                                                        clone_lib="Research Genetics human BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                /note="single stranded/single chemistry 26909. .26986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="single clone coverage"
18212. 28306.
note="por product sequence only"
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                                                                                                                                                          organism="Homo sapiens"
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db_xref="taxon:9606"
                                             db_xref="taxon:9606"
                                                                                                                                                                                                                                  clone="SCb-316M22
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64828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neighboring sequence information:
This entry is part of a larger genomic contig. The start of this sequence is directed towards the centromere. The end (318188 . 320187) of this sequence overlaps with the start of Acc number AF049895. It covers RGP-64M4, SCb-282k6, SCb-273G1 entirely and is overlapped by SCb-296N11, SCb-316M22.
                     Direct Submission
Submitted (04-NOV-2003) Genome Analysis, Institute of Molecular Submitted (04-NOV-2003) Genome Analysis, Institute of Molecular Biotechnology, Buttenbergstr. 11, Jena, Thuringia 07745, Germany On Nov 4, 2003 this sequence version replaced gi:4151947.

Center: Institute of Molecular Biotechnology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                                             Dye;
                                                                                                                                                                                                                                                                                                                                   Sequencing vector: Misaple, 100% of reads Sequencing vector: Misaple, 100% of reads Consensus quality: 319496 bases at least Q40 Consensus quality: 320184 bases at least Q30 Consensus quality: 320187 bases at least Q20 Quality coverage: 7.63
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62823..145565
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200838. .320187
                                                                                                                                                                          Center code: IMB
Web site: http://genome.imb-jena.de/
Contact: gscj-submit@genome.imb-jena.de
Conter: Project Information
Center project name: NBSlocusA
Center clone name: RGP-64M4 to SCb-316M22
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/mol type="genomic DNA"
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     Platzer, M
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AUTHORS
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SCP-228C20"

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TCAGAACGTCTGCAGCCTGGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATT	
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  REFERENCE I (bases 1 to 2024)  AUTHORS Hillman,J.L., Lal,P., Tang,T.Y., Corley,N.C., Guegler,K.J., Baughn,M.R., Patterson,C., Bandman,O., Young,J.A., Gorgone,G.A., Yue,H., Azimzai,Y., Reddy,R., Lu,D.A.M. and Shih,L.L.  TITLE Phosphorylation effectors JOHNNAL PATENT: JP 2005256035-8 6 20-AUG-2002;
	INCYTE PHARMACEUTICALS INC OS Homo sapiens (human) PN JP 2002526035-A/6 PD 20-AUG-2099 JP 2000562510 PR 28-JUL-1999 US 60/155213,14-SEP-1998
	14-OCT-1998 US 60/155239,03-NOV-1998 US 60/106889 PR 19-NOV-1998 US 60/109093,22-DEC-1998 US 60/113796 PR 12-JAN-1999 US 60/155233 PI JENNIFER L HILLMAN, PREETI LAL, TOM Y TANG,NEIL C CORLEY, KARL J PI GIRGIER
1037 GAAATGIGTTTCATAAAAGGATATTTATATCTCTGTTGCTTTGACTTTTTATATAAAA 1096 	PI MARIAH R BAUGHN, CHANDRA PATTERSON, OLGA BANDMAN, JANICE AU YOUNG, GINA A GORGONE, HENRY YUE, YALDA AZIMZAI, ROOPA REDDY, DYUNG AINA DI MIJI
1097 TCCGTGAGTATTAAAGCTTTATTGAAGCTTCTTTGGGTAAATATTAGTCTCCCTCC	61P
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03-OCT-2003

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 1886)
I (clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P. E., Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P. E., Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoeffeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagis, A., Vandlen, R., Watanabe, C., Wieand, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I. and Godowski, P., Zhang, M., Zhang, Z., The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / translation="MTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMASLSQSRSS
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PSLNLLQNKSM"
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CA 94080, USA
                                         1920 CITTATIGAAGGIICTITGGGIAAATATIAGICICCCICCAIGACACIGCAGIATITIT
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  CTITATIGAAGGITCTITGGGTAAATATIAGTCTCCCTCCATGACACTGCAGTATITITT
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Homo sapiens clone DNA43306 RIPKZ (UNQ277) mRNA, complete cds.
AY358813
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Submitted (01-AUG-2003) Department of
Inc., 1 DNA Way, South San Francisco,
Location/Qualifiers
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Genome Res. 13 (10), 2265-2270 (2003)
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FLI_CDNA.
Homo sapiens (human)
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A61P31/04,
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A61P37/00,
A61P37/08,CO7K16/40,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/
12,C12N9/16,
C12Q1/68,GQ1N33/50,GQ1N33/566,C12N15/00,C12N5/00,A61K37/02 CC
reclone Number: 156108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             512
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                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                         'organism='Homo sapiens (human)'
                                                                                                                                                                                                                                                                                                                                                           DB 6; Length 2024;
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1. .2024
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100.0%; Pred. No. 0;
ive 0; Mismatches

    .2024
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

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Matches 879; Conservative
  PC A611
PC A611
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Primer for synthesizing full-length cDNA and use thereof.
BD127583
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                       BD127583.1 GI:2322528
JP 2002017375-A/3014.
Homo sapiens (human)
Homo sapiens
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DEFINITION
ACCESSION
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SOURCE
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RESULT 6
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07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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HELLIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN J2-2002(1375-A/3014
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZU PI ISHII,
YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI SHINICHI KOJIMA,
PI TETSUJI OTSUKI, HISASHI KOGA
PC CIZNIS/09, CO7K14/47, CO7K16/18, CIZNI/15, CIZNI/19, CIZNI/21, CIZNS/
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Oy 993 ATTTACTTCAAATAAACCATGTAAGTCACTGTTTTCAAGAAGAATGTGTTTCATAA 1052	AK075213 LOCUS LOCUS LOCUS AK075213 LOCUS LOCUS DEFINITION Homo sapiens CDNA FLJ90732 fis, clone PLACE1010081, highly similar LOCUS LOCUS DEFINITION Homo sapiens serine/threonine kinase RICK (RICK) mRNA. AK075213 AK075213 GI:22761157 AK075213 AK075213 GI:22761157 AK075213 AK075213 GI:22761157 EXYMODE Oligo cappiens (full insert sequence). Homo sapiens ENARYOLA METAZOA; CATATATATATATATATATATATATATATATATATATAT		ORIGIN A X-765 = "RENA"   Mol_type="mRNA"   Mol_type="mRNA"   Mol_type="mRNA"   Mol_type="mRNA"   Mol_type="mRNA"   Mol_type="mRNA"   A X-61 = "a axon. 1960"   A x-61 = "placenta"   A tissue_type="placenta"   A

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Patent: EP 1201765-A 13 02-MAY-2002;
Axxima Pharmaceuticals Aktiengesellschaft (DE)
Location/Qualifiers rarcragaaaagcrcaagacrgrrarrrargaagcrgcarcacrgrccrggaaarcaca GTTGGGATAGCACCATTTCTGGTTCTCAAAGGGCTGCATTCTGTGATCACAAGACCACTC CATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAGC 333 AGTTACAGAGTGTTTCAAGTGCCATTCACCTATGTGACAAGAAAAATGGAATTATCTC 1162 AGTTACAGAGTGTTTCAAGTGCCATTCACCTATGTGACAAGAAAAAAAGGAATTATCTC TGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCATG TGAACATACCTGTAAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCATG AAAATAGTGGTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTT TATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCCTGGAAATCACA GITGGGATAGCACCATICTGGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCACTC CATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAGC CTGGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAAACCAAATGACAG AAGCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGG ACTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACA CTACTGACATCCAAGGAGGAATTTGCCAAAGTTATAGTACAAAAATTGAAAGGTAAACA AACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTAA Gaps ; Indels Length ۲; 1. .2501 /organism="synthetic construct" /mol\_type="unassigned DNA" /bo xref="taxon:32630" /note="N/A" 9 DB Score 812; DB Pred. No. 0; 0; Mismatches ucn al Similarity 99.9%; 862; Conservative 1822 1053 1882 -8 qq ò 임

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AX429236 Sequence 13 from Patent AX429236 AX429236.1 GI:21540548

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1 (bases 1 to 2501)
1 nohara,N., del Peso,L., Koseki,T., Chen,S. and Nunez,G.
RICK, a novel protein kinase containing a caspase recruitment domain, interacts with CLARP and regulates CD95-mediated apoptosis J 8101. Chem. 273 (20), 12296-12300 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 2501)
Inohaza,N., Koseki,T., Chen,S., del Peso,L. and Nunez,G.
Direct Submission
Submitted (01-OCT-1997) Dept. Pathlogy, Comprehensive Cancer &
Geriatrics Center, 4-131 CCGC 1500 E. Medical Center Dr, Ann Arbor,
MI 48109, USA
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                1942 CTTTATTGAAGGTTCTTGGGTAAATATTAGTCTCCCTCCATGACACTGCAGTATTTTTT
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/note="CARD domain protein; phosphorylated protein;
phosphorylated protein; apoptosis regulator"
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/organism="Homo sapiens"
/mol type="mRNA"
/db Xref="taxon:9606"
/chromosome="8"
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                                                                                                                                         Length 2502;
           1 (bases 1 to 2502)
Nunez,G., Inohara,N. and Koseki,T.
Compositions and methods for identifying apoptosis
pathway inhibitors and activators
Patent: US 6348573-A 2 19-PEB-2002,
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/organism="unknown"
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                                                                                                                                                        unclassified.
1 (Dases 1 to 2098)
Boldin,M. and Wallach,D.
MODULATORS OF INTRACELLULAR INFLAMMATION, CELL DEATH AND CELL
SURVIYAL PATHWAYS
PATHWAYS
PATHMAYS
BOLDIN MARK (IL); MALLACH DAVID (IL)
LOCATION/Qualifiers
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    DNA
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46.9%; Score 783; DE
Best Local Similarity 100.0%; Pred. No. 0;
Matches 783; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                               /organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
2098 bp
from Patent WO9855507.
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Mockernan, K.J., Malek, J.A., Gunatrane, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Boutferd, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Stalska, U., Sanilus, D.E.,
Schnerch, A., Schein, J.B., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 1889)

                                                                                                                                                                     1557 CTGGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAAATGACAG
                                                                                                                                                                                                                                     AAGCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGG
   CATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAGC
                                    1497 CATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAGC
                                                                                                                    CTGGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAAATGACAG
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BC004553.2 GI:33871163
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GANISM artificial sequences.

**Tricial sequences**

**Tricial sequ
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100.0%; Pred. No. 0;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Length 1889; Indels 1319

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1140 AGTTACAGAGTGTTTCAAGTGCCATTCACCTATGTGAGAAGAAGAAAATGGAATTATCTC 1199
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 8, clone RP13-706H15
                                      DB 9;
0;
                   43.9%; Scor.
100.0%; Pred. No. v.
... 0; Mismatches
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AC139421.1 GI:28195932
HTG; HTGS PHASE0.
Homo sapiens (human)
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                                Query Match 43.9
Best Local Similarity 100.
Matches 733; Conservative
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/translation="MNGEAICSALPTIPYHKLADLRYLSRGASGTVSSARHADWRVQV
AVKHAHITHYLDSERKOVERARILHKARFSYILPILGICVBEFLGITTERWBNGS
LNELLHRKTEYPDAPELRF HEIFALGWYLHANNFPLLHDLKTQNILLDNEFHV
KTADFGLSKWRMMSLSQSRSSKSABEGGTIIYMPENYEHPDLKTQNILLDNEFHY
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PDBRPSPIRKCLIELEPULETFEITTFEITTFIBAVIQLKKTKLGSVSSAIHLCOKKKMELSLN
IPVNHGPQEESGCSSQLHENGSSPETSRSLPAPQDNDFLSRRAQDVFWKLHFPCPGN
SWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQPGIAQQWIQSKREDIVU
MTRACLNQSLALLSRDLIMKEDYELUSYSKPRTSKVRQLLDTTDIGGEEFAKVIVQK
                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Boutfard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,E.D.
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1508. .1774
/note="CARD, Region: Caspase recruitment domain. Motif contained in proteins involved in apoptotic signaling.

Predicted to possess a DEATH (pfam00531) domain-like fold"
/db_xref="CDD:pfam00619"
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 20127435.
Location/Qualifiers
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/products_receptor_interacting serine-threonine kinase 2"
/protein_id="AAH04553_1"
/db_xref="GI:13528714"
                                                                            Submitted (14-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Thsue Procurement: ATCC/CTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
AND Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replaced gi:13528713.
Contact: MGC help desk
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/mol_type="taxon:9606"

/clone="MGC:10684 IMAGB:4026156"

/tissue_type="Skin, melanotic melanoma."

/lone_lb="NB-NIH MGC 20"

/lab_host="DH108-R"

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/db_xref="MIM:603455"
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/gene="RIPK2"
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Submitted (03-FEB-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker: html
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Center: Whitehead Institute/ MIT Center for Genome Research
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
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Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
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Search completed: April 1, 2004, 08:35:46 Job time : 6746 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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March 29, 2004, 14:25:53; Search time 31.5 Seconds (without alignments) 10193.248 Million cell updates/sec
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283366 segs, 96191526 residues Searched:

Xgapop 60.0 , Xgapext 60.0 Ygapop 60.0 , Ygapext 60.0 Fgapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0

20 Word size:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=Frame+ n2p. model - DEV=xlp
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-Q-/cgn12 | /USFPT0-gpool | DVS09771161/runat\_29032004\_124857 | 14342/app\_query.fasta\_1.1863
-DSE=PIR 78 -QFRT=Fastan - SUFFIX=01120n2p.rpr -MINNATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=01150 -TRANS=human40.cdi
-USFST=0 -UNITS=bits -START=1 -END=-1 -MATRIX=01150 -TRANS=human40.cdi
-USFR=USO9771161 @CGN - HRAPSTIZE=50 -MINLEND - MAXLEN=200000000
-USER=USO9771161 @CGN 1 1 44 @runat\_29032004 124857 14342 -NCPU=6 -ICPU=3
-UN MAAP -LARGEGGERRY -MESS=0 -MAHIT -DSPENCCK=100 -LONGLOG
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6

PIR\_78:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Score Match Length DB Result Š.

Description

No matches found

Search completed: March 29, 2004, 14:36:33 Job time : 31.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using frame_plus_n2p model
  OM nucleic
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Seconds March 29, 2004, 14:23:38; Search time 20.5 Run on:

(without alignments)
8478.545 Million cell updates/sec

US-09-771-161A-2 Title: Perfect score:

1 acctagtttatacccagata...........caacagcctgatgtgaaaa 1669 Sequence:

OLIGO Scoring table:

Xgapop 60.0 , Xgapext 60.0 Ygapop 60.0 , Ygapext 60.0 Fgapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0

141681 segs, 52070155 residues Searched:

20 Word size: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2\_1/USFO spool\_D/US09771161/runat\_29032004\_124856\_14314/app\_query.fasta\_1.1863
-Q=/cgn2\_1/USFO spool\_D/US09771161/runat\_29032004\_124856\_14314/app\_query.fasta\_1.1863
-DB=SwissProt\_42-OFWT=fastan -SUFFIX=oli20n2p.rsp -MINMATCH=0.1 -LGOPCL=0
-LGOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR\_SCORE=quality -THR\_MIN=20 -ALIGN=15 -MODE=LOCAL
-UST=40-NOME=ext -HEAPSIZES=500 -MINLEN=0 -MAXISH=2000000000
-USER=US09771161\_@CGN 1 1 19 @runat\_29032004\_124856\_14314 -NCPU=6 -ICPU=3
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=IO0 -LONGLOG
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LOSPBLOCK=IO0 -KGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DBLOP=6 -DBLDEXT=7

SwissProt 42:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	043353 h receptor- P58801 mus musculu
	540 1 RIK2 HUMAN 539 1 RIK2 MOUSE
08	
Length	540
% Query Match	227 42.7 27 5.1
% ult Query No. Score Match Length DB ID	1 227 42.7 540 1 2 27 5.1 539 1
Result No.	77

### ALIGNMENTS

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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 41, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37)
(RIP-like interacting CLARP kinase) (Receptor-interacting protein 2)
(RIP-2) (CRAD-containing incerleukin-1 beta converting enzyme associated kinase) (CARD-containing IL-1 beta ICE-kinase).
RIPK2 OR RICK OR RIP2 OR CARDIAK.
                                            540 AA
                                            PRT;
                                              .
                                            STANDARD;
```

TISSUE SPECIFICITY: Detected in heart, brain, placenta, lung, peripheral blood leukocytes, spleen, kidney, testis, prostate, pancreas and lymph node.

SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SIMILARITY: Contains 1 CARD domain.

PTM: Autophosphorylated

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RESUBLEACE TO TABORD STATE OF THE STATE OF T
                                                                                                                                        MEDLINE=98241586; PubMed=9575181;
Inohara N., del Peso L., Koseki T., Chen S., Nunez G.;
NICK, a novel protein kinase containing a caspase recruitment domain,
interacts with CLARP and regulates CD95-mediated apoptosis.";
J. Biol. Chem. 273:12296-12300(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98381580; PubMed=9705938;
Jhome M., Hofmann K., Burns K., Martinon F., Bodmer J.-L.,
Mattmann C., Tschopp J.,
"Identification of CARDIAK, a RIP-like kinase that associates with
                           Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.
TISSUB-Endothelial cells;
MEDLINE=99307936; Pubmed=9642260;
MCCarthy Jv., Ni Jv., Ni Jr. V.M.;
"RIP2 is a novel NF-kappaB-activating and cell death-inducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ozersky P., Holmes A., Broy M.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Platzer M., Varon R.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND MUTAGENESIS OF ASP-146.
                                                                                                                      SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.
                                                                                                                                                                                                                                                                                                                                                                                                                    kinase.";
J. Biol. Chem. 273:16968-16975(1998)
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     caspase-1.";
Curr. Biol. 8:885-888(1998).
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                                                                           NCBI_TaxID=9606;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this etatement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334 AsnileProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHisGlu 353
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                                                                                                                                                                                                                                   R GO; GO: 0004674; F: protein serine/threonine kinase activity; TAS.
R GO; GO: 0004871; F: signal transducer activity; TAS.
R GO; GO: 0004871; F: signal transducer activity; TAS.
R GO; GO: 00006915; P: siapptosals; TAS.
R GO; GO: 0007165; P: signal transduction; TAS.
R GO: GO: 0007165; P: signal transduction; TAS.
R InterPro; IPR001315; CARD.
R InterPro; IPR001315; CARD;
R InterPro; IPR001315; CARD; I.
R Pfam; PF00069; PK10389.
R Pfam; PF00069; PK10389.
R PRINTS; PR00109; TYRKINASE.
R PRNATT; SN00114; CARD; I.
R PROSITE; PS50209; CARD; I.
R PROSITE; PS50209; CARD; I.
R PROSITE; PS500107; PROTEIN KINASE DOM; I.
R PROSITE; PS00107; PROTEIN KINASE DAY; FALSE NEG.
R Transferaese; Serine-threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K->A: ABOLISHES KINASE ACTIVITY.
K->M: REDUCES FRA-MEDIATED APOPTOSIS.
D->N: ABOLISHES KINASE ACTIVITY.
575A692239505792 CRC64;
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ATP.
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Matches:
Conservative:
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Indels:
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                                                                                                           EMBL; AF027706; AAC34970.1; EMBL; AF0278530; AAC27722.1; EMBL; AF064824; AAC25668.1; EMBL; AC04003; AAC24561.1; EMBL; AF17829; AAD04634.1; EMBL; BC094553; AAH04553.1; Genew; HGNC.10020; RIPKZ.
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540 AA;
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Best Local Similarity:
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DOMAIN
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                                     413
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                                                                                                                                                                                                                                                                 394 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrPro
                                                                                                     414 CysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro
                                                                                                                                                                                                                                                                                                                                                 474 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr
                                                                                                                                                                                                                                                                                                                                                                                                                             494 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys
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                                                                             TGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAGCCT
                                                                                                                                                           695 GGTATAGCCCCAGCAGTGGATCCAGAGCAAAAGGGGAAGACATTGTGAACCAAATGACAGAA
                                                                                                                                                                                                                                            GCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAGAGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                        875 ACTGACATCCAAGGAGAAGAATTTGCCAAAGTTATAGTACAAAAATTGAAAGATAACAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CS7BL/6;
MEDLINE=21891093; PubMed=11894097;
Chin A.I., Dempsey P.W., Bruhn K., Miller J.F., Xu Y., Cheng G.;
"Involvement of receptor-interacting protein 2 in innate and adaptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRAFE. MAY DESCRIPTION. ACTIVATES PRO-CASPASE-1 and pro-CASPASE-8. Potentiates CASP-8-mediated apoptosis. Activates NF-kappa8 (By similarity).
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- SUBDUIT: Binds to CFLAR/CLARP and CASP1 via their CARD domains.
Binds to BIRC3/C-IAP1 and BIRC2/C-IAP2, TRAFI, TRAF2, TRAF5 and TRAF6. May be a component of both the TNFRSF1A and TNRFSF5/CD40 receptor complex (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- FUM: Autophosphorylated (By similarity).
-!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
-!- SIMILARITY: Contains 1 CARD domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update).
10-OCT-2003 (Rel. 42, Last annotation update)
Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            539 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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P58801;
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LaterPro; Ripk2.

AnterPro; IPR0001315; CARD.

InterPro; IPR0001245; Prot kinase.

BR InterPro; IPR001245; Tyr_Dkinase.

BR Pron; PR001245; Tyr_Dkinase.

BR Pron; PR001245; Tyr_Dkinase.

BR PRINTS; PR00109; PYRXINASE.

BR PRINTS; PR00109; TYRXINASE.

BR PROSTTE; PR500101; PROTEIN KINASE DOM; I.

BR PROSTTE; PS50010; PROTEIN KINASE ATP; FALSE NEG.

BR PROSTTE; PS00107; PROTEIN KINASE ATP; PALSE NEG.

BR PROSTTE; PS00107; PROTEIN KINASE ST; I.

KW PROSTTE; PS00107; PROTEIN KINASE ST; I.

KW POSPHOTYJALLON; APOPTORIN KINASE.

FT DOMAIN 431 523 CARD.

FT RINDING 47 47 3.

TAGT_SITE 146 147 3.

C SEQUENCE 57.
```

Length:
Matches:
Conservative:
Mismatches:
Indels: 4.28e-20 27.00 100.00% 100.00% 5.08% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores:

US-09-771-161A-2 (1-1669) x RIK2\_MOUSE (1-539)

743 CAAATGACAGAAGCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATC 802 ð 요

803 ATGAAAGAGGACTATGAACTT 823

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Search completed: March 29, 2004, 14:32:12 Job time: 22.5 secs

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Command line parameters:
-MODEL_frame+ n2p.model -DEV=Xlp
-MODEL_frame+ n2p.model -DEV=Xlp
-C_GGNZ_1/USFPC_spool p/USC09771161/runat_29032004_124857_14326/app_query.fasta_1.1863
-D=SGPTREMEL_25 -QFMT=fastan -SUFFIX=0.120n2p.rspt -MINNATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -ŪNITS=bits -START=1 -RND=-1 -MATRIX=0.1go -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=20 -ALIGN=15 -MODE=LOCAL
-OUTRAT=ptc -NORM=ext -HRAFSIZE=500 -MINIEN0 -MAXIEN=200000000
-USER=US09771161_@CGN 1 1 95_@runat_29032004 124857_14326 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NGG_SCORES=0 -WAIT -USPBADCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
                                                                                                                                            March 29, 2004, 14:24:58; Search time 87.5 Seconds (without alignments) 12036.569 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                   1 acctagtttatacccagata.......caacagcctgatgtgtaaaa 1669
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                OM nucleic - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1017041 segs, 315518202 residues
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Ygapext 60.0
Fgapext 7.0
Delext 7.0
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sp_human:*
sp_invertebrate:*
sp_mammal:*
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531
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No matches found
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Search completed: March 29, 2004, 14:35:18 Job time : 87.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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RESULT 1

OM protein - protein search, using sw model

March 29, 2004, 14:08:46; Search time 59 Seconds Run on:

(without alignments)
1111.034 Million cell updates/sec

US-09-771-161A-93

232 1 MYSLOLOSVSSAIHLCDKKK.....PEILVVSRSPSLNLLONKSM 232 Perfect score: Sequence:

OLIGO Scoring table:

Gapop 60.0 , Gapext 60.0

1586107 seqs, 282547505 residues Searched:

20

Word size :

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

22

Post-processing: Listing first 45 summaries

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* A\_Geneseq\_29Jan04:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2004s:\* Database :

d. No. is the number of results predicted by chance to have a re greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution. Pred. No. score and

#### SUMMARIES

Description	Aay59406 Human RIC	Aay59405 Human RIC	. Aay59404 Human RIC	Aaw92795 Human B1	Aay68774 Amino aci	Aam93621 Human pol	Aau80369 Human cel	Aae27882 Human rec	Aab43570 Human can	Adc99079 Human KPP	Aay59407 Human RIC	Aay31140 Human CAR	Aab20079 Human CAR	Abg31075 Human cas	Aao22107 Protein o	Abu56269 Human Cas	Adb81362 Human cas	Abu56272 Human CAR	Aao22110 Protein o	Aao22109 Protein o	Abu56271 Human Cas	Abj04754 RICK prot
ID	AAY59406	AAY59405	AAY59404	AAW92795	AAY68774	AAM93621	AAU80369	AAE27882	AAB43570	ADC99079	AAY59407	AAY31140	AAB20079	ABG31075	AA022107	ABU56269	ADB81362	ABU56272	AA022110	AA022109	ABU56271	ABJ04754
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This sequence is a tragment or the number KILK interface included the day cappage during the invention. RICK acts as a positive regulator of apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10 curing capptosis signalling. The invention provides methods for identifying apoptosis signalling. The invention provides methods for identifying apoptosis signalling pathway inhibitors and activators, and methods and compositions for screening compositions dentified: RKC, RICK, and the CIDE family of activators (CIDE-A, CIDE-B and DRED-1). RICK is useful in screening assays for agents, useful in the diagnosis, prognosis or treatment of disease associated with excess cell growth and dysregulation of capptosis. Complexes containing RICK and CLARP can be used in drug screening assays to identify inhibitor molecules blocking CD95-mediated apoptosis. Overexpression of ARC in an in vitro cell system can be used to therapy treatment of disease with increased cell death in muscle tissue therapy treatment of disease with increased cell death in muscle tissue therapy treatment of disease with increased cell death in muscle tissue therapy treatment of disease with increased cell death in muscle tissue can be used as reagents for the preparation of affinity chromotation of the preparation of affinity chromatography media, and for diagnostically measuring RICK levels. A specific inhibitor of an essential step in the biochemistry of apoptosis is needed. RICK interaction with intracellular factors such as CLARP and FADD appears to be essential for apoptosis, inhibitors of RICK levels. This sequence was a specification given in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence is a fragment of the human RICK (RIP-like interacting CLARP
                                                                                                                                                                                                          caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway; CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation; gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS; aplastic anaemia; ischaemic injury; toxin-induced liver disease.
                                                                                                                                                                                          RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Compositions for identifying apoptosis signaling pathway inhibitors
                                                                                                                                                 Human RICK protein sequence residues 248-531.
               AAY59406 standard; protein; 284 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US009183.
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                                                           AAY59406;
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AAY59406
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Gaps

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0; Indels

97.8%; Score 227; DB 3; Le 100.0%; Pred. No. 5.5e-222; ive 0; Mismatches 0;

Best Local Similarity 100.0 Matches 227; Conservative

Query Match

Sequence 284 AA;

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kinase) protein of the invention. RICK acts as a positive regulator of apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10 during CD95 signalling. The invention provides methods for identifying apoptosis signalling. The invention provides methods for identifying compositions for screening compounds which will modulate the interactions of the various compositions identified: ARC, RICK, and the CIDE family of activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening assays for agents, useful in the diagnosis, prognosis or treatment of disease associated with excess cell growth and dysregulation of apoptosis. Complexes containing RICK and CLARP can be used in drug creening assays to identify inhibitor molecules blocking CD95-mediated apoptosis. Overexpression of ARC in an in vitro cell system can be used to therapy treatment of disease with increased cell death in muscle tissue and cardiac disorders. Therapeutic compositions of CIDEs can be used to treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia, ischaemic injury, and toxin-induced liver disease. AntiRICK antibodies can be used can be used as reagents for the preparation or affinity chromatography
LQSVSSAIHLCDKKKWELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDFL 117
                                                           125
                                                                                                                                        GIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRFTSKVRQLLDT 185
                                                                                                                                                                               237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC; caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway; CIDE-A; CIDE-B; DREP-1; disgnosis; cell growth; apoptosis dysregulation; gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS; aplastic anaemia; ischaemic injury; toxin-induced liver disease.
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                                                                                   SRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQP
                                                           SRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQP
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media, and for diagnostically measuring RICK levels. A specific inhibitor of an essential step in the biochemistry of apoptosis is needed. RICK interaction with intracellular factors such as CLARP and FADD appears to be essential for apoptosis, inhibitors of RICK binding to intracellular apoptosis factors are potential drug candidates. Note: This sequence was created using information given in the specification
                                                                                                                                                                                                                                                                                                    125
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                                                                                                                                                                                                                                                     252 LQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDFL
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compositions for screening compounds which will modulate the interactions of the various compositions identified: ARC, RICK, and the CIDE family of activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.8%; Score 227; DB 3; Length 531; 100.0%; Pred. No. 9.9e-222; ative 0; Mismatches 0; Indels
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                                            New B1 protein regulates cell death and cell survival pathways -derivatives, DNA and antibodies, also regulate intracellular inflammation; for treating AIDS, cancer.
                                                                                                                                                       can interact with, intracellular mediators or modulators of inflammation, cell death and/or cell survival pathways, directly or indirectly. Cells can be modulated or mediated in inflammation, cell death or cell survival pathways or another intracellular signalling-activity using B1.
Conditions such as AIDS and cancer can be treated using B1. Antibodies, oligonucleotides and ribozymes can also be used to regulate the above
                                                                                                                                                                                                                                                                                                                                                                                                             373
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                                                                                                                                                                                                                                                                                                                                                                                                                                              66 SRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQP 125
                                                                                                                                          This invention describes the isolation of a novel human B1 protein which
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100.0%; Pred. No. 1e-221;
ive 0; Mismatches 0
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WPI; 1999-070258/06.
N-PSDB; AAX02558.
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Reddy R, Lu DAM, Shih LL;
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22-DEC-1998;
12-JAN-1999;
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03-NOV-1998
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98US-0155196P. 98US-0155239P. 98US-0106889P. 98US-0109093P. 98US-0113796P. 99US-0155233P. 98US-0155213P. 99WO-US017132

Lal P, Tang YT, Corley NC, Guegler KJ, Baughn MR; , Bandman O, Au-Young J, Gorgone GA, Yue H, Azimzai Y;

human phosphorylation effectors useful for the diagnosis, treatment prevention of proliferative, immune and neuronal disorders. and

Claim 1; Page 84-85; 142pp; English.

AAY68769-95 and AAY68797-99 represent human phosphorylation effectors (PHSP), designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not given in the specification). The sequences were isolated from cDNA libraries prepared from various human tissues. The PHSP proteins are useful for the diagnosis, treatment and prevention of proliferative disorders, immune disorders and neuronal disorders. The PHSP proteins form pharmaceutical compositions which useful for treating or preventing disorders associated with decreased PHSP expression/activity. PHSP antagonists are useful for treating or preventing disorders associated with increased PHSP expression/activity.

Sequence 540 AA;

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                                                              114 IQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDFL
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                Length 540;
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                                                                                                                                                                  Human; full length cDNA; cDNA synthesis; oligo-capping
; Score 227; DB 3; Lens
          97.8%; Scor.
100.0%; Pred. No. 100.0%; Mismatches
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                        Best Local Similarity 100.
Matches 227; Conservative
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830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation. 830

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Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y; Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga

WPI; 2001-524255/58. N-PSDB; AAK94554.

11-JAN-2000; 2000JP-00118774.

02-MAY-2000; 2000JP-00183765

(HELI-) HELIX RES INST.

Claim 8; SEQ ID NO 3454; 1380pp + Sequence Listing; English.

The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5' and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length not form DNA of the invention. Note: The sequence data for this patent did format directly from EPO

Sequence 540 AA;

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                                                                                                                             SRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQP 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, virucide, cytomegalovirus infection, CMV; cellular kinase, RICK,
RIP, Nck-Interacting kinase, MKK3; SRPK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying agents for treatment or prevention of cytomegalovirus infection, comprises contacting test compound with cellular kinase and detecting change in cellular kinase activity.
                                                                                                                                                                                     SRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQP
                                                                                                     LQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDFL
                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                              TDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM 540
                       Length 540;
                                                                                                                                                                                                                                                                                                                                                         TDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM
                                                              Indels
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                     Score 227; DB 4;
Pred. No. 1e-221;
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        97.8%; Scor.
100.0%; Pred. No. 10.
10.0%; Pred. No. 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 23-24; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cellular kinase RICK protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU80369 standard; protein; 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2000; 2000US-0240750P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schubart D, Habenberger P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                              Conservative
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                                        Similarity
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                                                            227;
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                       Query Match
Best Local 9
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                                           Best Loca
Matches
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97.8%; Score 227; DB 5; Length 540; 100.0%; Pred. No. 1e-221;

Query Match Best Local Similarity

Sequence 540 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense oligonucleotide that targets regions of a nucleic acid
encoding human receptor interacting protein (RIP)2, for treating diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 SRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQP 125
                                                                                                           SRKAQDCYFMKLHHCPGNHSWDST1SGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQP 125
                                                                                                                                                 SRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQP 433
                                                                                                                                                                                                                                                                     GIAQQWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDT 493
                                  LQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDFL 373
                                                                                                                                                                                                                            GIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65
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LQSVSSAIHLCDKKKMELSLNI PVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; receptor interacting protein; RIP2; antisense; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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100.0%; Pred. No. 1e-221;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                           TDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human receptor interacting protein (RIP)2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 15; Col 49-54; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE27882 standard; protein; 540 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            associated with RIP2 expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-2001; 2001US-00920663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ward DT, Cowsert LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-673017/72.
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Length 544;

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nootropic, anticonvulsant; antiarteriosclerotic; antiasthmatic; immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological; antidiabetic; neuroprotective; osteopathic; antiarthritic; antiparasitic; antihelminthic; antiporal; uropathic; ophthalmological; antiparasitic; antihelminthic; antibocriatic; virucide; protozoacide; fungicide; kinase; phosphatase; KPP; cancer; developmental; mental retadation; neurological; hepatitis; cancer; developmental; mental retadation; neurological; Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's; diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anti-HIV; antiallergic; antiinflammatory; antianaemic; antiparkinsonian;
                                                                                                                                                                                                                                                                                                                       6 LQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDFL
                                                                                                                                                                                                                                                                                                                                                                              318 LQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 GIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    498 TDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 TDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM
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                                                                                                                                                       97.8%; Score 227; DB 3; L. 100.0%; Pred. No. 1e-221; ive 0; Mismatches 0;
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2001US-0333098P.
2001US-0332424P.
2001US-0334288P.
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                                                                                                                                                                                             Local Similarity 100. es 227; Conservative
the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-403214/38.
                                                                               Sequence 544 AA;
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Thornton MB, Tr
Zebarjadian Y;
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16-NOV-2001;
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                                                                                                                                                               Query Match
                                                                                                                                                                                                                                           Matches
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                                 GIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDT 185
                                                                           Human; cancer associated gene; cancer antigen; detection, cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidhabetic; antistentitic; antistritic; antiviral; antiinflammatory; antithyroid; antialeragic; antibacterial; cardiant; dermacological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haemacopoletic cell disorder; autoimmune disorder; haemacopoletic cell disorder; autoimmune disorder; haemostatic; cardiovascular disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer.
                                                                                                                                                                                         TDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cancer associated protein sequence SEQ ID NO:1015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 1595-1597; 2352pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB43570 standard; protein; 544 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAR-2000; 2000WO-US005882.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-587533/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAC77779
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Yue

Duggan BM;
AE, Griffin JA;
Lee EA, Lee SY;
DB, Arvizu CS;
Tang YT;

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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         433
                                                                                                                    The invention relates to a novel isolated polypeptide which is a human kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides, agonists and antagonists are useful for diagnosing, treating or preventing cell proliferative disorders such as atherosclerosis, cirrhosis, hepatitis and cancer, developmental disorders e.g. mental retardation, neurological disorders including Alzheimer's disease and Parkinson's disease, autoimmune and inflammatory disorders such as Crohn's disease and diabetes mellitus and finally, viral, bacterial, fungal, parasitic, protozoan or helminthic infections. Furthermore, the polynucleotides encoding KPP may be useful for creating transgenic animals to model human disease, as well as during gene therapy procedures. The current sequence is that of the human KPP protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                         96 AAFCDHKTTPCSSAIINPLSTAGNSERLQPGIAQQMIQSKREDIVNQMTEACLNQSLDAL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIQGEEFAKVIVQKLKDNKQMGLQPYPEI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  434 LSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIQGEEFAKVIVQKLKDNKQMGLQPYPEI 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway; CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation; gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                        95
                         New human kinases and phosphatases and polynucleotides, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AlDS, allergy or anemia), multiple sclerosis, osteoarthritis, cancer or hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             374 AAFCDHKTTPCSSAIINPLSTAGNSERLQPGIAQQWIQSKREDIVNQMTEACLNQSLDAL
                                                                                                                                                                                                                                                                                                                                                                                                        36 ESCGSSQLHENSGSPETSRSLPAPQDNDFLSRKAQDCYFMXLHHCPGNHSWDSTISGSQR
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aplastic anaemia; ischaemic injury; toxin-induced liver disease.
                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                              84.9%; Score 197; DB 7; Length 510; 100.0%; Pred. No. 3e-191; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human RICK protein sequence residues 365-531.
                                                                                               Claim 1; SEQ ID NO 32; 424pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY59407 standard; protein; 167 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           494 LVVSRSPSLNLLQNKSM 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216 LVVSRSPSLNLLQNKSM 232
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Best Local Similarity 100.
Matches 197; Conservative
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                                                                                                                                                                                                                                                                                                                       Sequence 510 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09955134-A2
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                                                                                                                                                                                                                                                                                             invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY59407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
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This sequence is a trademin or the numera rate, interacting characteristics of the invention. RICK acts as a positive regulator of apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10 during CDSs signalling. The invention provides methods for identifying apoptosis signalling pathway inhibitors and activators, and methods and compositions for screening compounds which will modulate the interactions of the various compositions identified: RC, RICK, and the CIDE family of activators (CIDE-A, CIDE-B and DRE-1). RICK is useful in screening casays for agents, useful in the diagnosis, prognosis or treatment of disease associated with excess cell growth and dysregulation of caspotosis. Complexes containing RICK and CLARP can be used in drug screening assays to identify inhibitor molecules blocking CDS-mediated apoptosis. Ownerspression of ARC in an in vitro cell system can be used to contained the enzymatic activity of caspase-8.

Confidentify inhibitors of the enzymatic compounds may be useful for gene therapy treatment of disease with increased cell death in muscle tissue and candiac disorders. Therapeutic compositions of CIDEs can be useful or to use used as reagents for the preparation or affinity chromatography media, and for diagnostically measuring RICK levels. A specific inhibitor of an essential step in the biochemistry of apoptosis is needed. RICK interaction with intracellular factors such as CLARP and FADD appears to be essential for apoptosis, inhibitors of RICK levels. This sequence was a poptosis factors are potential draw and canding capting information given in the specification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 GIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GIAQQWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDT 120
                                                                                                                                                                                                                                                                                                                                        the human RICK (RIP-like interacting CLARP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRKAODCYFMKLHHCPGNHSWDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                    Compositions for identifying apoptosis signaling pathway inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.0%; Score 167; DB 3; L6
100.0%; Pred. No. 3.3e-161;
ive 0; Mismatches 0;
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Koseki T;
                                                                                                                                                                                                                                                                                                                                sequence is a fragment of se) protein of the inventio
                                                                                                                                                                                                                                                                 Claim 6; Page; 93pp; English.
                                                                                                                                                                                               useful for treating diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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Best Local Similarity 100.
Matches 167; Conservative
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   Inohara N,
                                                                          WPI; 2000-072163/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 167 AA;
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   Ö
       Nunez
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413 PCSSAIINPLSTAGNSERLOPGIAQOWIQSKREDIVNOMTEACLNOSLDALLSRDLIMKE 472

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myelodysplastic syndrome; myocardial infarction; cell proliferation; cell differentiation; cell survival; CARD-4L; CARD-4S; CARD-4Y; CARD-4Z;
spinal muscular dystrophy; cerebellar degeneration; anaemia; drug;
                                                                                                                                                                                                                                                 Novel CARD-3 and CARD-4 genes and polypeptides used or treating regulation of cellular proliferation and differentiation and cell
                                                                            301. .431
/note= "predicted linker domain"
432. .540
                                                                    "predicted kinase domain"
                                                                                                   /note= "predicted CARD domain"
                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                Example 2; Fig 2; 181pp; English.
                                                                                                                                                                      98US-00099041.
                                                                                                                                                 99WO-US002544
                                                                                                                                                               98US-00019942
                                                                                                                                                                                             (MILL-) MILLENNIUM PHARM INC
                                                             1. .300
/note= "
                                                                                                                                                                                                                           WPI; 1999-494269/41.
N-PSDB; AAZ09246.
                                       Homo sapiens
                                                                                                                                                05-FEB-1999;
                                                                                                                  WO9940102-A1
                                                                                                                                                                       17-JUN-1998;
08-DEC-1998;
                                                                                                                                                                06-FEB-1998;
                                                                                                                                  12-AUG-1999
                                                                                                                                                                                                             Bertin J;
                                                                                                                                                                                                                                                                   survival
                         human.
                                                             Domain
                                                                            Domain
                                                                                            Domain
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This invention describes the isolation of novel human caspase recruitment domain, CARD-3 and CARD-4 polynucleotides and proteins and a partial article for the invention are involved in the regulation of caspase activation. The caspase cartivation are involved in the regulation of caspase activation. The caspase and articlodies can be used in screening assays, polypeptides, homologues and medicine and therapeutic and prophylactic methods of treatment. The medicine and therapeutic and prophylactic methods of treatment. The medicine and therapeutic and prophylactic methods of treatment. The medicine associated with abnormal level or rate of apoptotic cell death, abnormal activity of the TMF receptor complex, or abnormal activity of a caspase. Since that may be treated include cancer (particularly follicular lymphoma, carcinomas associated with mutations in p53 and hormone-cappendent tumours), autoimmune disorders (e.g. systemic lugus erythematosis, immune-mediated glomerulonephritis), viral infections, Alzheimer's disease, Parkinson's disease, amyocirophic lateral sclerosis, retuinitis pigmentosa, spinal muscular dystrophy, cerebellar degeneration, anaemia, myelodysplastic syndrome, myocardial infarction, and stroke.

CARD-3 protein interacts with other cellular proteins, and so can be used for regulation of cellular proliferation and differentiation and cell survival. The CARD proteins may also be used to for screen drugs or compounds which modulate their activity. The CARD-4 spen can express a long transcript that encodes CARD-4, a short transcript that encodes CARD-4s and CARD-4s and cARD-42. This sequence in expersents the human CARD-13 protein described in the method of the invention

Query Match

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Sequence 540 AA;

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0
                                                                            105 PCSSAIINPLSTAGNSERLQPGIAQQMIQSKREDIVNQMTEACLNQSLDALLSRDLIMKE 164
                                           Gaps
                                           ;
0
55.2%; Score 128; DB 2; Length 540; 100.0%; Pred. No. 4.4e-121; ive 0; Mismatches 0; Indels
                                       Conservative
                    Best Local Similarity
Matches 128; Conserva
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The present sequence is that of human caspase recruitment domain 3 (CARD-3), an intracellular protein predicted to be involved in regulating caspase activation. The sequence is predicted from an isolated cDNA clone (see AAR30001). Methods of diagnosing and treating patients suffering from a disorder associated with an abnormal level or rate of apoptotic cell death, abnormal activity of the Ras/APO-1 receptor complex, abnormal activity of the traceptor receptor complex, abnormal activity of a caspase involve administering a compound that modulates the expression or activity of CARD-3, CARD-5 or CARD-6 e.g. using expression or activity of CARD-3, CARD-6, CARD-6 or CARD-6 e.g. using autoimmune disorders, neurological disorders, hamatoly disorders include cancer, viral infection, autoimmune disorders and immune disorders. CARD-3, -4, -5 and -6 inflammatory disorders and immune disorders. CARD-3, -4, -5 and -6 conceins can be used to regulate cell proliferation, cell survival and cell growth. They can also be used to screen drugs or compounds that modulate their activity or expression and to treat disorders associated 224 532 Isolated intracellular proteins predicted to be involved in regulating caspase activation are used for diagnosis and treatment of e.g. cancer, viral infections, autoimmune diseases, neurological diseases and CARD-3; caspase recruitment domain; human; cancer; infection; autoimmune disease; neurological disease; haematological disease; inflammation; antitumour; antiseptic; immunomodulator; antiinflammatory; apoptosis; diagnosis; gene therapy. DYELVSTKPTRTSKVRQLLDTTD1QGEFAKV1VQKLKDNKQMGLQPYPE1LVVSRSPSL DYELVSTKPIRTSKVRQLLDTTDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSL 1. .400 /note= "kinase domain" 401. .431 /note= "linker domain" Location/Qualifiers AAB20079 standard; protein; 540 AA. Claim 9; Fig 2; 208pp; English. 432. .540 /note= "CARD" 28-JUN-2000; 2000WO-US017691. 99US-00340620 (MILL-) MILLENNIUM PHARM INC (first entry) hematological disorders. NLLQNKSM 232 NLLQNKSM 540 Human CARD-3 protein. WPI; 2001-061973/07. N-PSDB; AAF30001. WO200100826-A2 28-JUN-1999; Homo sapiens 23-APR-2001 04-JAN-2001 473 Bertin J; 165 225 533 AAB20079; Key Domain Domain Domain RESULT 13 AAB20079 셤 g à ò

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US6369196-B1.
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                                                                                                                                                                                                                                                                Query Match
Best Local S
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                                                                                                         164
                                                                                                                                                      224
                                                                                                                                                                              532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to identifying (M1) a compound which modulates a human or marine caspase recruitment domain (CARD)-4L (Iong form) polypeptide with a by contracting the polypeptide with a test compound and determining the effect of the test compound on the activity of the polypeptide to identify a compound which modulates the polypeptide. The method may be adapted for identifying a compound which binds to the LRR (leucine rich repeat) domain of CARD-4. Also included is a method of
                                                                                                                              472
                                                                                                                                                                                                                                                                                                                                                                               Human; caspase recruitment domain; CARD-3; CARD-4; IRR; leucine rich repeat; LPS; lipopolysaccharide; NF-kB; nuclear factor-kappa B; cancer; viral infection; autoimmune disorder; systemic lupus erythematosus; immune-mediated glomerulonephritis; arthritis; immune disorder; multiple sclerosis; Hashimoto's thyroiditis; atopic condition; asthma; allergy; psoriasis; contact dermatitis; gastrointestinal allergy; insulin-dependent diabetes; bacterial infection; tuberculosis; lepromatous leprosy; cell signalling disorder; tissue disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARD-
                                                                                                                       PCSSAIINPLSTAGNSERLQPGIAQQMIQSKREDIVNQMTEACLNQSLDALLSRDLIMKE
                                                                                                                                                                    PCSSAIINPLSTAGNSERLQPGIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKE
                                                                                                                                                      DYELVSTKPTRTSKVRQLLDTTDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSL
                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying modulators of long form of caspase recruitment domain, (4L useful for treating cancer, infections, and immune disorders, by contacting test compound with CARD-4L and determining effect of the
 9-
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  or
 CARD-3, -4, -5
                                                         55.2%; Score 128; DB 4; Length 540; 100.0%; Pred. No. 4.4e-121; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Girardin S;
                                                                                                                                                                                                                                                                                                                                                             Human caspase recruitment domain protein CARD-3.
with insufficient or excessive production of (
protein, or production of an aberrant protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sansonetti P,
                                                                                                                                                                                                                                                                                         ABG31075 standard; protein; 540 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Fig 2; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-DEC-2001; 2001WO-US049798.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                  Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bertin J, Philpott D,
                                                                                                                                                                                                     NLLQNKSM 232
                                                                                                                                                                                                                             533 NLLQNKSM 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-583627/62.
                                                                      Similarity
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                                  Sequence 540 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                         105
                                                                                                                              413
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                                                          Query Match
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                                                                      Local
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ABG31075
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mediated activation of nuclear factor-kappa B (NF-kB), by providing a call expressing a polypeptide comprising the LRR domain of CARD-4 and call expressing a polypeptide comprising the LRR domain of CARD-4 and harbouring LPS, exposing the cell to a test compound and measuring NF-kB activation, where altered NF-kB activation polypeptide in the presence of the test compound compared to the binding in the absence of the test compound indicates that the test compound is a candidate compound for modulating LPS-mediated activation of NF-kB. Modulators identified by CKM) are useful for treating a disorder characterised by aberrant CARD-4 protein or nucleic acid. Compounds that medulate the activity of CARD-44 are useful to treat or diagnose disorders such as cancer, viral continented disorders e.g. systemic lupus erythematosus, immune-mediated glomerulonephritis and arthritis, immune disorders, such as multiple sclerosis, Hashimoto's thyroiditis, atopic conditions such as an ultiple sclerosis, Hashimoto's thyroiditis, gastrointestinal callergies, insulin-dependent diabetes, bacterial infections, including tuberculosis, and lepromatous leptosy, disorders of cell signalling and disorders of tissues. The present sequence represents human CARD-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytostatic, virucide, immunomodulatory, neuroprotective; antialzheimers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cerebroprotective; antiparkinsonian; antisclerotic; ophthalmological; nootropic; antianaemic; Caspase Recruitment Domain; CARD; CARD-41; p53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 DYELVSTKPTRTSKVRQLLDTTDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSL
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100.0%; Pred. No. 4.4e-121;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein of human CARD-3 SEQ ID No 2.
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WPI; 2002-391988/42.
N-PSDB; AAL40752, AAL40753.
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Isolated Caspase Recruitment Domain (CARD) polypeptides (CARD-4L and CARD-4S) useful for diagnosing and treating e.g. Parkinson's and Alzheimer's disease, cancers and viral infections.

# Example 2; Fig 2; 116pp; English

The invention relates to novel isolated Caspase Recruitment Domain (CARD) polypeptides, CARD-4L and CARD-4S. The CARD proteins of the invention may be used to treat disorders associated with decreased CARD expression by supplementing the patient's own production of CARD. Disorders associated with the expression and activity of CARD include cancers (particularly follicular lymphomas, carcinomas associated with mutations in p53, and normone-dependent tumours such as breast cancer, prostate cancer, and ovarian cancer), autoimmune-mediated glomerulonephritis), viral infections erythematosus, immune-mediated glomerulonephritis), viral infections (such as those caused by herpes viruses, postviruses, and ademoviruses), neurological diseases (such as Alzeimer's disease, Parkinson's disease, amylotrophic lateral sclerosis (ALS) retinitis pigmentosa, spinal muscular atrophy, and various forms of cerebellar degeneration), anaemia associated with chronic disease, aplastic anaemia, and the myelodysplastic syndromes. This sequence represents a human CARD protein relating to the invention

## Sequence 540 AA;

PCSSAIINPLSTAGNSERLQPGIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKE 472 105 PCSSALINPLSTAGNSERLQPGIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKE 164 473 DYELVSTKPIRTSKVRQLLDTTDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSL 532 DYELVSTKPTRISKVROLLDTTDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSL 224 0; Gaps 55.2%; Score 128; DB 5; Length 540; 100.0%; Pred. No. 4.4e-121; 0; Indels 100.0%; Pred. nc. Best Local Similarity 100. Matches 128; Conservative 413 165 Query Match g g ò

Search completed: March 29, 2004, 14:12:52 Job time : 60 secs

NLLQNKSM 232 NLLONKSM 540

225 533

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                   Copyright
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OM protein - protein search, using sw model
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March 29, 2004, 14:11:47 ; Search time 22 Seconds
(without alignments)
544.419 Million cell updates/sec Run on:

232 1 MYSLQLQSVSSAIHLCDKKK.....PEILVVSRSPSLNLLQNKSM 232 US-09-771-161A-93 Perfect score:

Sequence:

Gapop 60.0 , Gapext 60.0 OLIGO Scoring table:

389414 segs, 51625971 residues

Searched:

Total number of hits satisfying chosen parameters: 20 Word size :

25

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Issued Patents AA:\*

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(cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Sequence 5,	Seguence 4,	3 Sequence 3,	1 Sequence 1,	27 Sequence 27,	28 Sequence 28,	6 Seguence 6,	1 Sequence 1,	-2 . Sequence 2,	Sequence 2,	1 Sequence 1,	Sequence 2,	-2 Sequence 2,	Sequence 2,	_	6 Sequence 6,	Sequence 6,	6 Seguence 6,	Sequence 6,	Sequence 6,		Seguence 5,	Seguence 5,		S entraines
QI	US-09-069-023-	US-09-069-023-4	US-09-069-023-	US-09-069-023-	US-09-069-023-	US-09-345-473E-			US-09-099-041A	US-09-245-281-	US-09-470-271-	US-09-207-359B-	US-09-340-620A	US-09-865-364-	US-09-748-537-1	US-09-207-359B-6		US-09-099-041A-6	US-09-245-281-6	US-09-340-620A-6	US-09-099-041A-5	US-09-245-281-5	US-09-207-359B-5	US-09-340-620A-5	110-00-065-364-0
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Length	284	478	530	531	540	540	167	540	540	540	540	540	540	540	540	110	110	109	109	109	131	131	131	131	121
% Query Match	97.8	97.8	97.8	97.8	97.8	97.8	72.0	55.2	55.2	55.2	55.2	55.2	55.2	55.2	55.2	47.4	47.4	47.0	47.0	47.0	42.2	42.2	42.2	42.2	42.2
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## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 GIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDT 237
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                                                              GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Inhohara, Machino
APPLICANT: Inhohara, Machino
APPLICANT: Moschi, Takeyoshi,
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
CURRENT APPLICATION NUMBER: US/09/069,023A
CURRENT FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 5.
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APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohiro
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS.AND ACTIVATORS
FILE REFERENCE: UM-03333
CURRENT APPLICATION NUMBER: US/09/069,023A
CURRENT FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 284;
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hes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                97.8%; Score 227; DB 4; Le
100.0%; Pred. No. 3.9e-220;
ive 0; Mismatches 0;
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100.0%; Pred. No. 6.2e-22;
iive 0; Mismatches 0
US-09-069-023-5; Sequence 5, Application US/09069023A; Patent No. 6348573
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US-09-069-023-4
; Sequence 4, Application US/09069023A
; Patent No. 6448573
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 227; Conservative
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Matches 227; Conservative
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ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-09-069-023-5
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TYPE: PRT
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                                      SRKAQDCYFMKLHHCPGNHSWDST1SGSQRAAFCDHKTTPCSSA1INPLSTAGNSERLQP
                                                                                                                 6 LOSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDFL
                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09069023A

Patent No. 6348573
GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Nonez, Gabriel
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
CURRENT APPLICATION NUMBER: US/09/069,023A

CURRENT FILING DATE: 1998-04-27

NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Inchara, Nachiro
APPLICANT: Inchara, Nachiro
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
CURRENT APPLICATION UMBER: US/09/069,023A
CURRENT FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
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Best Local Similarity 100.
Matches 227; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 530
TYPE: PRT
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US-09-069-023-3
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LENGTH: 531
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Patent No. 6348573

GENERAL INFORMATION

APPLICANT: Nunez, Gabriel

APPLICANT: Inohara, Nachiro

APPLICANT: Inohara, Nachiro

APPLICANT: East Takeyoshi

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS

TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS

TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS

CURRENT APPLICATION NUMBER: US/09/069,023A

CURRENT FILING DATE: 1998-04-27

NUMBER OF SEQ ID NOS: 38

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 27

IENGTH: 540

TENGTH: 540

TENGTH: 540

US-09-069-023-27
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                                                                   Length 531;
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                                                                                           6.9e-220;
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100.0%; Pred. No. 7e-220;
ive 0; Mismatches 0;
                                                                   97.8%; Score 227; DB 4;
100.0%; Pred. No. 6.9e-22
ive 0; Mismatches 0
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US-09-345-473E-28
; Sequence 28, Application US/09345473E
; Patent No. 6558903
; GENERAL INFORMATION:
                                                                   Query Match
Best Local Similarity 100.0
Matches 227; Conservative
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Best Local Similarity 100.
Matches 227; Conservative
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ORGANISM: Homo sapiens
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Sequence 1, Application US/09019942
Patent No. 6033855
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Sequence 6, Application US/09069023A

Sequence 6, Application US/09069023A

GENERAL INFORMATION:

APPLICANT: Nunez, Gabriel

APPLICANT: Inohara, Nachiro

APPLICANT: Inohara, Nachiro

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS

TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS

FILE REFERENCE: UM-0333

CURRENT APPLICATION NUMBER: US/09/069,023A

CURRENT FILING DATE: 1998-04-27

NUMBER OF SEQ ID NOS: 38

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 6
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                                                                                                                                                                                                                                                                                  Query Match 97.8%; Score 227; DB 4; Length 540; Best Local Similarity 100.0%; Pred. No. 7e-220; Matches 227; Conservative 0; Mismatches 0; Indels
  TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof
FILE REFERENCE: 35800/183781
                                         CURRENT APPLICATION NUMBER: US/09/345,473E
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 62
SEQ ID NO 28
LENGTH: 540
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TYPE: PRT
CRGANISM: Homo sapiens
US-09-069-023-6
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ORGANISM: Homo sapiens
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US-09-069-023-6
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RESULT 8 US-09-019-942-1

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105 PCSSAIINPLSTAGNSERLQPGIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKE 164
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Batent No. 6340576

GENERAL INFORMATION:

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

FILE REFERENCE: 07334-076001

CURRENT APPLICATION NUMBER: US/09/099,041A

CURRENT FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                 APPLICANT: Bertin, John
TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
TITLE OF INVENTION: DOMAIN POLYBEPTIDES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADBRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.2e-120;
                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,942
FILING DATE: 06-FEB-1998
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
RICHARD SAME NORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
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ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 200154
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 540 amino acids
amino acid
                                                                                                                                                                                                          STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.0
Matches 128; Conservative
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GENERAL INFORMATION:
                                                                                                                                                                                       Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-099-041A-2
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LENGTH:
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APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES-OF THE CARD-RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REPRENCE: 0734/118001
CURRENT APPLICATION NUMBER: US/09/245,281
CURRENT PILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: US 09/207,359
EARLIER FILING DATE: 1998-12-08
EARLIER PILING DATE: 1998-06-17
EARLIER PILING DATE: 1998-06-17
EARLIER FILING DATE: 1998-06-06
NUMBER OF SEQ ID NOS: 44

SOFTWARE: FASTEN FARENCE: 1998-06-06

LENGTH: 5-0
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                                                                                                                                            55.2%; Score 128; DB 4; L6 100.0%; Pred. No. 2.2e-120; ive 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: GENES ENCOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09245281
Patent No. 6369196
GENERAL INFORMATION:
                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 128; Conservative
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                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-091A-2
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-09-245-281-2
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413 PCSSAIINPLSTAGNSERLQPGIAQQWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKE 472
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; Sequence 2, Application US/09207359B
; Patent No. 6469140
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: NOWBER: US 09/09/207,359B
; CURRENT APPLICATION NUMBER: US 09/09/207,359B
; CURRENT FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastESEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/470,271
FILING DATE:
APPLICATION NUMBER: 09/019,942
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/068001
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELEFRONE: 617/542-5070
                              Richardson P.C.
CORRESPONDENCE ADDRESS:
ADDRESSEB: Fish & Richardsc
STREET: 225 Franklin Street
CITY: Boston
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-09-470-271-1
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ORGANISM: Homo sapiens
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USA
                                                                                                                   STATE: M2
COUNTRY:
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APPLICANT: Bertin, John
APPLICANT: Bertin, John
APPLICANT: Chao, Mosee Wolf Culture, Grand-Related Protein Famile AND USES THEREC
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILE AND USES THEREC
FILE REFERENCE: 07334-316001
CURRENT APPLICATION NUMBER: US/09/748,537
CURRENT FILING DATE: 2000-112-26
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR PILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PREASEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 540
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PRIOR APPLICATION NUMBER: US 09/207,359
PRIOR FILING DATE: 1998-12-08
PRIOR FILING DATE: 1998-12-08
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 47-
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2.
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; Sequence 1, Application US/09748537
; Patent No. 6680167
                                                                                                                                                                                                                                                                                                                                                                                 Matches 128; Conservative
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ORGANISM: Homo sapiens
US-09-865-364-2
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ORGANISM: Homo sapiens
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Best Local Similarity
                                                                                                                                                                                                                   LENGTH: 540
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TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
FILE REFERENCE:: 07334-124001
                                                                                                                                                                            413 PCSSAIINPLSTAGNSERLQPGIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKE 472
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                                                   Query Match 55.2%; Score 128; DB 4; Length 540; Best Local Similarity 100.0%; Pred. No. 2.2e-120; Matches 128; Conservative 0; Mismatches 0; Indels
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Parent No. 6613521
GENERAL INFORMATION:
APPLICANT: BETTIN, JOHN
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-112001
CURRENT APPLICATION NUMBER: US/09/865;364
CURRENT FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT PEDILCATION NUMBER: US/09/340,620A
CURRENT FILING DATE: 1999-06-28
PRIOR APPLICATION NUMBER: US 09/245,281
PRIOR PILING DATE: 1999-02-05
PRIOR FILING DATE: 1998-12-08
PRIOR FILING DATE: 1998-12-08
PRIOR FILING DATE: 1998-12-08
PRIOR FILING DATE: 1998-06-17
PRIOR PELING DATE: 1998-06-17
PRIOR PELING DATE: 1998-06-17
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 71
SOFTWARE: FASTESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09340620A
Patent No. 6482933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
       US-09-207-359B-2
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US-09-865-364-2
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Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 10, Appl Sequence 10, Appl

Title: Perfect score:

Sequence:

OM protein

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Scoring table:

Word size :

Searched:

Database :

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DNDFLSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNS 120
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100.0%; Pred. No. 6.6e-218;
ive 0; Mismatches 0;
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Patent No. US20020110811A1
GENERAL INFORMATION:
TITLE OF INVENTION: et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT FILING DATE: 2001-01-26
PRIOR PILING DATE: 2000-11-28
PRIOR PILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-11-26
PRIOR FILING DATE: 2000-11-26
PRIOR FILING DATE: 2000-11-26
PRIOR FILING DATE: 2000-01-26
PRIOR FILING DATE: 2000-01-26
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APPLICANT: LEVINE, et al.

TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILLE REPERENCE: 802620-2005.1

CURRENT APPLICATION NUMBER: US/09/771,161A

CURRENT FILING DATE: 2001-01-26

PRIOR PILLING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: 136776

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-04-12

NUMBER OF SEQ ID NOS: 273

SOFTWARE: Patentin version 3.0

SEQ ID NO 93

LENGTH: 232
                US-10-105-931-5

US-10-118-984-5

US-10-118-984-5

US-10-014-269-21

US-10-014-269-21

US-10-014-506-21

US-09-931-071-11
                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 93, Application US/09771161A Patent No. US20020110811A1 GENERAL INFORMATION:
  Query Match 100.
Best Local Similarity 100.
Matches 232; Conservative
131
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ORGANISM: Homo sapiens
US-09-771-161A-184
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Sequence 14, Appl
Sequence 1015, Ap
Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
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Sequence 6, Appli
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Sequence 184, App
Sequence 28, Appl
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1411.757 Million cell updates/sec
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US-09-771-161A-184
US-09-862-027-28
US-09-981-397A-14
US-09-925-301-1015
US-09-748-537-1
US-09-748-537-1
US-09-748-537-1
3 US-10-133-780-1
3 US-10-139-984-2
1 US-10-295-981-2
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                     GenCore version (c) 1993 - 2004
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Maximum DB seq length: 2000000000
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Match Length DB
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US-10-105-931-6 US-10-118-984-6 US-10-295-981-6

Score

Result

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0; Gaps

Length 232; 0; Indels

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Fatent No. US2002014428A1

GENERAL INFORMATION:

FAPLICANT: Hodge, Martin R.

TITLE OF INVENTION: No. US20020142428A1e1 Kinases and Uses Thereof

TITLE OF INVENTION: No. US2002014228A1e1 Kinases and Uses Thereof

CURRENT APPLICATION NUMBER: US/09/862,027

CURRENT PILING DATE: 2001-05-21

FRIOR FILING DATE: 1999-06-30

FRIOR FILING DATE: 1999-06-30

NUMBER OF SEQ ID NOS: 82

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 540
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                                                                                                                                                                                                             97.8%; Score 227; DB 9; Length 540; 100.0%; Pred. No. 1.1e-212; ive 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: Patentin version 3.0
SEQ ID NO 184
LENGTH: 540
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Best Local Similarity 100.(
Matches 227; Conservative
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ORGANISM: Homo sapiens
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US-09-771-161A-184
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Best Local Similarity
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US-09-862-027-28
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RESULT

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APPLICANT: Schubart, Daniel
APPLICANT: Schubart, Daniel
APPLICANT: Habenberger, Peter
APPLICANT: Habenberger, Peter
APPLICANT: Stein-Gerlach, Matthias
APPLICANT: Bevec, Dorian
TITLE OF INVENTION: Callular Kinases Involved in Cytomegalovirus Infection and their
TITLE OF INVENTION: Inhibition
FILE REPERRNCE: AXM-004.1 US
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: 00/240,750
PRIOR APPLICATION NUMBER: 60/240,750
PRIOR PILING DATE: 2000-10-16
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 GIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRISKVRQLLDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 LOSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPRENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR PILING DATE: 1999-03-12
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Parentin Ver. 2.0
SEQ ID NO 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.8%; Score 227; DB 10; Length 540; 100.0%; Pred. No. 1.1e-212; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 TDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM 232
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0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.1e-212;
Matches 227; Conservative 0; Mismatches 0;
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Sequence 1015, Application US/09925301

; Patent No. US20020052308A1

; GENERAL INFORMATION:
Sequence 14, Application US/09981397A Publication No. US20030082519A1 GENERAL INFORMATION:
                                                                                             APPLICANT: Axxima Pharmaceuticals AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 227; Conservative
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TYPE: PRT
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105 PCSSAIINPLSTAGNSERLQPGIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKE 164
                                                                                                                                                                                                                                                                                                          472
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                                                                                                                                                                        55.2%; Score 128; DB 9; Length 540; 100.0%; Pred. No. 4e-116; Live 0; Mismatches 0; Indels
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; Publication No. US20020123115A1
; GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
DOMAIN POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
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APPLICATION NUMBER: US/10/133,780
FILING DATE: 26-Apr-2002
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/019,942
FILING DATE: 06-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Weiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/068001
TELEFORMUNICATION INFORMATION:
TELEFORM: 617/542-6970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Richardson P.C.
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
LENGTH: 540
; TYPE: PRT
GRANISM: HOMO Sapien8
US-09-728-721-2
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardso
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 540 amino acids TYPE: amino acid
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SEQUENCE CHARACTERISTICS
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Matches 128; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                           225 NLLQNKSM 232
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COUNTRY: USA
                                                                                                                                                                          Query Match
Best Local Similarity
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Sequence 2, Application US/09728721
Patent No. US20020061845A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
FILE REFERENCE: 07334-124001
CURRENT PAPLICATION NUMBER: US/09/728,721
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: 09/340,620
PRIOR APPLICATION NUMBER: US 09/207,359
PRIOR FILING DATE: 1998-10-08
PRIOR FILING DATE: 1998-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bertin, John
APPLICANT: Chao, Moses V.
APPLICANT: Chao, Moses V.
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILE AND USES THERE
PILE REFERENCE: 07334-316001
                                                                                                                                                            DYELVSTKPTRISKVRQLLDTTDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSL 224
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                                                                                        437
                                                                                                                                 GIAQOWIQSKREDIVNOMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDT 185
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    LQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDFL 377
                                                                        SRKAQDCYFWKLHHCPGNHSWDST1SGSQRAAFCDHKTTPCSSA11NPLSTAGNSERLQP
                                                  SRKAODCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/748,537
CURRENT FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09748537 Patent No. US20020061833A1 GENERAL INFORMATION:
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GRGANISM: Homo sapiens
US-09-748-537-1
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RESULT 11
US-10-295-981-2
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413 PCSSAIINPLSTAGNSERLQPGIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKE 472
                                                                                 413 PCSSAIINPLSTAGNSERLQPGIAQOWIOSKREDIVNOMTEACLNOSLDALLSRDLIMKE 472
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Sequence 2, Application US/10118984

Publication No. US20020197693A1

Publication No. US20020197693A1

TITLE OP INVENTION:

TITLE OP INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY

TITLE OP INVENTION: NOVEL 1001

CURRENT PELICATION NUMBER: US/10/118,984

CURRENT FILING DATE: 2002-04-09

PRIOR PELICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281

PRIOR PILICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/207,359

PRIOR PILING DATE: EARLIER FILING DATE: 1999-02-05

PRIOR PILING DATE: EARLIER FILING DATE: 1998-12-08

PRIOR PILING DATE: EARLIER FILING DATE: 1998-02-05

PRIOR PILING DATE: EARLIER FILING DATE: 1998-02-05

PRIOR PILING DATE: EARLIER FILING DATE: 1998-02-06

PRIOR PILING DATE: EARLIER FILING DATE: 1998-02-06

PRIOR PILING DATE: EARLIER FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 44
                                                       165 DYELVSTKPTRISKVRQLLDTTDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSL
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Sequence 2, Application US/10105931

Bublication No. US20020150987A1

GENERAL INFORMATION:
TITLE OF INVENTION: John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

FILE REFERENCE: 07334-07601

CURRENT APPLICATION NUMBER: US/10/105,931

CURRENT FILING DATE: 2002-03-25

PRIOR APPLICATION NUMBER: 09/099,041

PRIOR PILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Homo sapiens
US-10-105-931-2
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nes 128; Conserv
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Sequence 2, Application US/10295981

Publication No. US20030120055A1

GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE.

TITLE OF INVENTION: NOWEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE.

TOURERN APPLICATION NUMBER: US/10/295,981

CURRENT FILING DATE: 1099-02-10-15

PRIOR FILING DATE: 1099-02-05

PRIOR FILING DATE: 1099-02-05

PRIOR FILING DATE: 1099-02-05

PRIOR PLING DATE: 1099-02-06

PRIOR FILING DATE: 1999-02-06

PRIOR FILING DATE: 1999-02-06

NUMBER OF SEQ ID NOS: 71

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 540

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          413 PCSSAIINPLSTAGNSERLQPGIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 DYBLVSTKPTRTSKVRQLLDTTDIQGEBFAKVIVQKLKDNKQMGLQPYPBILVVSRSPSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 540;
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100.0%; Pred. No. 4e-116;
iive 0; Mismatches 0;
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-09-728-721-6
Sequence 6, Application US/09728721
Patent No. US20020061845A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 128; Conservative
                                                                                      LENGTH: 540
TYPE: PRT
CRGANISM: Homo sapiens
US-10-118-984-2
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Best Local Similarity
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APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREC
FILE REFERENCE: 07334-124001
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                    GENERAL INFORMATION:
APPLICANTON
APPLICANTON
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
APPLICANTON
TITLE OF INVENTION:
TITLE OF INVENTION:
AND USES THEREOF
FILE REFERENCE: 07334/118001
CURRENT APPLICATION NUMBER: US/10/118,984
CURRENT FILING DATE: 2002-04-09
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US/09/245,281
PRIOR PELICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/207,359
PRIOR PLING DATE: EARLIER PILING DATE: 1998-12-08
PRIOR PLING DATE: EARLIER FILING DATE: 1998-12-08
PRIOR PELING DATE: EARLIER FILING DATE: 1998-02-06
PRIOR PELING DATE: EARLIER FILING DATE: 1998-02-06
PRIOR PELING DATE: EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FASTER APPLICATION NUMBER: US 09/019,942
NUMBER OF SEQ ID NOS: 44
SEQ ID NOS: 44
SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QPGIAQQWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 QPGIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.0%; Score 109; DB 13; Length 109; 100.0%; Pred. No. 3.4e-98; rive 0; Mismatches 0; Indels
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100.0%; Pred. No. 3.4e-98;
ive 0; Mismatches 0;
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CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: US/09/340,620
PRIOR FILING DATE: 1999-06-28
PRIOR FILING DATE: 1999-06-28
PRIOR FILING DATE: 1999-06-05
PRIOR PILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: US 09/207,359
PRIOR APPLICATION NUMBER: US 09/207,359
PRIOR PILING DATE: 1998-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-295-981-6; Sequence 6, Application US/10295981; Publication No. US20030120055A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-118-984-6
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APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/10105931
| Publication No. US20020150987A1
| GENERAL INFORMATION:
| TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED |
| TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF |
| TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF |
| TITLE OF INVENTION: NUMBER: US/10/105,931 |
| CURRENT APPLICATION NUMBER: 09/099,041 |
| PRIOR FILING DATE: 1998-06-17 |
| PRIOR FILING DATE: 1998-06-17 |
| PRIOR FILING DATE: 1998-06-17 |
| NUMBER OF SEQ 10 NOS: 37 |
| SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 3.4e-98;
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Pred. No. 3.4e-98;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.0%; Scc...
V 100.0%; Pred. No. 3...
O; Mismatches
                                                   TILE REFERENCE: 07334-12401

CURRENT APPLICATION NUMBER: US/09/728,721

CURRENT FILMG DATE: 2000-12-01

PRIOR PELLING DATE: 1999-06-28

PRIOR PELLING DATE: 1999-06-28

PRIOR PELLING DATE: 1999-12-08

PRIOR PELLING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: US 09/099,041

PRIOR PELLING DATE: 1998-06-17

PRIOR PELLING DATE: 1998-06-17

PRIOR FILING DATE: 1998-02-06

PRIOR FILING DATE: 1998-02-06

PRIOR FILING DATE: 1998-02-06

PRIOR FILING DATE: 1998-02-06
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100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 109; Conservative
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, ORGANISM: Homo sapiens
US-10-105-931-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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Best Local Similarity
Matches 109; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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US-10-118-984-6
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Search completed: March 29, 2004, 14:16:23 Job time : 43 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

March 29, 2004, 14:10:51; Search time 20 Seconds (without alignments) 1115.822 Million cell updates/sec

US-09-771-161A-93 232 1 MYSLQLQSVSSAIHLCDKKK......PEILVVSRSPSLNLLQNKSM 232 Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

283366 seqs, 96191526 residues

Searched:

Word size :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description Query Score Match Length DB ID

No matches found

No. Result

Search completed: March 29, 2004, 14:14:52 Job time : 20 secs

Ipis bade Blank (nsbto)

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version 5.1.6
- 2004 Compugen Ltd.
GenCore (c) 1993
           Copyright
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OM protein - protein search, using sw model

March 29, 2004, 14:09:41; Search time 17 Seconds (without alignments) 710.604 Million cell updates/sec Run on:

US-09-771-161A-93

Perfect score:

1 MYSLQLQSVSSAIHLCDKKK......PEILVVSRSPSLNLLQNKSM 232 Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

141681 segs, 52070155 residues Searched:

20 Word size : Total number of hits satisfying chosen parameters:

N

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Listing first 45

SwissProt 42:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Descripti	043353 h receptor- P58801 mus musculu
	540 1 RIKZ HUMAN 539 1 RIKZ MOUSE
80	
Š.	
% Query Match	227 97.8 27 11.6
	!
Result No.	H 73

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[1]
SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.
MEDLINE=98241596; PubMed=9575181;
Inohara N., del Peso L., Koseki T., Chen S., Nunez G.;
Inohara N., del Peso L., Koseki T., Chen S., Nunez G.;
IRICK, a novel protein kinase containing a caspase recruitment domain,
interacts with CLARP and regulates CD95-mediated apoptosis.";
J. Biol. Chem. 273:12296-12300(1998).
                                                                                                                                                                                     Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37) (RIP-like interacting CLARP kinase) (Receptor-interacting protein 2) (RIP-2) (CARD-containing interleukin-1 beta converting enzyme associated kinase) (CARD-containing IL-1 beta ICB-kinase).
                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                     (Rel. 41, Last sequence update) (Rel. 42, Last annotation update)
                                                                                             540 AA
ALIGNMENTS
                                                                                                                                                                                                                                                                  RIPK2 OR RICK OR RIP2 OR CARDIAK. Homo sapiens (Human).
                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                         10-OCT-2003
                                                                                                                                                     28-FEB-2003
                                                                                             RIK2 HUMAN
                                                                                                             043353;
```

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EMBL; AF027706; AAC34970.1; -.

AAC25668.1; -.

AF064824; AF078530;

EMBL: EMBL;

AC004003; AAC24561.1; AF117829; AAD04634.1;

EMBL;

[2] SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47. TISSUE=Endothelial cells;

SUBCELLULAR LOCATION: Cytoplasmic (Probable).
TISSUE SPECIFICITY: Detected in heart, brain, placenta, lung, peripheral blood leukocytes, spleen, kidney, testis, prostate, pancreas and lymph node.

receptor complex.

-!- PTM: Autophosphorylated. -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. -!- SIMILARITY: Contains 1 CARD domain.

```
MEDLINE=22388257; PubMed=12477932;

A KIRDLINE=22388257; PubMed=12477932;

A Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B.B., Buctow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B.B., Buctow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

A Altschul S.F., Zeeberg B.B., Bonaldo M.F., Carninci P., Prange C.,

B And S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Roads S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hales S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Nilalon D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski W.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski W.I., Skalska U., Smailus D.E.,

H. Mannar J.M., Maran D.M., Marra M.A.,

Butterfield Y.S.N., Krzywinski W.I., Skalska U., Smailus D.E.,

H. Mannar J.M., Maran M.A.,

Beneration and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human and mouse CDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
-!- FUNCTION: Activates pro-caspase-1 and pro-caspase-8. Potentiates
CASP-8-mediated apoptosis. Activates NF-kappaB.
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- SUBUNIT: Binds to CFLAR/CLARP and CASPI via their CARD domains.
Binds to BIRC3/C-1API and BIRC3/C-1AP2, TRAFI, TRAF2, TRAF5 and
TRAF6. May be a component of both the TNFRSF1 and TNRFSF5/CD40
                                                                                                                              MEDINE-98381580; PubMed-9705938;
Thome M., Hofmann K., Burns K., Martinon F., Bodmer J.-L.,
Mattmann C., Tschopp J.;
"Identification of CARDIAK, a RIP-like kinase that associates with
MEDLINE-98307936; PubMed-9642260;
McCarthy J.V., Ni J., Dixit V.M.;
"RIP2 is a novel NF-kappaB-activating and cell death-inducing
                                                                                                                                                                                                                                                                                        Ozersky P., Holmes A., Broy M.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                    Platzer M., Varon R.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                  AND MUTAGENESIS OF ASP-146
                                                          nase.";
Biol. Chem. 273:16968-16975(1998).
                                                                                                                                                                                                                caspase-1.";
Curr. Biol. 8:885-888(1998)
                                                                                                                SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                          kinase.
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Search completed: March 29, 2004, 14:13:21
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Matches
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MEDLINE=21891093; PubMed=11894097;
Chin A.I., Dempsey P.W., Bruhn K., Miller J.F., Xu Y., Cheng G.;
"Involvement of receptor-interacting protein 2 in innate and adaptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 LOSVSSAIHLCDKKKMELSLAIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDFL
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37).
RIPK2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                               R GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
R GO; GO:0004871; F:signal transducer activity; TAS.
R GO; GO:0004871; F:signal transducer activity; TAS.
R GO; GO:0006915; P:signal transducer activity; TAS.
R GO; GO:0007165; P:signal transduction; TAS.
R InterPro; IPR0011315; CARD.
R InterPro; IPR001215; Prot_kinase.
R InterPro; IPR001245; Tyr_pkinase.
R InterPro; IPR001245; Tyr_pkinase.
R Pfam; PF00069; pkinase; I.
R PFam; PF00069; pkinase; I.
R PRNTS; PR00109; TYRKINASE.
R PROD; PS500109; TYRKINASE.
R PROSITE; PS500109; RRDF; I.
R PROSITE; PS500109; RROTEIN KINASE DOM; I.
R PROSITE; PS00107; PROTEIN KINASE DAY; I.
TYRAIS FROUNDER FOUNDER KINASE ST; I.
TYRAIS FROUNDER FOUNDER FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ->M: REDUCES FAS-MEDIATED APOPTOSIS.
->N: ABOLISHES KINASE ACTIVITY.
575A6922339505792 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazaa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.8%; Score 227; DB 1; Length 540; 100.0%; Pred. No. 5.4e-233; ive 0; Mismatches 0; Indels
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ATP (BY SIMILARITY)
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Matches 227; Conservative
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P58801;
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NP BIND
BINDING
ACT SITE
MUTAGEN
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                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROSITE; PS001017; PROTEIN KINASE ATP; FALSE NEG.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
Prosphorylation; Apoptosis.
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42951BF97CA15DFA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            449 OMTEACLNQSLDALLSRDLIMKEDYEL 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:1891456; Ripk2.
InterPro; IPR001315; CARD.
InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser thr pkin AS.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00619; CARD; 1.
Pfam; PF0069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Prot kinase; 1.
SWART; SM00114; CARD; 1.
PROSITE; E550209; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF461040; AAL96436.1; -.
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nes 27; Conservative
Nature 416:190-194(2002).
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March 29, 2004, 14:10:16 ; Search time 45 Seconds
    (without alignments)
    1626.672 Million cell updates/sec
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                                                                                                                                                                                                                                                     232
1 MYSLQLQSVSSAIHLCDKKK.....PEILVVSRSPSLNLLQNKSM 232
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                          1017041 segs, 315518202 residues
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                                                                                          OM protein - protein search, using sw model
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fung:*
4: sp_human:*
5: sp_invertebrate:*
5: sp_mammal:*
6: sp_mammal:*
6: sp_mammal:*
7: sp_mammal:*
7: sp_mammal:*
8: sp_mammal:*
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sp_vertebrate:*
sp_unclassified:*
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Description

ij

Query Score Match Length DB

Result

No matches found

Search completed: March 29, 2004, 14:14:19 Job time: 45 secs

SUMMARIES

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AK075213 Homo sapi
AR2777 Sequence 2
BD106658 Modulator
AK22453 Sequence
AK22706 Homo sapi
AR194318 Sequence
AK194318 Sequence
AK194318 Sequence
AK19435 Sequence
AK26525 Sequence
AK262513 Sequence
AK262513 Sequence
AK262513 Sequence
AK262513 Sequence
AK291600 Sequence
AK291600 Sequence
AK29125 Sequence
AK29125 Sequence
AK29125 Sequence
AK21256 Sequence
AK21256 Sequence
AK21256 Sequence
AK26252 Sequence
AK26252 Sequence
AK26253 Sequence
AK26253 Sequence
AK26253 Sequence
AK26253 Sequence
AK39199 Sequence
AK36299 Novel mol
AK117829 Homo sapi
AC139421 Homo sapi
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Homo sapiens receptor interacting protein 2 (RIP2) mRNA, complete
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BC004553 Homo Bapi
AF064824 Homo Bapi
BD251808 Phosphory
BD127583 Primer fo
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AF461040
AF487539
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-MODBL=frame+ p2n.mcdel -DEV=x1h
-Q=/Cgn2_1/USPTO_gepool/USO9771161/runat_29032004_124851_19858/app_query.fasta_1.391
-Q=/Cgn2_1/USPTO_gepool/USO9771161/runat_29032004_124851_19858/app_query.fasta_1.391
-DB=CenEmb1 -QFWT=fastap -SUFFTX=0130p_Zn.rge -MINMATCH=0.1 -LOOPGTL=0
-LOOPEXT=0 -UNITS=bits -STRAT=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=20 -ALIGN=15 -MODE=LOCAL
-UTFRT=pto -NORM=ext -HEAPSIZE=500 -MILCEN=0 -MAXLEN=2000000000
-USER=USO9771161_@CGN 1_1_2496_@runat_29032004_124851_19858 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQGERY -NEG SCORESe=0 -WAIT -DSPBIGCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=0 -THREADS=1 -XGAPO=60 -XGAPEXT=60 -FGAPOP=6
                                                                                                                          April 1, 2004, 11:22:08 ; Search time 4002 Seconds (without alignments) 2512.640 Million cell updates/sec
                                                                                                                                                                                                                                   1 MYSLQLQSVSSAIHLCDKKK......PEILVVSRSPSLNLLQNKSM 232
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                         nucleic search, using frame_plus_p2n model
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AY335645.1 GI:33303916
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synthetic construct
synthetic construct
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McCarthy,J.V., Ni,J. and Dixit,V.M.
MrRP2 is a novel NF-kappaB-activating and cell death-inducing kinase J. Biol. Chem. 273 (27), 16968-16975 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIADPGLSKWRWMSLSQSRSSKSAPEGGTIIYMPPENYEPGQKSRASIKHDIYSYAVI
TWEVLSKROPPEDVTWPLQIYYSVSQCHRPVINEESLEVDIPBIRBARMISLIESGWAQN
PDERPSFLKCLIELEPVLRYFEELIFLEAVIQLKKTKLASVSAIHLCDKKKWELSLA
IPVNHGPQEESCGSOLHENSGSPETFREADAPQDNDFLSRKAQDCYFWKLHHCPGNH
SWDSTISGSQRAFCDHKTTFCSSAIINDLGSTAGNSRELQPGTAQOWIQSKREDIVNQ
MTBACLNOSLDALLSRDLINKEDYELVSTKFTSKWRQLLDTTDIGGEEFAKVIVQK
LKDNKQMGLQPYPELIVVSRRSPSLNLLONKSM"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVKHLHIHTPLLDSERKDVLREAEILHKARFSYILPILGICNEPEFLGIVTEYMPNGS
LNELLHRKTEYPDVAWPLRPRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNBFHV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MNGEAICSALPTIPYHKLADLRYLSRGASGTVSSARHADWRVQV"
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                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                2 (bases 1 to 1623)
McCatthy,J.V. Ni,J. and Dixit,V.M.
Direct Submission
Submitted (15-JUL-1998) Molecular Oncology, Genentech Inc, 1 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                   function="activtes NF-kappaB"
function="induces cell death"
'note="RIP2; serine/threonine kinase homolog; contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuGInSerValSerSerAlaileHisLeuCysAspLysLysMetGluLeuSerLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product="receptor interacting protein 2"
protein id="AAC27722.1"
db_xref="GI:3342910"
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                   Way, South San Francisco, CA 94080, USA Location/Qualifiers
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    .1623
/organism="Homo sapiens"

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/db_xref="taxon:9606"
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               sapiens (human)
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Direct Submission

Submitted (02-JUL-2003) Biological Chemistry and Molecular

Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,

Cambridge, MA 02141-2023, USA

This CDS clone is a part of a collection of human full-length

expression clones generated by Harvard Institute of Proteomics.

Each CDS has been cloned without stop-codon (to allow fusion with

C-terminal tag). The CDS has been directionally cloned using BD

In-Fusion (TW) cloning system between the Sall and HindIII sites of

the pDNR-Dual vector. Additional sequences in the clone: 'ACC'

sequence; 'GG' after last codon and before HindIII site to maintain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1479
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1180 TGGGACAGCACTTTCTGGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCACTCCA 1239
                                                                                                                                                                                                                                                                         1300 GGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAAATGACAGAA 1359
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                                                                                                                                                                                                                                                                                                                                              146 AlacysLeubsnGlnSerLeubspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186 ThraspileGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206 GlnMetGlyLeuGlnProTyrProGlulleLeuValValSerArgSerProSerLeuAsn
                                                                 106 CysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro
                                                                                                                                   1240 recrercadeaaraaraaraceacrercaacrecagaaacreagaacerecagaecer
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1 (bases 1 to 1623)
Park, J., Rolfs, A., Hu, Y., Shen, B., Vannberg, F., Moreira, D.,
Kelley, T., Zuo, D., Raphael, J., Baqui, M., Jepson, D., Harlow, B.,
LaBaer, J., and Brizuela, L.
Cloning of human full-length CDS FLEXGene kinases in
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2 (bases 1 to 1623)

Park, J. Rolfe, A., Hu, Y., Shen, B., Vannberg, F., Moreira, D.,

Kelley, T., Zuo, D., Raphael, J., Bagui, M., Jepson, D., Harlow, E.,

LaBaer, J., and Brizuela, L.
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/clone=lib="MGC clone templates"
/lab_host="DHSalpha T1 resistant"
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/db_xref="taxon:32630"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

13 (bases 1 to 1886)

14 (bases 1 to 1886)

15 Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., John,Y., Johnson,S., Lee,J., Liao,D., Mark,M., Robbie,B., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K., Xie,M.H., Yansuran,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.

The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Beffort to Identify Novel Human Secreted and Transmembrane Proteins:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAQ89172.1"
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GSPETSRSLPAPQDNDFLSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTP
                            1540 CAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAAAT 1599
                                                                                                                                                                                                                                                                      AY358813 1886 bp mRNA linear PRI 03-OCT-2003
Homo sapiens clone DNA43306 RIPK2 (UNQ277) mRNA, complete cds.
AY358813
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EDYELVSTKPTRTSKVRQLLDTTDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRS
PSLNLLQNKSM"
206 GlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsn 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
Location/Qualifiers
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/organism="Homo sapiens"
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483. .1694
/locus_tag="UNQ277"
/note="PRO34092"
                                                                                                           A Bioinformatics Assessment
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FLI_CDNA.
Homo sapiens (human)
Homo sapiens
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TITLE
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                                                                                                                                                                                                                                                                                                  /trānslation="MNGEAICSALPTIPYHKLADLRYLSRGASGTVSSARHADWRVQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrPro 105
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                                                                                                           /gene="RIPK2"
/note="Mutations: Stop->Leu
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     'note="Vector: pDNR-Dual"
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                         1. .>1623
/gene="RIPK2"
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Young, A., Zhang, L.-H. and Green, E.D.
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/gene="RIPK2"
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Contact: MGC help desk
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1. (Dasas 1 to 1889)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Morce, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstean, M.J., Usdin, T.B., Toshiyuki, S., Carnioci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bossak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gay, L.J., Hulyk, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1251 TGGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCACTCCA 1310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1311 recrerreacearaaraareceacrereaceacacaaaacreagaacereacacea 1370
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                                   1071 AACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCATGAA 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTGACATCCAAGGAGAAGTTTGCCAAAGTTATAGTACAAAATTGAAAGATAACAAA 1610
                                                                                                                                                                                                                                                             1131 AATAGTGGTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTTTA 1190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeulleMetLysGluAsp 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 GlylleAlaGlnGlnTrplleGlnSerLysArgGluAsplleValAsnGlnMetThrGlu 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185
                                                                                                                                                                                                                                                                                                                                                                                                                        TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLySThrThrPro 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125
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                                                                                                                                                                                                                                                                                                            SerArglysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85
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                                                                                                                                                                                                            AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu
LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu
                                                                                                      AsnileProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHisGlu
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Louract: much usek

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing Center (NISC),

Gailthersburg, Maryland;

Web site: http://www.nisc.nih.gov/

Contact: nisc_mgc@nhgri.nih.gov/

Contact: nisc_mgc@nhgri.nih.gov/

Akhter,N., Ayele,K., Backstrom-Sternberg,S.M., Benjamin,B.,

Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,

Blakesley,R.W., Granite,S., Guan,X., Gupta,J., Haghighi,P.,

Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,

Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,

McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,

Tsurgeon,C., Voget,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
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PUBRRSFLKCLIELEPVLRTFEEITFLEAVIOLKKTKLQSVSSAIHLCDKKKMELSLN
IPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDFLSRRAQDCYFMKLHHCPGNH
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 20127435.
Location/Qualifiers
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jonee, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (14-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product="receptor-interacting serine-threonine kinase
/protein_id="AAH04553.1"
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On Aug 19, 2003 this sequence version replaced gi:13528713
                                                                                                                                                                                                                                                                                                                                                                              human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/db xref="LocusID:8767"
/db xref="MIM:603455"
203. .1825
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/clone lib="NIH MGC 20"
/lab host="DH10B-R"
/note="Vector: pOTB7"
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/clone="MGC:10684 IMAGE:4026156"
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Homo sapiens
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Switzerland
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AF064824.1
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Best Local Similarity:
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DB:
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AUTHORS
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                                    263. .1063
Anote="Mokinase; Region: Protein kinase domain"
/db xref="CDD:pfam00069"
1508. .1774
/note="CARD: Region: Caspase recruitment domain. Motif
contained in proteins involved in apoptotic signaling.
Predicted to possess a DEATH (pfam00531) domain-like fold"
/db_xref="CDD:pfam00619"
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MTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIQGEEFAKVIVQK
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227
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                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                           LKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM"
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/product = "CARD-containing ICE associated kinase"
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/db_cref="GI-2390172"
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SWDSTISGSQRAAFCDHYTTPCSSAIINPLGSTAGNSBRLQPGTAQQWIQSKREDIVNQ
WTEACLNQSLDALLSRDLIMKEDYELVSTKETTSKVRQLLDTTDIQGEEFAKVIVQK
AF064824 1902 bp mRNA linear PRI 07-JUL-1998
Homo sapiens CARD-containing ICE associated kinase mRNA, complete
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Thome,M., Hofmann,K., Burns,K., Martinon,F., Bodmer,J.-L.,
Mattmann,C. and Tschopp,J.
Identification of CARDIAK, a RIP-like kinase that associates with
                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (12-MAY-1998) Institute of Biochemistry, University Lausanne, Chemin des Boveresses, 155, Epalinges, CH 1066,
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/note="encodes intermediate domain"
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Conservative:
Mismatches:
Indels:
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/note="encodes CARD motif"
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(bases 1 to 1902)
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Homo sapiens (human)
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                       A61P5/14, A61P5/38,

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A61P21/04,
PC A61P25/00, A61P25/08, A61P25/14, A61P25/16, A61P25/18, A61P25/28,
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PC A61P37/08, C07K16/40, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/PC A61P37/06, PC A61P37/06, PC A61P37/06, PC A61P37/06, PC A61P37/06, PC A61P37/06, PC A61P37/10, PC A61P37/1
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C12N15/09, A61K38/00, A61K45/00, A61P1/04, A61P1/16, A61P3/10 PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1502 GGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAAATGACAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1142 TTACAGAGTGTTTCAAGTGCCATTCACCTATGTGACAAGAAGAAAATGGAATTATCTCTG
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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1 (bases 1 to 2024)

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1 (bases 2 to 2024)

1 (bases 3 to 2025)

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M LU,
LEO L SHIH
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                                        AATAGTGGTTCTCCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGTTTTTA
                                                                                                                                                                   TCTAGAAAAGCTCAAGACTGTTATTTTTATGAAGCTGCATCACTGTCCTGGAAATCACAGT
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MARIAH R BAUGHN, CHANDRA PATTERSON, OLGA BANDMAN, JANICE
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JP 2002526035-A/6.
Homo sapiens (human)
Homo sapiens
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Unpublished

E (bases 1 to 2033)

Isogai, T. and Otsuki, T.

Direct Submission

Submitted (25-MR2-2002) Takao Isogai, Helix Research Institute,

Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

ECONOW, Trade and Industry of Japan; CDNA full insert sequencing:

Research Association for Biotechnology; CDNA full insert sequencing:

Research Association for Biotechnology; CDNA full insert sequencing:

Restructure, Human Genome Center; CDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens cDNA FLJ90732 fis, clone PLACE1010081, highly similar to Homo sapiens serine/threonine kinase RICK (RICK) mRNA.
                                                                                                                                                                                                                  1578 GCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGGAC 1637
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                                                             1398 researadeaccartricresarcreaasescrecarrerereacaccacacacacteca 1457
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                                                                                                                                                                                           GlylleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145
                                                                                                                                                                                                                                                                             146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                       CysSerSerAlallelleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro
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                      TrpAspSerThr11eSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrPro
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/mol_type="mRNA"
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TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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Ota; T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
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Primer for synthesizing full-length cDNA and use thereof FH K
Location/Qualifiers
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6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu
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for synthesizing full-length cDNA and use thereof.
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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JP 2002017375-A/3014.
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PP 07-JUL-2000
PI TOSHIO OTA, I
PI VISHI,
PI VISHI KAWAI,
PI TETSUJI OTSU
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227
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1 (bases 1 to 2098)
Boldin,M. and Wallach,D.
MODULATORS OF INTRACELLULAR INFLAMMATION,
SURVIVAL PATHWAYS
PATHWAYS
BOLDIN MARK (IL); WALLACH DAVID (IL)
LOCATION/QUalifiers
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Matches:
Conservative:
Mismatches:
Indels:
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Ward, D.T. and Cowsert, L.M.
Antisense modulation of RIP2 expression
Patent: US 6456221-A 3 30-JUL-2002;
Location/Qualifiers
1. 2501
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Matches:
Conservative:
Mismatches:
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Sequence 3 from patent US 6426221.
AR221453.1 GI:23328503
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                                                                                                                                                                                                                                              PI DAVID WALLACH, MARK BOLDIN, NIKOLAI MALININ
PC CLANIS/12, CO7K14/47, CO7K16/18, C12Q1/68, A61K38/17, G01N33/68
Strandedness: Single;
CC Topology: Linear;
FH Kev
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                                                                                                                                                          cell
                                                                                                                                                          cell death and
                                               BD106558 1 G1:33201476

BD106658 1 G1:33201476

Synthetic construct

SM Synthetic construct

artificial sequences.

1 (bases 1 to 2098)

Mallach, D. Boldin, M. and Malinin, N.

Modulactors of intracellular inflammation, cell deat survival pathways

Patent: JP 2002502258-A 1 22-JAN-2002;

YEDA RESEARCH AND DEVELOPMENT CO LTD

PN JP 2002502258-A/1

PP 22-JAN-2002

PF 01-UN-1998 JP 1999501993

PR 05-JUN-1997 IL 121746

PI DAUTO WALLACH MARK BOLDIN, NIKOLAI MALININ

PC CLANIS/12, CO7K14/47, CO7K16/18, C1201/68, A6IK38/
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Conservative:
Mismatches:
Indels:
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    ..2098
    ^organism="synthetic construct"
/mol type="genomic DNA"
    /db_xref="taxon:32630"

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                               survival pathways.
BD106658
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Best Local Similarity:
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AF027706 2501 bp mRNA linear PRI 10-SEP-1998
Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete
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95241896
9575181
2 (bases 1 to 2501)
Inohara,N., Koseki,T., Chen,S., del Peso,L. and Nunez,G.
Direct Submission
Submitted (01.0CT-1997) Dept. Pathlogy, Comprehensive Cancer &
Geriatrics Center, 4-131 CCGC 1500 E. Medical Center Dr. Ann Arbor,
MI 48109, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 1764 CAAAIGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAAAT 1823
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 2501)
Inohara,N., del Peso,L., Koseki,T., Chen,S. and Nunez,G.
RICK, a novel protein kinase containing a caspase recruitment
domain, interacts with CLARP and regulates CD95-mediated apoptosis
J. Biol. Chem. 273 (20), 12296-12300 (1998)
1404 TGGGATAGCACCATTTCTGGTTCTCAAAGGGCTGCATTCTGTGATCACAAGACCACTCCA
                                                                                                                               126 GlylleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu
                                                                                                                                                      1524 GGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAAAATGACAGAA
                                                                                                                                                                                                                             1584 GCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGGAC
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                                                                         1464 TGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAGCCT
                                                                                                                                                                                                        146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp
                                                                                                                                                                                                                                                                               166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr
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AF027706.1 GI:3123886
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     1524 GGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAAAACCAAATGACAGAA 1583
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Patent: EP 1201765-A 13 02-MAY-2002;
Axxima Pharmaceuticals Aktiengesellschaft (DE)
Location/Qualifiers
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                                                                             1584 GCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGGAC
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                                          AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp
                                                                                                                 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr
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Mismatches:
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/noce="N/A"
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Sequence 13 from Patent EP1201765.
AX429236
AX429236.1 GI:21540548
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20-APR-2002

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1225 AACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCATGAA 1284
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Unclassified.
1 (bases 1 to 2502)
Nunez,G., Inohara,N. and Koseki,T.
Compositions and methods for identifying apoptosis signaling pathway inhibitors and activators
Patent: US 6348573-A 2 19-FEB-2002;
Location/Qualifiers
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                                                                                                                  2502 bp
patent US 6348573.
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Seguence 2 from patent 0
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          / CTAINSTALL OND = "MNGEAICSALPTIPYHKIADIRYLSRGASGTVSSARHADWRVQV
AVKHLHIHTPLLDSBRKDVLREABILHKARFSYILPILGICNEPEFGIVTBYWRNGS
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1 (bases 1 to 2521)

2 Clark H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P. B., Hadens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Mark, M., Robbis, E., Sanchez, C., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vags, A., Woods, K., Watanabe, C., Wieand, D., Woods, K., Xie, M.H., Yansura, D., Yi.S., Yu.G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I. and Godowski, P.

The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment
                                                                                                                                                                                                                                                             AX358814 2521 bp mRNA linear PRI 03-OCT-2003
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LNELLHRKTEYPDVAWPLRPRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNBFHV
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Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
Location/Qualifiers
ThrAspileGlnGlyGluGluPheAlaLysVallleValGlnLysLeuLysAspAsnLys
                                                                              GlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsn
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Homo sapiens (human)
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Conservative:
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein March 29, 2004, 13:59:15; Search time 61 Seconds (without alignments) 1074.607 Million cell updates/sec Run on:

US-09-771-161A-93 1206 1 MYSLQLQSVSSAIHLCDKKK.....PEILVVSRSPSLNLLQNKSM 232 Perfect score:

Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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tion	6 Human	5 Human	4 Human		4 Amino	1 Human	9 Human	2 Human		0 Human	9 Human	-		_		_			Ξ.	2 Human			3 Human	4 Human	3 Human
Description	Aay59406	Aay59405	Aay59404	Aaw92795	Aay68774	Aam9362	Aau80369	Aae2788	Aab43570	Aay31140	Aab20079	Abg31075	Aao22107	Abu56269	Adb81362	Adc99079	Aay59407	Aao22109	Abu56271	Abu56272	Aao22110	Abj04754	Aam79473	Aay31144	Aab20083
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## ALIGNMENTS

AAY59406 standard; protein; 284 AA AAY59406

AAY59406;

(first entry) 21-MAR-2000 Human RICK protein sequence residues 248-531.

RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC; caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway; CIDE-A; CIDE-8; DREP-1; diagnosis; cell growth; apoptosis dysregulation; gene therapy; cardiac disorder; autocodegenerative disorder; AIDS; aplastic anaemia; ischaemic injury; toxin-induced liver disease. 

Homo sapiens.

WO9955134-A2.

04-NOV-1999.

99WO-US009183. 27-APR-1999; 98US-00069023. 27-APR-1998;

(UNMI ) UNIV MICHIGAN.

Koseki T; Inohara N, Nunez G,

WPI; 2000-072163/06.

Compositions for identifying apoptosis signaling pathway inhibitors useful for treating diseases.

Claim 6; Page; 93pp; English.

This sequence is a fragment of the human RICK (RIP-like interacting CLARP kinase) protein of the invention. RICK acts as a positive regulator of apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10 during. CD95 signalling. The invention provides methods for identifying apoptosis signalling pathway inhibitors and activators, and methods and composations for screening compounds which will modulate the interactions of the various compositions identified ARC, RICK, and the CIDE family of activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening assays for agents, useful in the diagnosis or treatment of disease associated with excess cell growth and dysregulation of apoptosis. Complexes containing RICK and CLARP can be used in drug

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apoptosis. Overexpression of ARC in an in vitro cell system can be used to identify inhibitors of the enzymatic activity of caspase-8. Identification of ARC-like inhibitory compounds may be useful for gene therapy treatment of disease with increased cell death in muscle tissue and cardiac disorders. Therapeutic compositions of CIDEs can be used to treat e.g. cancer, AIDS; neurodegenerative disorders, aplastic anaemia, ischaemic injury, and toxin-induced liver disease. AntiRICK antibodies can be used as reagents for the preparation or affinity chromatography media, and for dispnostically measuring RICK levels. A specific inhibitor of an essential step in the blochemistry of apoptosis is needed. RICK interaction with intracellular factors such as CLARP and FADD appears to be essential for apoptosis, inhibitors of RICK binding to intracellular apoptosis factors are potential drug candidates. Note: This sequence was created using information given in the specification
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screening assays to identify inhibitor molecules blocking CD95-mediated
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Compositions for identifying apoptosis signaling pathway inhibitors useful for treating diseases.

98US-00069023

27-APR-1998;

(UNMI ) UNIV MICHIGAN Nunez G, Inohara N, WPI; 2000-072163/06.

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This sequence is a fragment of the human RICK (RIP-like interacting CLARP kinase) protein of the invention. RICK acts as a positive regulator of this apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10 during CD95 signalling apoptosis induced by caspase-8 and caspase-10 apoptosis signalling. The invention provides methods for identifying compositions for screening compounds which will modulate the interactions of the various compositions identified aRC, RICK, and the CIDE family of activators (CDE-A, CIDE-B and DREP-1). RICK is useful in screening assays for agents, useful in the diagnosis, prognosis or treatment of disease associated with excess cell growth and dysregulation of apoptosis. Complexes containing RICK and CLARP can be used in drug creening assays to identify inhibitor molecules blocking CD95-mediated apoptosis. Overexpression of ARC in an in vittor cell system can be used to contain the inhibitory compounds may be useful for gene therapy treatment of disease with increased cell death in muscle tissue and cardiac disorders. Therapoutic compositions of CIDEs can be used to treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia, ischaemic injury, and toxin-induced liver disease. AntiRICK antibodies can be used as reagents for the preparation or affinity chromatography media, and for diagnositically, measuring RICK levels. A specific inhibitor of an essential step in the biochemistry of apoptosis is needed. RICK interaction with intracellular factors such as CLARP and FADD appears to apoptosis factors are potential drug candidates. Note: This sequence was a essential drug apoptosis is the preparation of the preparation of a created using information given in the specification
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                      Claim 6; Page; 93pp; English
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Nunez G,

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This invention describes the isolation of a novel human B1 protein which can interact with, intracellular mediators or modulators of inflammation, cell death and/or cell survival pathways, directly or indirectly. Cells can be modulated or mediated in inflammation, cell death or cell survival pathways or another intracellular signalling activity using B1. Conditions such as AIDS and cancer can be treated using B1. Antibodies, oligonucleotides and ribozymes can also be used to regulate the above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New B1 protein regulates cell death and cell survival pathways - derivatives, DNA and antibodies, also regulate intracellular inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           373 LSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               433 PGIAQOWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             313 KLÓSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDF
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                                                                                                B1 protein; intracellular mediator; modulator; inflammation; cell dea
cell survival pathway; intracellular signalling; AIDS; cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1182; DB 2;
Pred. No. 5.6e-115;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Malinin N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Fig 3A; 90pp; English.
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971L-00121199.
971L-00121746.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; for treating AIDS, cancer.
  (first entry)
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Matches 227; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wallach D, Boldin M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-070258/06.
                                               Human B1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAX02558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 540 AA;
                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                         WO9855507-A2
  07-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence is the human RICK (RIP-like interacting CLARP kinase)

Co fapoptosis, potentiating apoptosis induced by caspase-8 and caspase-10

during CD95 signalling. The invention provides methods for identifying

apoptosis signalling pathway inhibitors and activators, and methods and

compositions for screening compounds which will modulate the interactions

CC activators (CIDE-A, CIDE-B and DREP-1). RICK, and the CIDE family of

activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening

compositions identified: ACC, RICK, and the CIDE family of

activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening

compositions complexes containing RICK and CLARP can be used in drug

co asays for agents, useful in the diagnosis, prognosis or treatment of

disease associated with excess cell growth and dysregulation of

conpositions. Overexpression of ARC in an in vitro cell system can be used

co identify inhibitors of the enzymacic activity of caspase-B

co identify inhibitors of the enzymacic activity of caspase-B

co identification of ARC-like inhibitory compounds may be useful for gene

therapy treatment of disease with increased cell death in muscle tissue

condition of a disease with increased cell death in muscle tissue

condition and for diagnostically measuring RICK levels. A specific inhibitor

condition and for diagnostically measuring RICK levels. A specific inhibitor

condition with intracellular factors such as CLARP and FADD appears to

be essential for apoptosis, inhibitors of RICK binding to intracellular

conditions are poptential drug candidates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  364 LSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 KLOSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSOLHENSGSPETSRSLPAPQDNDF 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          424 PGIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 483
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                                                                                                                                                                                                                                                                                                                               Compositions for identifying apoptosis signaling pathway inhibitors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 531;
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                                                                                                                                                                                                    Koseki T;
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 7a; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                       useful for treating diseases.
                                                 99WO-US009183
                                                                                                98US-00069023
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nes 227; Conservative
                                                                                                                                                (UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                    Inohara N,
                                                                                                                                                                                                                                                   WPI; 2000-072163/06
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                                                 27-APR-1999;
                                                                                                27-APR-1998;
04-NOV-1999.
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Gaps

; 0

Length 540; Indels 372 124

Amino acid sequence of a human phosphorylation effector PHSP-6.

16-MAY-2000 (first entry)

AAY68774;

AAW92795 standard; protein; 540

AAW92795

AAW92795 ID AAW9 XX AC AAW9: XX

RESULT 4

125

185 484

65

Query Match

Best Loca Matches

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Gordone GA,
 Au-Young J,
                                                                               Claim 1; Page 84-85; 142pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                       AAM93621 standard; protein; 540 AA
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Wakamatsu A, Sugiyama T, Nagai
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2000JP-00118774.
2000JP-00183765.
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                                                                                                                                                                                                                 98.0%;
99.6%;
C, Bandman O, A
Lu DAM, Shih LL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                  Matches 227; Conservative
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                          WPI; 2000-183125/16
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Best Local Similarity
                                     N-PSDB; AAZ46143
                                                                                                                                                                                                Sequence 540 AA;
Patterson C,
Reddy R, Lu
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11-JAN-2000;
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                                                              18. .287
note= "protein kinase family signature sequence"
         PHSP; proliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guegler KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                "potential phosphorylation site"
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                                                                                                                                                                                                                 "potential phosphorylation
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                                                    ocation/Qualifiers
         phosphorylation effector; Pr
disorder; neuronal disorder.
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98US-0155239P.
98US-0106889P.
98US-0109093P.
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03-NOV-1998;
19-NOV-1998;
22-DEC-1998;
12-JAN-1999;
                                     Homo sapiens
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          Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY68769-95 and AAY68797-99 represent human phosphorylation effectors (PHSP), designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not given in the specification). The sequences were isolated from cDNA libraries prepared from various human tissues. The PHSP proteins are useful for the diagnosis, treatment and prevention of proliferative disorders, immune disorders and neuronal disorders. The PHSP proteins form pharmaceutical compositions which useful for treating or preventing disorders associated with decreased HSPP expression/activity. PHSP antagonists are useful for treating or preventing disorders associated with increased PHSP expression/activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64
                                                                                                                                                                                                                                                  treatment
Azimzai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               313 KLQSVSSAIHLCDKKKKMELSLNIPVNHGPQEBSCGSSQLHENSGSPETSRSLPAPQDNDF
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K, Kojima S, Otsuki T, Koga H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                    prevention of proliferative, immune and neuronal disorders.
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                                                                                                                                                                                                                                          human phosphorylation effectors useful for the diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1182; DB 3; Length 540;
Pred. No. 5.6e-115;
1; Mismatches 0; Indels
Yue H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGIAQOWIOSKREDIVNOMTEACLNOSLDALLSRDLIMKEDYELVSTKP
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for treating and/or preventing cytomegalovirus (CMV) infection and/or related diseases. The method of the invention comprises contacting a test compound with at least one of the cellular kinases RICK, RIP, NCK-Interacting kinase, MKK3 and SRPK-2 and detecting any change in kinase activity. The method of the invention can be used to treat and/or prevent CMV infections and related diseases. Oligonucleotides that can detect the specified kinases can also be used for diagnosis of infection. The present amino acid sequence represents the human cellular kinase RICK protein of the invention, as described above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 433 PGIAQOWIQSKREDIVNOMTEACLNOSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antisense oligonucleotide that targets regions of a nucleic acid
encoding human receptor interacting protein (RIP)2, for treating diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
                                                                                                                                                                                 present invention relates to a new method for identifying compounds
                                        Identifying agents for treatment or prevention of cytomegalovirus infection, comprises contacting test compound with cellular kinase and detecting change in cellular kinase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               313 KLQSVSSAIHLCDKKKKMELSINIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      373 LSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1182; DB 5;
Pred. No. 5.6e-115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human receptor interacting protein (RIP)2.
                                                                                                                                      Disclosure; Page 23-24; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              540 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98.0%;
99.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE27882 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cowsert LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-673017/72.
N-PSDB; AAD45172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 227; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 540 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65
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                                                                                                                                                                                                                        clones. 830 cDNA molecule persociation and the protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA molecules have been determined. Primers for synthesised by the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention. Note: The sequence data for this patent did form part of the printed specification, but was obtained in CD-ROM format directly from EPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372
                                                                                    synthesizing full length cDNA clones and their use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            373 LSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytomegalovirus infection; CMV; cellular kinase; RICK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              313 KLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 QLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                       The invention relates to primers for synthesising full length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM 540
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                                                                                                                                                            SEQ ID NO 3454; 1380pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1182; DB 4;
Pred. No. 5.6e-115;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stein-Gerlach M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIP; Nck-Interacting kinase; MKK3; SRPK-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cellular kinase RICK protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU80369 standard; protein; 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2000; 2000US-0240750P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.6
Matches 227; Conservative
                                                                                                                 genetic manipulation
                                                                                      830 Primers useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AXXI-) AXXIMA PHARM
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                     WPI; 2001-524255/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 540 AA;
                                                N-PSDB; AAK94554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP1201765-A2.
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Length 540; Indels 372

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                                             The invention relates to antisense compounds targetted to a nucleic acid encoding human receptor interacting protein (RIP)2 to inhibit its expression. Antisense compounds are used for treating diseases associated with RIP2 expression. They are also useful in antisense gene therapy. The present sequence is human RIP2 protein
                                                                                                                                                                                                       313 KLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDF 372
                                                                                                                                                                                                                                                      LSRKAQDCYFWKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 432
                                                                                                                                                                                                                                                                                                  PGIAQQWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492
                                                                                                                                                                                                                                                                                    PGIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
                                                                                                                                                                                         64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antinflammatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus, host disease; organ rejection;
                                                                                                                                                                                        QLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDF
                                                                                                                                                                                                                                      LSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ
                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          haemostatic; thrombolytic; cardiovascular disorder; infection;
neurological disease; drug screening.
                                                                                                                                                                                                                                                                                                                                                         540
                                                                                                                                                                                                                                                                                                                                  TTDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM 232
                                                                                                                                         Score 1182; DB 5; Length 540;
Pred. No. 5.6e-115;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cancer associated protein sequence SEQ ID NO:1015.
                      49-54; 35pp; English.
associated with RIP2 expression.
                                                                                                                                                                                                                                                                                                                                                                                                                  AAB43570 standard; protein; 544
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                                                                                                                                           98.0%;
99.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                       Query Match
Best Local Similarity 99.6
Matches 227; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruben SM;
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N-PSDB; AAC77779.
                                                                                                                   Sequence 540 AA;
                        Example 15; Col
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AAB43570
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antilinflammatory; antilatements; antilatements; antivatements; coagulant; contrological conditions and diagnosing pathological conditions. CC polymuclocides and polypeptides, antibodies, agonists and antaquists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of or immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate confirmantion, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB42440 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                         qiven in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                AAC77607 to AAC78448 encode the human cancer associated proteins giv
AAB43398 to AAB44239. The proteins can have activities based on the
tissues and cells the genes are expressed in. Example of activities
include: cytostatic; proliferative; vulnerary; immunomodulator;
antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.0%; Score 1182; DB 3; Length 544; 99.6%; Pred. No. 5.7e-115; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTDI QGEEFAKVI VQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM
Claim 11; Page 1595-1597; 2352pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY31140 standard; protein; 540 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 99.6
Matches 227; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 544 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens,
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This invention describes the isolation of novel human caspase recruitment domain, CARD-3 and CARD-4 polymucleotides and proteins and a partial comutine CARD-4 protain and genes. The genes and proteins of the invention are involved in the regulation of caspase activation. The caspase activation are involved in the regulation of caspase activation. The caspase and antibodies can be used in screening assays, detection assays, predictive methods may be used to disponse and treat patients which are suffering cardivity of the TNF receptor complex, abnormal activity of the TNF receptor complex, or abnormal activity of a caspase. Captured and prophylactic methods which are suffering activity of the TNF receptor complex, or abnormal activity of a caspase. Captured with mutations in p53 and hormone-captured may be treated include cancer (particularly follicular lymphoma, carcinomas associated with mutations in p53 and hormone-captured associated with mutations in p53 and hormone-captured may be used include cancer (particularly follicular supering associated with mutations in p53 and hormone-captured spidenate tumours), autoimmune disorders (e.g. systemic lupus carcinomas associated with mutations in p53 and hormone-captured spidenate spidenate spidenate distance and sister and stroke.

Alzheimar's disease, parkinson's disease, amyorchophy, cerebellar degeneration, anaemia, myelodysplastic syndrome, myocardial infarction, and stroke.

CARD-3 protein interacts with other cellular proteins, and so can be used for regulation of cellular proliferation and differentiation and cell survival. The CARD proteins may also be used to for screen drugs or compounds which modulate their activity. The CARD-4 and CARD-4 encodes CARD-4 splice variants, CARD-4 and CARD-42. This sequence compounds which modulation described and activated in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel CARD-3 and CARD-4 genes and polypeptides used or treating regulation of cellular proliferation and differentiation and cell survival.
                  'note= "predicted kinase domain"
                                      301. .431
/hote= "predicted linker domain"
432 .540
/note= "predicted CARD domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Fig 2; 181pp; English.
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98US-00099041.
98US-00207359.
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.300
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                                                                                                                                                   WO9940102-A1
                                                                                                                                                                                                                                     05-FEB-1999;
                                                                                                                                                                                                                                                                                  06-FEB-1998;
                                                                                                                                                                                                                                                                                                                         08-DEC-1998;
                                                                                                                                                                                                                                                                                                      17-JUN-1998;
                                                                                                                                                                                            12-AUG-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                 Bertin J;
  Domain
                                           Domain
                                                                                      Domain
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# Sequence 540 AA;

invention

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313 KLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDF 372
                                                                                                                                                    LSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124
                                                                                                                                                                         373 LSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTIPCSSAIINPLSTAGNSERLQ 432
                                                                             5 QLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDF 64
                                             Gaps
                                           ;
0
Score 1176; DB 2; Length 540;
Pred. No. 2.4e-114;
1; Mismatches 1; Indels (
       97.5%;
                        Best Local Similarity 99.1
Matches 226; Conservative
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         Query Match
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433 PGIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492 TTDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM 540 TIDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM 185 ð 셤

AAB20079 standard; protein; 540 AA

AAB20079;

(first entry) 23-APR-2001

Human CARD-3 protein.

CARD-3; caspase recruitment domain; human; cancer; infection; autoimmune disease; neurological disease; haematological disease; inflammation; antitumour; antiseptic; immunomodulator; antiinflammatory; apoptosis; diagnosis; gene therapy.

Homo sapiens.

#01. .431
/note= "linker domain"
432. .540
/note= "CARD" . .400 note= "kinase domain" location/Qualifiers Domain Domain Domain 

WO200100826-A2

04-JAN-2001

28-JUN-2000; 2000WO-US017691.

MILL-) MILLENNIUM PHARM INC

99US-00340620.

28-JUN-1999;

Bertin J;

WPI; 2001-061973/07.

N-PSDB; AAF30001

Isolated intracellular proteins predicted to be involved in regulating caspase activation are used for diagnosis and treatment of e.g. cancer, viral infections, autoimmune diseases, neurological diseases and hematological disorders.

Claim 9; Fig 2; 208pp; English.

The present sequence is that of human caspase recruitment domain 3 (CARD-3), an intracellular protein predicted to be involved in regulating caspase activation. The sequence is predicted from an isolated cDNA clone (see AAF30001). Methods of diagnosing and treating patients suffering from a disorder associated with an abnormal level or rate of apoptotic cell death, abnormal activity of the Fas/APO-1 receptor complex, abnormal activity of a caspase involve administering a compound that modulates the expression or activity of CARD-3, CARD-4, CARD-5 or CARD-6 e.g. using expression or activity of GARD-3, CARD-4, CARD-5 or CARD-6 e.g. using ene therapy methods. Such disorders include cancer, viral infection, autoimmune disorders and immune disorders. CARD-3, -4, -5 and -6 proteins can be used to regulate cell proliferation, cell survival and proteins can be used to regulate cell proliferation, cell survival and cell growth. They can also be used to screen drugs or compounds that modulate their activity or excessive production of CARD-3, -4, -5 or -6 protein, or production of an aberrant protein

Sequence 540 AA;

PGIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184

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                                                                                                                                                                       LSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124
                                                          64
                                                                                                                                                                                                                                                                                                                                                                                  Human; caspase recruitment domain; CARD-3; CARD-4; LRR; leucine rich repeat; LPS; lipopolysaccharide; NF-kB; nuclear factor-kappa B; cancer; viral infection; autoimmune disorder; systemic lupus erythematosus; immune-mediated glomerulonephritis; arthritis; immune disorder; multiple sclerosis; Hashimoto's thyroiditis; atopic condition; asthma; allergy; psoriasis; contact dermatitis; gastrointestinal allergy; insulin-dependent diabetes;
                                                                        LSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTIPCSSAINPLSTAGNSERLQ
                                                                                                                                                        PGIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD
                                                          QLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying modulators of long form of caspase recruitment domain, C
4L useful for treating cancer, infections, and immune disorders, by
contacting test compound with CARD-4L and determining effect of the
                                   ö
                                                                                                                                                                                                                  TTDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM 540
                                                                                                                                                                                                      TIDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM 232
            Length 540;
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bacterial infection; tuberculosis; lepromatous leprosy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bertin J, Philpott D, Sansonetti P, Girardin S;
            Score 1176; DB 4;
Pred. No. 2.4e-114;
                                                                                                                                                                                                                                                                                                                                                              Human caspase recruitment domain protein CARD-3.
                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell signalling disorder; tissue disorder.
                                                                                                                                                                                                                                                                                         ABG31075 standard; protein; 540 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Fig 2; 139pp; English.
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           97.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-DEC-2001; 2001WO-US049798
                                                                                                                                                                                                                                                                                                                                       (first entry)
                                    Matches 226; Conservative
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                         Best Local Similarity
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             Query Match
                                                                                                                                                                                                                                                                  RESULT 12
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The invention relates to identifying (MI) a compound which modulates a human or murine caspase recruitment domain (CARD)-4£ (long form) polypeptide with a by contacting the polypeptide with a test compound and determining the effect of the test compound on the activity of the polypeptide to identify a compound which modulates the polypeptide. The method may be adapted for identifying a compound which binds to the LARD (leucine rich repeat) domain of CARD-4. Also included is a method of

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identifying a candidate compound for modulating LPS (lipopolysaccharide)-
mediated activation of nuclear factor-kappa B (NF-kB), by providing a
cell expressing a polypeptide comprising the LRR domain of CARD-4 and
harbouring LPS, exposing the cell to a test compound and measuring NF-kB
activation, where altered NF-kB activation polypeptide in the presence of
the test compound compared to the binding in the absence of the test
compound indicates that the test compound is a candidate compound for
modulating LPS-mediated activation of NF-kB. Modulators identified by
compound indicates that the test compound is a candidate compound for
modulating LPS-mediated activation of NF-kB. Modulators identified by
compound indicates that a disorder characterised by abstract CARD-4
protein or nucleic acid. Compounds that modulate the activity of CARD-4
care useful to treat or diagnose disorders such as cancer, viral
infections, autoimmune disorders e.g. systemic lupus erythematosus,
immune-mediated glomerulonephritis and arthritis, immune disorders, such
as multiple sclerosis, Hashimoto's thyroiditis, acopic conditions such as
as multiple sclerosis, Hashimoto's thyroiditis, acopic conditions such as
as multiple sclerosis, and lepromatous leprosy, disorders of cell signaling and
tuberculosis, and lepromatous leprosy, disorders of cell signaling and
disorders of tissues. The present sequence represents human CARD-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97.5%; Score 1176; DB 5;
99.1%; Pred. No. 2.4e-114;
iive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein of human CARD-3 SEQ ID No 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAO22107 standard; protein; 540 AA
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98US-00099041.
98US-00207359.
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Best Local Similarity 99.1'
Matches 226; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 540 AA;
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17-JUN-1998;
08-DEC-1998;
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Homo sapiens.

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The invention relates to novel isolated Caspase Recruitment Domain (CARD) polypeptides, CARD-41 and CARD-45. The CARD proteins of the invention may be supplementing the patient's own production of CARD. Disorders associated with decreased CARD expression by supplementing the patient's own production of CARD. Disorders associated with the expression and activity of CARD include cancers (particularly follicular lymphomas, carcinomas associated with mutations in p53, and hormone-dependent tumours such as brass cancer, prostate cancer, and ovarian cancer, autoimmune-mediated glomerulonephritis), viral infections erythematosus, immune-mediated glomerulonephritis), viral infections cured by herspes viruses, poxviruses, and adenoviruses), neurological diseases (such as Alzheimer's disease, Parkinson's disease, amylotrophic lateral sclerosis (ALS) retinitis pigmentosa, spinal muscular atrophy, and various forms of cerebellar degeneration), anemia and the myelodysplastic syndromes. This sequence represents a human CARD protein relating to the invention
                                                                                                                                            Isolated Caspase Recruitment Domain (CARD) polypeptides (CARD-4L and CARD-4S) useful for diagnosing and treating e.g. Parkinson's and Alzheimer's disease, cancers and viral infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  313 KLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDF 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   373 LSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTIPCSSAIINPLSTAGNSERLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 540;
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Pred. No. 2.4e-114;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Caspase recruitment domain protein, CARD-3.
                                                                                                                                                                                                                                 Example 2; Fig 2; 116pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU56269 standard; protein; 540
  (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.1%;
Matches 226; Conservative
                                                                                                   N-PSDB; AAL40752, AAL40753.
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                                                                                  2002-391988/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 540 AA;
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                                           Bertin J;
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The invention relates to an isolated polypeptide, comprising at least 25 contiguous amino acids of a human caspase recruitment domain (CARD)-47, human CARD-42 or murine CARD-41 (all splice variants of CARD-4)

contiguous amino acids of a human caspase recruitment domain (CARD)-47, human CARD-42 or murine CARD-41 (all splice variants of CARD-41)

colypeptide. Also included is an isolated fusion protein, comprising the CARD polypeptide is useful in screening assays, colypeptide. The CARD polypeptide is useful in screening assays, catection assays (e.g. chromosomal mapping, tissue typing and forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, conjocing clinical trials and pharmacogenomics), and in therapeutic and prophylactic treatments (in diseases associated with apoptotic call death e.g. cancers, autoimmune disorders (e.g. systemic lupus erythematosus and immune related glomerulonephitatis), viral infections, AIDS (acquired immunodeficiency syndrome), neurological disease (e.g. Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis dismentosa, spinal muscular atrophy and cereballar degeneration), heamatological diseases (e.g. anaemia, neutropaenia and myelodysplastic syndromes), myocardial infarction and stroke). The CARD polypeptide is useful as bait protein in a two-hybrid assay or three hybrid assay to identify other proteins, which bind to or interact with other CARD conteins, ABDS (accepted on chromosome 7. The present sequence is a human care care and an enterpresent sequence is a human care care and care ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated human caspase recruitment domain (CARD)-4Y or CARD-4Z polypeptide, or murine CARD-4L polypeptide, useful in screening assays, detection assays, predictive medicine, and in therapeutic applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           313 KLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDF
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                                                                                                                                                       98US-00207359.
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98US-00099041
                                                                                                                                                                                                                                                                                    (MILL-) MILLENNIUM PHARM INC
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N-PSDB; ABX75869, ABX74870.
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                                                US6469140-B1
                                                                                                                                                     08-DEC-1998;
                                                                                                                                                                                                        06-FEB-1998;
                                                                                                                                                                                                                              17-JUN-1998;
                                                                                                    22-OCT-2002
                                                                                                                                                                                                                                                                                                                                          Bertin J;
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ADB81362 standard; protein; 540 AA.

RESULT 15

ADB81362 П us-09-771-161a-93.rag

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This invention relates to two novel genes CARD-3 and CARD-4 (caspase recruitment domains), which are mediators of apoptosis and are useful in the identification of compounds that modulate apoptosis. Specifically, CARD-3 (also known as RIPZ, RICK and CARDIAK) is known to be a mediator. of p75 (a member of the tumour necrosis factor (TNF) family), and is believed to provide the switch for cell survival and cell death decisions mediated by this p75 neutrophin receptor. Accordingly these genes, and the proteins encoded thereof, are linked to certain disorders associated with an increased number of cells surviving and proliferating when apoptosis is inhibited. These include cancer, autoimmune disorders e.g. systemic lupus and immune mediated glomerulonephritis, viral infections such as those caused by the herpesvirus, neurological disorders such as retinitis pigmentosa, haematologic diseases including chronic neutropenia, as well as myocardial infarction and strokes. The present compound alters the binding of CARD-3 to p75, which comprises measuring the death domain of p75, which comprises measuring the binding of a polypeptide containing the presence and absence of the test compound, and determining is placered. This polypeptide is the human CARD-3 protein sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 1; 40pp; English
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Gaps

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97.5%; Score 1176; DB 7; Length 540; 99.1%; Pred. No. 2.4e-114; Live 1; Mismatches 1; Indels C

Conservative

Best Local Similarity Matches 226; Conserv

Query Match

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tumour necrosis factor; TNF; neutrophin receptor; cancer; autoimmune disorder; systemic lupus; immune mediated glomerulonephritis; viral infection; neutrological; retinitis pigmentosa; haematologic; chronic neutropenia; myocardial infarction; seroke; RIP; RICK; CARDIAK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting compounds which alter binding of the caspase recruitment doma. (CARD) of CARD-3 polypeptide to the neurotrophin receptor p75 is useful to provide compounds for treating CARD-3 mediated disorders.
                                                                                                                                     human; CARD-3; CARD-4; caspase recruitment domain; apoptosis; p75;
                                                                                       Human caspase recruitement domain 3 (CARD-3) protein.
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                                                                                                                                                                                                                                                                                                                                                                        = Kinase_domain
                                                                                                                                                                                                                                                                                                                                                                                                                      = Linker_domain
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N-PSDB; ADB81363.
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CHAO M V.
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17-JUN-1998;
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ADB81362;
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(CHAO/)
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64
                313 KLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDF
                                                                                           5 QLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDF
                                                                     LSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLO
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; APPLICANT: Koseki, Takeyoshi
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Sequence 41, Appl
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Sequence 4, Appli
Sequence 3, Appli
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Sequence 28,
Sequence 1, 7
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(cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

(cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

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(cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

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   version 5.1.6 - 2004 Compugen Ltd.
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US-09-470-271-1
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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1111222244460000011110000111100000000000	tion US/ : Gabriel ' Nachir ' Nachir : COMPOS : SIGNAL : SIGNAL N NUMBER E: 1998- OS: 38 Ver. 2.	98.0% imilarity 99.6% Conservative OLGSVSSAIHLCDKKKW KLQSVSSAIHLCDKKKKH KLQSVSSAIHLLDKKKKHHCP ILSRKAQDCYFWKLHHCP ILSRKAQDCYFWKLHHCP ILSRKAQDCYFWKLHHCP ILSRKAQDCYFWKLHHCP ILSRKAQDCYFWKLHHCP ILSRKAQDCYFWKLHHCP ILSRKADDCYFWKLHHCP ILSRKADDCYFWKLHHCP ILSRKADCYFWKLHHCP ILSRKADCYFWKLHHCP ILSRKADCYFWKLHHCP ILSRKADCYFWKLHHCP ILSRKADCYFWKLHHCP ILSRKADCYFWKLHHCP ILSRKADCFFWKLHCHCP ILSRKADCFFWKLHCP ITDIGGEEFAKVIVQKL ITDIGGEEFAKVIVQKL ITDIGGEEFAKVIVQKL Application US/09 3348573 Numaz, Gabriel Inobjara, Naohiro
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9-207-359B-41 9-340-620A-41 9-265-364-41 9-265-364-41 9-207-359B-39 9-307-359B-39 9-307-359B-46 9-207-359B-46 9-207-359B-8 9-207-359B-8 9-207-359B-8 9-207-359B-8 9-207-359B-8 9-207-359B-8 9-207-359B-8 9-207-359B-8 9-340-620A-8 9-340-620A-8 9-340-620A-8 9-340-620A-10	RESULT 1 US-09-069-023-5 Sequence 5, Application US/09069023A Sequence 5, Application US/09069023A Sequence 1. Application US/09069023A GENERAL INFORMATION: APPLICANT: Innohara, Takeyoshi TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDE TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDE TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDE TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND FILE REFERENCE: US-0333A CURRENT FILING DATE: 1998-04-27 CURRENT FILING DATE: 1998-04-27 SOFTWARE: RECENTION VOY: 2.0 SEQ ID NO 5 LENGTH: 284 LENGTH: 284 LYPE: PRT ORGANISM: Homo sapiens US-09-069-023-5	98.0%; Score 1182; DB 4; Length 2
Sequence 41, Sequence 41, Sequence 41, Sequence 39, Sequence 39, Sequence 39, Sequence 46, Sequence 46, Sequence 8, A Sequence 8, A Sequence 10, Seq	IDENTIFYING APOPTOSIS AND ACTIVATORS	98.0%; Score 1182; DB 4; Length 284; imilarity 99.6%; Pred. No. 1.9e-125; Conservative 1; Mismatches 0; Indels 0; Gaps CLOSSENAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPODNDF CLSKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ LSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ LSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ LSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ PGIAQQWIGSKREDIVNQWTEACLNGSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD PGIAQQWIGSKREDIVNQWTEACLNGSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD TTDIQGEEFAKVIVQKLKDNKQMGLQPYPEILLVVSRSPSLNLLQNKSM 232 TTDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM 232 TTDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM 284 AAPDIcation US/09069023A RMATION: Numez, Gabriel Inobara, Nachiro
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TYPE: PRT
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Patent No. 6348573

Patent No. 6348573

Patent No. 6348573

Patent No. 6348573

APPLICANT: INFORMATION:
APPLICANT: Indhara, Nachiro
APPLICANT: Inchara, Nachiro
APPLICANT: Expension: Compositions and METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333

CURRENT APPLICANION NUMBER: US/09/069,023A

CURRENT FILING DATE: 1998-04-27

NUMBER OF SEQ ID NOS: 38

SOFTWARE: Patentin Ver. 2.0
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS FILE REFERENCE: UM-03333 CURRENT APPLICATION NUMBER: US/09/069,023A CURRENT FILING DATE: 1998-04-27 NUMBER OF SEQ ID NOS: 38 SOFTWARE: PATENT VET. 02: 2.0
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Pred. No. 4.2e-125;
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Best Local Similarity 99.6'
Matches 227; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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                                                                                                              Sequence 1, Application US/09069023A
| Sequence 1, Application US/09069023A
| Patent No. 6346573
| GENERAL INFORMATION:
| APPLICANT: Nunez, Gabriel
| APPLICANT: Inohara, Naohiro
| APPLICANT: Koseki, Takeyoshi
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
| TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
| FILE REFERENCE: UM-03333
| CURRENT APPLICATION NUMBER: US/09/069,023A
| CURRENT PAPLICATION NUMBER: 1998-04-27
| NUMBER OF SEQ ID NOS: 38
| SOGTWARE: PatentIn Ver. 2.0
| SEQ ID NO: 18
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APPLICANT: Nunez, Gabriel
APPLICANT: Inchara, Nachiro
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
CURRENT APPLICATION NUBER: US/09/069,023A
CURRENT FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.0
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483 TIDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM 530
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Pred. No. 5e-125;
1; Mismatches 0;
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99.6%; Pred. No. 5.1e-125;
live 1; Mismatches 0;
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Best Local Similarity 99.6%;
Matches 227; Conservative
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Matches 227; Conservative
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Best Local Similarity
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65 LSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124
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TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-076001
CURRENT APPLICATION NUMBER: US/09/099, 041A
CURRENT FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,942 102 & FILING DATE: 06-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FILING DATE:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REGISTRATION VUMBER: 07334/068001
TELECOMMUNICATION INFORMATION:
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99.1%; Pred. No. 2.5e-124;
iive 1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                       TELEX: 200154
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                              TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
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Matches 226; Conservative
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MOLECULE TYPE: protein
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CORGANISM: Homo sapiens
US-09-099-041A-2
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LENGTH: 540
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                                                                                                                     125 PGIAQOWIQSKREDIVNOMTEACLNOSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
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Patent No. 6558903
GENERAL INFORMATION:
TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof
FILE REFERENCE: 35800/183781
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSEQ for Windows Version 4.0
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Patent NO. 6033855
GENERAL INCRMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
TITLE OF INVENTION: DOMAIN POLYPEPTIDES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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99.6%; Pred. No. 5.1e-125;
iive 1; Mismatches 0;
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225 Franklin Street
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Best Local Similarity 99.6'
Matches 227; Conservative
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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CITY: Boston
STATE: MA
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US-09-345-473E-28
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LENGTH: 540
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US-09-019-942-1
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                                              373 LSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTIPCSSAIINPLSTAGNSERLO 432
                                                                                                                                                                                   313 KLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDF 372
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LSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124
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Patent No. 6369196

GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: 07334/118001

CURRENT APPLICATION NUMBER: US/09/245,281

CURRENT FILING DATE: 1999-02-05

BEARLIER APPLICATION NUMBER: US 09/207,359

EARLIER PELICATION NUMBER: US 09/207,359

EARLIER PILING DATE: 1998-06-17

FEARLIER APPLICATION NUMBER: US 09/099,041

EARLIER PILING DATE: 1998-06-17

MUMBER OF SEQ ID NOS: 44

SOFFWARE: FREUSE FALSE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 QLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDF 64
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Patent No. 6410689
GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
TITLE OF INVENTION: DOMAIN POLYPEPTIDES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
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99.1%; Pred. No. 2.5e-124;
tive 1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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STREET: 22.
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LENGTH: 540
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US-09-470-271-1
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STATE:
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313 KLQSVSSAIHLCDKKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDF 372
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; Sequence 2, Application US/09207359B
; Patent No. 646540
; GENERAL INFORMATION:
    APFLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/207,359B
; CURRENT APPLICATION NUMBER: US 09/099,041
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-06-17
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOOTWARE: FastSEQ for Windows Version 4.0
; TENGTH: 540
                                                                                                                                                            COMPUTER: 110m COMPUTER:
OPERATING SYSTEM: Windows 95
SOFTWARE: FEASTER: Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/470,271
FILING DATE:
PRIOR APPLICATION NUMBER: 09/019,942
FILING DATE:
APPLICATION NUMBER: 09/019,942
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Weiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/068001
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFAX: 20154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TENTAL AND ASSIGNED A
                                                                                                                                 COMPUTER: IBM Compatible
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amino acid
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Matches 226; Conservative
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                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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02110-2804
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APPLICANT: Bertin, John
APPLICANT: Chao, Moses V.

ITLE OF INVENTION: NOUSE MOLECULES OF THE CARD-RELATED PROTEIN FAMILE AND USES THEREC
FILE REFERENCE: 07334-316001
CURRENT APPLICATION NUMBER: US/09/748,537
CURRENT PILING DATE: 2000-12-26
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 14
SSOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 540
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APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-112001
CURRENT APPLICATION NUMBER: US/09/865,364
CURRENT FILING DATE: 1904-12-08
PRIOR APPLICATION NUMBER: US 09/207,359
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR FILING DATE: 1998-12-08
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR PLILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 2
TOWNWEL FASTESEQ for Windows Version 4.0
SEQ ID NO 2
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99.1%; Pred. No. 2.5e-124;
iive 1; Mismatches 1;
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Pred. No. 2.5e-124;
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99.1%;
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Matches 226; Conservative
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; ORGANISM: Homo sapiens
US-09-748-537-1
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CORGANISM: Homo sapiens
US-09-865-364-2
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Best Local Similarity
Matches 226; Conserv
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TITLE OF INNENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
FILE REPERENCE: 07334-124001
CURRENT APPLICATION NUMBER: US/09/340,620A
CURRENT APPLICATION NUMBER: US 09/245,281
PRIOR APPLICATION NUMBER: US 09/245,281
PRIOR FILING DATE: 1999-02-05
PRIOR FILING DATE: 1999-102-05
PRIOR PILING DATE: 1998-12-08
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 71
SOFTWARE: FASTESEQ for Windows Version 4.0
                                                                                                                                           313 KLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDF 372
                                                                                                                                                                                                                   124
                                                                                                                                                                                                                                          433 PGIAQOWIQSKREDIVNOMTEACLNOSLDALLSRDLIMKEDYBLVSTKPTRTSKVRQLLD 492
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                                                               Gaps
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               Length 540;
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                                                               1; Indels
          Ouery Match 97.5%; Score 1176; DB 4;
Best Local Similarity 99.1%; Pred. No. 2.5e-124;
Matches 226; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 97.5%; Score 1176; DB 4;
Best Local Similarity 99.1%; Pred. No. 2.5e-124;
Matches 226; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09340620A Patent No. 6482933 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09865364
Patent No. 6613521
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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US-09-865-364-2
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                                                                                         PGIAQQWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492
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                                                                 PGIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
                                                                                                                                                                                                                                             RESULT 15
US-09-069-023-6
US-09-069-023-6
| Sequence 6, Application US/09069023A
| Patent No. 6346573
| GENERAL INFORMATION:
| APPLICANT: Nunez, Gabriel
| APPLICANT: Koseki, Takeyoshi
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
| TITLE OF INVENTION: COMPOSITIONS AND ACTIVATORS
| FILE REFERENCE: UM-03333
| CURRENT APPLICATION NUMBER: US/09/069,023A
| NUMBER OF SEQ ID NOS: 38
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NO 6
| LENGTH: 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                           TTDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM 540
                                                                                                                                                TIDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM 232
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Pred. No. 4e-90;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 71.9%; Score 867; DB Best Local Similarity 100.0%; Pred. No. 4e-Matches 167; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: March 29, 2004, 14:10:44 Job time : 23 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
US-09-069-023-6
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Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 5, Appli
Sequence 5, Appli
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Sequence 5, Appli
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Sequence 184, App
Sequence 28, Appl
Sequence 14, Appl
Sequence 1, Appl
Sequence 2, Appli
Sequence 2, Appli
                                                                                                                                                                                                                                (without alignments)
1411.757 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                1206
1 MYSLQLQSVSSAIHLCDKKK.....PBILVVSRSPSLNLLQNKSM 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US07_BUBW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

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19: /cgn2_6/ptodata/1/pubpaa/US107_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-771-161A-184
US-09-862-027-28
US-09-981-397A-14
US-09-982-301-1015
US-09-748-537-1
US-09-748-537-1
US-09-728-721-2
US-10-133-780-1
3 US-10-118-984-2
4 US-10-295-991-2
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US-10-105-931-5
US-10-118-984-5
US-10-295-981-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1065169 seqs, 261661801 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Perfect score:
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Maximum DB
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Sequence 6, Appli
Sequence 7, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 11, Appli
Sequence 71, Appli
Sequence 71, Appli
Sequence 71, Appli
Sequence 41, Appli
Sequence 39, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 10, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL LINCORTAILO...

JAPPLICANT: LEVINE. et al.

TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1

CURRENT PAPLICATION NUMBER: US/09/771,161A

CURRENT FILING DATE: 2001-01-26
PRIOR PILING DATE: 2000-11-28
PRIOR PILING DATE: 2000-06-15
PRIOR PLING DATE: 2000-06-15
PRIOR FILING DATE: 2000-04-12
                                                                                                                                                                                                                                               US-10-118-984-41

US-10-295-981-41

US-10-295-981-43

US-10-118-984-39

US-10-295-981-39

US-10-295-981-39

US-10-194-3

US-10-194-3

US-10-105-931-8

US-10-105-931-8

US-10-105-931-8

US-10-105-931-8

US-10-118-984-8

US-10-295-981-8

US-10-295-981-8

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US-10-295-981-8

US-10-295-981-8

US-10-295-981-8
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US-09-931-071-11
US-09-728-721-71
US-10-295-981-71
US-09-728-721-71
US-09-728-721-41
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Best Local Similarity 100.
Matches 232; Conservative
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US-09-925-301-1015
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US-09-981-397A-14
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Patent No. US20020142428A1
GENERAL INFORMATION:
APPLICANT: Hodge, Martin R.
TITLE OF INVENTION: No. US20020142428A1e1 Kinases and Uses Thereof
FILE REFERENCE: 35800/234862
CURRENT APPLICATION NUMBER: US/09/862,027
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 09/345,473
PRIOR FILING DATE: 1999-06-30
                                         QLLDTTDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM 232
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Patent No. US20020110811A1
GENERAL INFORMATION:
FILLS OF INVENTION: et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT FILING DATE: 2001-01-26
PRIOR PILING DATE: 2000-11-28
PRIOR PILING DATE: 2000-11-28
PRIOR PLING DATE: 2000-06-15
PRIOR PLING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
SPRIOR FILING DATE: 2000-06-15
SPRIOR FILING DATE: 2000-06-15
SURMER OF SEQ ID NOS: 273
SOFTWARE PATENTIN VERSION 3.0
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Pred. No. 2.7e-108;
1; Mismatches 0;
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SOFTHARRE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 540
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227; Conservative
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US-09-862-027-28
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CORGANISM: Homo sapiens
US-09-771-161A-184
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US-09-771-161A-184
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Best Local
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DB 9; Length 540;

Score 1182;

98.08;

Query Match

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APPLICANT: Schubart, Daniel
APPLICANT: Habenberger, Peter
APPLICANT: Habenberger, Peter
APPLICANT: Stein-Garlach, Matthias
APPLICANT: Stein-Garlach, Matthias
APPLICANT: Bevec, Dorian
TITLE OF INVENTION: Callular Kinases Involved in Cytomegalovirus Infection and their
TITLE OF INVENTION: Inhibition
FILE REFERENCE: AXM-004.1 US
CURRENT APPLICATION WUMBER: US/09/981,397A
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: 60/240,750
PRIOR FILING DATE: 2000-10-16
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
SEQ ID NO 14
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Fatent No. US20020052308A1
GENERAL INFORMATION:
APPLICATE ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
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                                Indels
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Pred. No. 2.7e-108;
1; Mismatches 0;
99.6%; Pred. No. 2.7e-108;
tive 1; Mismatches 0;
                           1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Axxima Pharmaceuticals AG
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Best Local Similarity 99.6
Matches 227; Conservative
     Best Local Similarity 99.6
Matches 227; Conservative
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APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREC
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREC
CURRENT APPLICATION NUMBER: US/09/728,721
CURRENT FILING DATE: 2000-12-01
PRIOR PELING DATE: 1999-06-28
PRIOR APPLICATION NUMBER: US 09/207,359
PRIOR PILING DATE: 1998-12-08
PRIOR PILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR PILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: US 09/019,942
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Publication No. US20020123115A1
GENERAL INPORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
DOMAIN POLYPEPTIDES
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Pred. No. 1.1e-107;
1; Mismatches 1;
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ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
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Patent No. US20020061845A1
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MEDIUM TYPE: Diskette
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Best Local Similarity 99.1%;
Matches 226; Conservative
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COUNTRY: USA
ZIP: 02110-2804
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CRGANISM: Homo sapiens
US-09-728-721-2
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US-10-133-780-1
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Patent No. US20020061833A1
GENERAL INFORMATION:
APPLICANT: Bertin, John
APPLICANT: Chao, Moses V.
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILE AND USES THERE
PILE REPERENCE: 07334-316001
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Pred. No. 1.1e-107;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                      Score 1182; DB 9;
Pred. No. 2.7e-108;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/748,537
CURRENT FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 1
SEQ ID NO 1
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver. 2.0
SERVANE: 544
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99.1%;
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Best Local Similarity 99.6°
Matches 227; Conservative
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Best Local Similarity 99.1
Matches 226; Conservative
                                                                                                                                                                                                                                                                     TYPE: PRT; ORGANISM: Homo sapiens
US-09-925-301-1015
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US-09-748-537-1
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US-10-295-981-2
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US-10-105-931-2

Sequence 2, Application US/10105931

Publication No. US20020150987A1

GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

FILE REFERENCE: 07334-076001

CURRENT APPLICATION NUMBER: US/10/105,931

CURRENT APPLICATION NUMBER: 09/099,041

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSEQ for Windows Version 4.0 '

SEQ ID NO 2

LENGTH: 540

TYPE: PRI

TYPE: PRI

SCALUS-105-931-2
OPERATING SYSTEM: Windows 95
SOFTWARE: FEALSEO for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/133,780
FILING DATE: 26-Apr-2002
PRIOR APPLICATION NUMBER: US/09/019,942
FILING DATE: 06-FEB-1998
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 35,23
REFERENCE/DOCKET NUMBER: 35,23
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-133-780-1
                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
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Best Local Similarity 99.1
Matches 226; Conservative
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APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREC
FILE REFERENCE: 07334-124001
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; Publication No. US20020197693A1
; GENREAL INFORMATION:
APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 07334/118001
; CURRENT FILING DATE: 2002-04-09
; FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281
; PRIOR FILING DATE: BARLIER FILING DATE: 1999-02-05
; PRIOR PELING DATE: BARLIER FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: BARLIER FILING DATE: 1998-06-17
; PRIOR FILING DATE: BARLIER FILING DATE: 1998-06-17
; PRIOR FILING DATE: BARLIER FILING DATE: 1998-06-17
; PRIOR FILING DATE: BARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FASESEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: SA0
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                                                                                                                                                65 LSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124
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64
5 QLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDF
                                                              313 KLÓSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 TIDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM 232
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; Publication No. US20030120055A1
; GENERAL INFORMATION:
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US-10-118-984-2
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Sequence 5. Application US/10118984

Sequence 5. Application WS/10118984

Publication No. US20020197693A1

GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY

CURRENT APPLICATION NUMBER: BEALIER APPLICATION NUMBER: US/09/245,281

PRIOR APPLICATION NUMBER: EARLIER PELICATION NUMBER: US 09/09,041

PRIOR APPLICATION NUMBER: EARLIER PELICATION NUMBER: US 09/099,041

PRIOR APPLICATION NUMBER: EARLIER PELICATION NUMBER: US 09/099,041

PRIOR APPLICATION NUMBER: EARLIER PLING DATE: 1998-06-17

PRIOR PLING DATE: EARLIER FILING DATE: 1998-06-17

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-06

NUMBER OF SEQ ID NOS: 44

SEQ ID NOS: 44

SEQ ID NOS: 44

SEQ ID NOS: 45

SEQ ID 
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13 KLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDF 72
                                                                                                                                       73 LSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTIPCSSAIINPLSTAGNSERL 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.4%; Score 632; DB 13; Length 131; 98.3%; Pred. No. 1.3e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-076001
CURRENT APPLICATION NUMBER: US/10/105,931
CURRENT APPLICATION NUMBER: 09/099,041
PRIOR APPLICATION NUMBER: 09/099,041
PRIOR FILING DATE: 1998-06-17
PRIOR PRIUMG DATE: 1998-06-17
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO SEQ ID NOS: 37
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                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/10105931 Publication No. US20020150987A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 98.3
Matches 117; Conservative
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ORGANISM: Homo sapiens
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CORGANISM: Homo sapiens
US-10-118-984-5
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US-10-118-984-5
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TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
FILE REFERENCE: 07334-124001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              372
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CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US/340,620
PRIOR FILING DATE: 1999-06-28
PRIOR FILING DATE: 1998-12-08
PRIOR FILING DATE: 1998-12-08
PRIOR FILING DATE: 1998-12-08
PRIOR FILING DATE: 1998-12-08
PRIOR FILING DATE: 1988-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 71
SOUTHARE: FRALESQ for Windows Version 4.0
SEQ ID NO 5
                                CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: US/09/340,620
PRIOR FILING DATE: 1999-06-28
PRIOR PELICATION NUMBER: US 09/245,281
PRIOR APPLICATION NUMBER: US 09/245,281
PRIOR APPLICATION NUMBER: US 09/207,359
PRIOR PELING DATE: 1998-12-08
PRIOR PELING DATE: 1998-06-17
PRIOR PELING DATE: 1998-06-17
PRIOR PELING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 71
SOFTWARE: FastSEQ for Windows Version 4.0
   CURRENT APPLICATION NUMBER: US/10/295,981
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99.1%;
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Best Local Similarity 99.1<sup>5</sup>
Matches 226; Conservative
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Best Local Similarity 98.3
Matches 117; Conservative
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, ORGANISM: Homo sapiens
US-09-728-721-5
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US-10-295-981-2
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RESULT 15

US-10-295-981-5

i Sequence 5. Application US/10295981

i Publication No. US20030120055A1

i GENERAL INFORMATION:

TITLE DESTRIPTION:

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE

FILE REFERENCE: 07334-124001

CURRENT APPLICATION NUMBER: US/09/340,620

PRIOR PILING DATE: 1999-06-28

PRIOR PILING DATE: 1999-06-26

PRIOR PILING DATE: 1999-06-17

PRIOR PILING DATE: 1999-06-17

PRIOR PILING DATE: 1998-12-06

PRIOR PILING DATE: 1998-12-06

PRIOR PILING DATE: 1998-06-17

LOSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDF 64
                                                               13 KLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDF 72
                                                                                                                                                            LSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERL 123
                                                                                                                                                                                                                                73 LSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTIPCSSAIINPLSTAGNSERL 131
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Best Local Similarity 98.3
Matches 117; Conservative
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ORGANISM: Homo sapiens
US-10-295-981-5
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Search completed: March 29, 2004, 14:11:39 Job time : 43 secs

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OM protein - protein search, using sw model

Run on:

March 29, 2004, 14:06:05; Search time 20 Seconds (without alignments) 1115.822 Million cell updates/sec

US-09-771-161A-93 1206 1 MYSLQLQSVSSAIHLCDKKK.....PEILVVSRSPSLNLLQNKSM 232 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
1: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	f22b7.5 protein -		hypothetical prote	ᅩ	hypothetical prote	MADS box protein D	hypothetical prote	Ė	RNA polymerase sig		Scythe protein - A	ESR1 protein - yea	ğ			transforming prote	DNA-binding protei	mycelial surface a	conserved hypothet	tryptophan dimethy	resistance protein	triacylglycerol li	genome polyprotein	MADS box protein T	hypothetical prote	Ψ	hypothetical prote	o	hypothetical prote
SUPPERMITES	ID	S44636	T00029	T32980	S68450	T29999	S71757	T33922	A55117	B81996	835551	T30561	S46005	T27389	F84869	T41987	S27774	T52092	T17415	G75458	JC4338	T30560	A24545	GNWVHC	S23728	869652	B89797	S66712 ·	I55449	T40953
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df		8.3	.8.1	7.7	7.7	7.5	7.4	7.4	7.4	7.3	٠	. 7.3	•	•	7.2	7.2	7.2	•	•	7.1	7.1	7.1	7.0	7.0	7.0	7.0	7.0	6.9	6.9	•
	Score	100.5	98	93	92.5	90	89	89	89	88	88	88	88	87.5	87	87	86.5	86.5	86.5	85.5	85.5	85.5	85	85	84.5	84.5	84	83.5	83.5	•
	sult No.	i	7	n	4	ស	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

Miranda protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: Jun-1999 #sequence\_revision 22-Jan-1999 #text\_change 17-Nov-2000
C;Accession: T00029
R;Ikeshima-Kataoka, H; Skeath, J.B.; Nabeshima, Y.; Doe, C.Q.; Matsuzaki, F.
Nature 390, 625-659, 1997
A;Title: Miranda directs Prospero to a daughter cell during Drosophila asymmetric divisic
A;Reference number: Z14067; MUID:98065952; PMID:9403694

RESULT 2

hypothetical prote	hypothetical prote		hypothetical prote	hypothetical prote	interleukin-1beta	G-box-binding prot	VPS27 protein - ye	gene Mx protein -	hypothetical prote	MADS box protein D	hypothetical prote	conserved hypothet	CHLPN 76 kDa homol	hypothetical 76K p
S59829	T29482	T25636	T25635	T25634	A56084	S53021	S45129	S31824	T40690	S71756	S50548	D72042	E86581	140729
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# ALIGNMENTS

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C; Accession: T29999
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A;Gene: CESP:ZC8.4
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C;Species: Caenorhabditis elegans
C;Species: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T32980
E;Accession: T32980
E;Accession: T32980
E;Accession: T32980
E;Du, Z.; Maggi, L.
Submitted to the EMBL Data Library, February 1998
A;Description: The sequence of C. elegans cosmid K02D7.
A;Reference number: Z21259
A;Reference undber: Z21259
A;Reference poly
A;Reference DNA
A;Molecule type: DNA
A;Residues: 1-692 < DUZ
A;Residues: 1-692 < DUZ
A;Residues: 1-692 < DUZ
A;Residues: BMBL:AF045645; PIDN:AAC02606.1; GSPDB:GN00022; CESP:T21D12.7
A;Experimental Bource: strain Bristol N2; clone K02D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 IAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDTT 186
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A;Molecule type: mRNA
A;Residues: 1-330 < IRS
A;Cross-references: EMBL:AB005661; NID:g2749776; PIDN:BAA24111.1; PID:g2749777
A;Experimental source: strain Canton-S
C;Genetics:
A;Cross-references: FlyBase:FBgn0021776
A;A;Map position: 92B-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      427 SFGAARHLCCKPRKKCVIPYVDPDKKR-----PIRCFPGDQSC------PIST 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 -IQSKREDIVNOMTEA-CLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIQ 189
                                                                                                                                                                                                                                                                                                                                                                                                  72 CYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQPGIAQQW 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 4
A;Introns: 29/1; 89/1; 127/1; 186/1; 233/1; 291/1; 379/3; 586/3; 611/3; 643/3
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                                                                                                                                                                                                               8.1%; Score 98; DB 2; Length 830; 21.3%; Pred, No. 2.7;
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                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                               39; Mismatches
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211 HKAL-----NEQMG-QEHADLL 226
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                                                                                                                                                                                                                                                                 44; Conservative
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Matches 44; Conserva
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C. Species: Homo sapiens (man)
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000
C; Accession: 868450
R; Liston, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani, Nature: 379, 340-353, 1996
A; Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP A; Reference number: A58182; MUID:96149249; PMID:8552191
A; Recession: S68450
A; Accession: S68450
A; Accession: S68450
A; Molecule type: mRNA
A; Residues: 1-618 < LIS>
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A;Introns: 43/2; 80/3; 110/3; 153/2; 274/3; 738/2; 1249/1; 1392/3; 1454/1; 1602/1; 1686/
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
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A;Nolecule type: DNA
A;Molecule type: DNA
A;Rossidues: 1-2288 <LAT>
A;Cross-references: EMBL:U64862; PIDN:AAB52624.1; GSPDB:GN00028; CESP:ZC8.4
A;Experimental source: strain Bristol N2; clone ZC8
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                                       85; Indels 54;
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submitted to the EMBL Data Library, July 1996
A;Description: The sequence of C. elegans cosmid ZC8.
A;Reference number: Z20719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
7.5%; Score 90; DB 2
Best Local Similarity 20.8%; Pred. No. 53;
Matches 47; Conservative 40; Mismatches
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Best Local Similarity 24.5%; Pred. No. 5.5;
Best Actobes 27; Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.7%; Score 92.5;
34.5%; Pred. No. 5.
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C,Superfamily: RING finger homology
C,Keywords: apoptosis; zinc finger
F,567-611/Domain: RING finger homology <RNG>
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627 SMSSECNTFDEAHFCKTI 644
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RNA polymerase sigma factor NWA0049 [imported] - Neisseria meningitidis (strain Z2491 ser C; Species: Neisseria meningitidis
C; Species: Neisseria meningitidis
C; Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C; Accession: B81996
R; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel]
HOlroyd, S; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A; Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A; Reference number: A81775; MUID: 20222556; PMID: 10761919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GB:AL162752; GB:AL157959; NID:g7378778; PIDN: CAB83366.1; PID:g7378824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is related to a mitotic checkpoir
                                                                                                                                                                                                                            10;
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                                                                                ------CYFMKLHHCPGNHSWDSTISGSQRAAFCD 100
                                                                                                                                                                                             ---SKREDIVNOM 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAPQDNDFLSRKAQDCYFMKLHHCP--GNHSWDSTISGSQRAAFCDHKTTPCSSAIINPL 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                342 PSISNMGVLSRA-----HSPALGVHSF----SGAORFNLSSHSOSPKRHSISHSP 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 STAGNSERLOPGIAQOWIQSKREDIVNOMTEACLNQSLDALLSRDLIMKEDYELVSTKPT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 28-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 17-Mar-2000 C;Accession: A55117  
R;Starborg, M.; Brundell, E.; Gell, K.; Hoeoeg, C. J. Biol. Chem. 269, 24133-24137, 1994  
A;Title: A novel murine gene encoding a 216-kDa protein is related to a mitc A;Reference number: A55117; MUID:95014147; PMID:7929068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 SLOLOSVSSAI - - HLCDKKKMELSLNIPVNH - - - - GPOEESCGSSOLHENSGSPETSRSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291 TLONATTSSSLTAHLRSLSKGESPVASPFONYSSIHSOSRSTSSPSLHSRS-----
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A;Cross-references: GB:X80169; NID:g562764; PIDN:CAA56450.1; PID:g642252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72; Indels
                                                                                                                                                                                             101 HKTTPCSSAIINP -- LSTAGNSERLOPGIAQOWIO--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             388 SGSFNDSFLAP-----ETEPIV---PELCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.4%; Score 89; DB 25.4%; Pred. No. 52; tive 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 RTSKVRQLLDTTDIQGEEFAKVIVQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tsg24 protein - mouse
N/Alternate names: bimE protein homolog
C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                             1138 GCACTGNATD 1147
                                                                                                                                                                                                                                                                                                       144 TEACLNQSLD 153
                                                                                   62 NDFLSRKAQD----
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C,Superfamily: bimE protein
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Best Local Similarity
Matches 52; Conservat
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A; Residues: 1-283 < PAR>
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Cross-references: EMBL:X95469; NID:g1239958; PIDN:CAA64743.1; PID:g1239959

Cross-references: EMBL:X95469; NID:g1239958; PIDN:CAA64743.1; PID:g1239959

Scrown Farmacription factor squa; serum response factor DNA-binding domain homoly skeywords: DNA binding; transcription regulation

Scrown Ferum response factor DNA-binding domain homology <SRF>
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introns: 43/3; 69/3; 134/3; 174/1; 604/2; 643/3; 718/3; 787/3; 848/2; 944/2; 1044/2;
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A;Cross-references: EMBLAF125461; PIDN:AAD12852.1; GSPDB:GN00020; CESP:Y8A9A.2
A;Experimental source: strain Bristol N2; clone Y8A9A
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 RKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQPG 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 SQQEYLKLKARYEALQRSQRNLLGEDLGPLNSKELESLERQLDMSLKQIRSTRTQAMLDT 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83
                                                                                                                                                                                                                 MADS box protein DEFH200 - garden snapdragon
C;Species: Antirrhinum majus (garden snapdragon)
C;Species: Antirrhinum majus (garden snapdragon)
C;Date: 11-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 20-Jun-2000
C;Accession: S71757
R;Davies, B.; Egea-Cortines, M.; de Andrade Silva, E.; Saedler, H.; Sommer,
EMBO J. 15, 4330-4343, 1996
A;Title: Multiple interactions amongst floral homeotic MADS box proteins.
A;Reference number: S71757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein Y8A9A.2 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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                                                            | : | | : :| | | : :-| | | KLENELEKLRNENKELVGKEARARDAANQQLSRANLLNKELEDTKQ 907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65; Indels
                               KEDYELVSTKPTRTSKVRQLLDTTDIQGEEF--AKVIVQKLKDNKQ
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R, Courtney, L.; Langston, Y.; Drone, K.; Mead, K.
submitted to the EMBL Data Library, February 1999
A, Description: The sequence of C. elegans cosmid Y8A9A.
A, Reference number: Z21439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 89; DB 2;
Pred. No. 3.1;
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; Pred. No. 32;
25; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.4%; Scor.
21.1%; Pred. No. 3.1.
'*** 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: nucleic acid sequence not shown
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Matches 39; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.Keywords: DNA C.E. Sponse to F;2-57/Domain: serum response to F;2-57/Domain: domain K <KDO>F;94-159/Domain: domain K
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Best Local Similarity
Matches 48; Conserv
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A,Map position: 2
A;Introns: 43/3: 69/3
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transcription factor IIF chain RAP74 - African clawed frog
('Species: Xenopus laevis (African clawed frog)
('Species: Xenopus laevis (African clawed frog)
('Date: 09-Dec-1993 #sequence_revision 26-May-1995 #text_change 21-Jul-2000
('Accession: 835551
R)Gong, D.W., Hasegawa, S.; Wada, K.; Roeder, R.G.; Nakatani, Y.; Horikoshi, M.
Nucleic Acids Res. 20, 6736, 1992
A)Title: Elucidation of three putative structural subdomains by comparison of primary st
A)Reference number: S35551, MUID:93126122; PMID:1480494
A)Accession: S35551
A,Status: preliminary; nucleic acid sequence not shown
A)Colocule Type: DNA
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                                                                                                                                                                                                                                                                                                                                                                 102 DQESACVHILIDFLDE-----QGYLTDSIEDILDHTPLEWMLDEAMLKQALTALKKF 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119
                                                                                                                                                                                                                     61 DNDFLSRKAQD-----CYFMKLHHCPGNHSWD--STISGSQ-----RAAFCDHKTT 104
                                                                                                                                                                                                                                                                       DNPLLERKDTDEFSDAEFSHYTAPARQIGGDEGEDMLSNIAGEQDFKQYLHAQVCEHPLS 101
                                                                                                                                                                                                                                                                                                                               105 PCSSAIINPLSTAGNSERLQPGIAQQWIQSKREDIVN-----QMTEACLNQSLDAL--- 155
                                                                                                                                                                                                                                                                                                                                                                                                                                    -----LSRDLIMK-EDYELVSTKPTRTSKVRQLLDTTDIQGEEFAKVIVQKLKDNK 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----SSDESETSEDSDIDGASSSLFMQKKKTPPKKDKKGGSNSSSRGNSRPGTPSPDTGN 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             402 TSSTLRAAASKLEQSKRGTVSN--TPAAKRLKMEAGPQNTSGKSTPQPQSGKSTPSSGDI 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 DPAGVAAADLNESLILQIERSGECAAKPSALHIVRNALDSIDGNRSQTLARIKKRLPQTD 213
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T30561
Scythe protein - African clawed frog
Scythe protein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000
C;Accession: T30561
S;Thress, K.; Henzel, W.; Shillinglaw, W.; Kornbluth, S.
EMBO J. 17, 6135-6143, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---RSLPAPODNDFLSRKAQDCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----CSSAIIN-----PLSTAGN
                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Cross-references: EMBL:217426; NID:g65029; PIDN:CAA78999.1; PID:g65030 C,Genetics:
A,Gene: RAP74
C,Keywords: DNA binding; transcription regulation
                                                                                                                                                                  90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 IMKED--YELVSTKPTRTSKVRQLLDT--TDIQGEEFAKVIVQKLK 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.3%; Score 88; DB 2; Length 283; Best Local Similarity 23.2%; Pred. No. 4.6; Matches 52; Conservative 27; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.3%; Score 88; DB 2; Length 524; Best Local Similarity 23.9%; Pred, No. 11; Matches 54; Conservative 22; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 SGTLEAALDLIASLNPFPAVGFASSTPTPYSDEALANLLAFRGM 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q-----MGLQPYPEILVVSRSPS-----LNLLQNKSM 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 SERLOPGIAQOWIQSKREDIVNOMTEACLNOSLDA-
A, Experimental source: serogroup A, strain 22491
C,Genetics:
A,Gene: NMA0049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 FMKLHHCPGNHSWDSTISGSQRAAFCDHKTTP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 IPVNHGPQEESCGSSQLHENSGSPETS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-524 <GON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346
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A,Accession: T30561
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: mRNA
A;Residues: 1-1135 < THR>
A;Residues: 1-1135 < THR>
A;Cross-references: EMBL:AF098511; NID:g3983138; PID:g3983139; PIDN:AAC83822.1
A;Cross-references: EMBL:AF098511; NID:g3983138; PID:g3983139; PIDN:AAC83822.1
A;Description: is a apoptotic regulator that is an essential component in the pathway of C;Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1.2368 <BEC.
A; Residues: 1.2368 <BEC.
A; Residues: 1.2368 <BEC.
A; Cross-references: BrBL: 236005; NID: 9536429; PIDN: CAA85094.1; PID: 9536430; MIPS: YBR136w
A; Experimental source: strain S288C
R; Becam, A.M.; Cullin, C.; Grzybowska, B.; Lacroute, F.; Nasr, F.; Ozier-Kalogeropoulos,
R; Becam, A.M.; S1-S11, 1994
A; Title: The sequence of 29.7kb from the right arm of chromosome II reveals 13 complete c
A; Reference number: S46569; MUID: 94378717; PMID: 8091856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Kato, R.; Ogawa, H. Wouleic Acids Res. 22, 3104-3112, 1994
A;Title: An essential gene, BSR1, is required for mitotic cell growth, DNA repair and mes A;Reference number: S47953; MUID:94344772; PMID:8065923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-196,'D',198-2368 <KAT>
A;Cross-references: EMBL:D11088; NID:9506874; PIDN:BAA01860.1; PID:d1002337; PID:9506876
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A;Molecule type: DNA
A;Residues: 1-2368 (ABZ)>
A;Cross-references: EMBL:X75891; NID:g496856; PIDN:CAA53494.1; PID:g496866
A;Experimental source: strain S288C
B;Kato, R.; Ogawa, H.
Submitted to the EMBL Data Library, May 1992
A;Description: An essential gene, ESR1, is required for mitotic cell growth, DNA repair a A;Reference number: S46662
A;Accession: S46663
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NiAlternate names: MEC1 protein; protein YBR1012; protein YBR136w
CiSpecies: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 29-Oct-1999
C;Accession: $46063; $46578; $46663; $47954; $64660
C;Accession: $46063; $46578; $46663; $50nimski, P.P.; Sagulski, M. R;Becam, A.M.; Herbert, C.J.; Nasr, P.; $10nimski, P.P.; Zagulski, M. Submitted to the Protein Sequence Database, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1002 HPTQEDGGSEQWAASVPPEWVPVIRQDMQNQRKIKQQPPLSDAYLSGMPAKRRKTMQGEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 -NQSLDALLSRDLIMKEDYELVSTKPTRTSK-VRQLLDTTDIQG---EEFAKVIVQKLKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 195-196,'D',198-322;671-744;848-1796;1803-2003;2004-2368 <KA2>
A;Cross-references: EMBL:D11088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 7.3%; Score 88; DB 2; Length 1135; Local Similarity 23.1%; Pred. No. 31; hes 30; Conservative 26; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 NPLSTAGNSERLQPGIAQQWIQSKREDIVNQ------MTEACL
A,Title: Scythe: a novel reaper-binding apoptotic regul.
A,Reference number: Z20860; MUID:99016035; PMID:9799223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Weinert, T.A.; Harlow, D.
submitred to the EMBL Data Library, July 1995
Kaference number: S64650
A;Accession: S64650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 NKQMGLQPYP 213
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.A.; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: F84669
A;Accession: F84669
A;Accession: F84669
A;Accession: F84669
A;Cross-references: GB:AE002093; NID:g2281098; PIDN:AAB64034.1; GSPDB:GN00139
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein U86 - human herpesvirus 7 (strain JI)
C;Species: human herpesvirus 7
A;Variety: strain JI
A;Variety: strain JI
A;Variety: abec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T41987
R;Nicholas, J.
R;Nicholas, J.
B;Nicholas, J.
A;Reference number: Z22022
A;Reference number: Z22022
A;Reference number: Z22022
A;Reference number: Z22022
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule Type: DNA
A;Residues: 1-1205
A;Cross-references: EMBL:U43400; PIDN:AAC54747.1
A;Experimental source: strain JI
C;Genetics:
A;Note: U86
                                                                       68 KMLDDIEDEYTDUNYNEGYSKMDTDGDLEWEEFKKLNKDPSKMEGERHRQMAKNRE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRSLPAPQDNDFLSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIIN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 PLSTAGN-----SERLQPG-----IAQQWIQSKREDIVNQMTEACLNQSLDA 154
                                   KR-EDIVNOMTEACLNOSLDAL-LSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIQGEE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOSILSPV-QDHINFTLOKAYFKCAYEC----FDRTRTHAE----ISRCAESCSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48; Gaps
                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein At2g43720 [imported] - Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43; Indels
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                                                                                                                                                                                                  193 FAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKS 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155 LLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTD 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.2%; Score 87; DB Best Local Similarity 24.2%; Pred. No. 2.3; Matches 37; Conservative 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 2
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Best Local S:
Matches 52
                                      135
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submitted to the EMBL Data Library, November 1998
A;Reference number: 220361
A;Accession: T27389
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Anlecule type: DNA
A;Residues: 1-340 'WILb>
A;Cross-references: EMBL:AL033514; NID:e1343251; FIDN:CAA22089.1; CESP:Y75B8A.29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 536 -SESLLSGILFSLHRIFSHFQPPKLTDGNGQINKSFKLVQKCFMNSNRYLRLLSTRIIPL 594
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T27389
R;Barlow, K.
A;Molecule type: DNA
A;Residues: 1-715,'P',717-1254,'Q',1256-1275,'G',1277-2368 <WEI>
A;Cross-references: EMBL:U31109; NID:g950172; PIDN:AAA74482.1; PID:g950173
C;Genetics:
A;Gene: SGD:ESR1, MECI
A;Cross-references: SGD:S0000340; MIPS:YBR136w
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                                                                                                                                                                                                                                             Appearation: required for mitotic cell growth, DNA repair, and meiotic r G; Keywords: ATP; P-loop; purine nucleotide binding; transmembrane protein G; Keywords: ATP; P-loop; purine nucleotide binding; transmembrane #status predicted <TM1.
F; 74-90, Domain: transmembrane #status predicted <TM2.
F; 71-787, Domain: transmembrane #status predicted <TM3.
F; 722-1169, Domain: transmembrane #status predicted <TM4.
F; 1152-1169, Domain: transmembrane #status predicted <TM6.
F; 1188-1304, Domain: transmembrane #status predicted <TM6.
F; 1288-1304, Domain: transmembrane #status predicted <TM7.
F; 1891-1934, Domain: transmembrane #status predicted <TM7.
F; 1918-1934, Domain: transmembrane #status predicted <TM8.
F; 1918-1934, Domain: transmembrane #status predicted <TM8.
F; 1918-1934, Domain: transmembrane #status predicted <TM8.
F; 1088, Binding site: ATP/GTP (Lys) #status predicted
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22.3%; Pred. No. 83;
tive 38; Mismatches 105; Indels
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Matches 56; Conservative
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A;Introns: 116/3; 216/3; 267/3
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schemefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
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REP1 ZYGBA
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	RA	Thome	., Ho	fmann F	(., Bur	ns	K., Martinon F.,	Bodmer J	L . ,	
	A F	Mattmann "Identif	Mattmann C., Tschopp J.; "Identification of Caphī	Techoi	JO J.;		a PID-like kinase that		associates with	
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        K->A: ABOLISHES KINASE ACTIVITY.
K->M: REDUCES FAS-MEDIATED APOPTOSIS.
                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Cytoplasmic (Probable).
TISSUE SPECIFICITY: Detected in heart, brain, placenta, lung, peripheral blood leukocytes, spleen, kidney, testis, prostate, pancreas and lymb node.
                                                                                                                                                                                                                                                                                                                                                         PTM: Autophosphorylated.
SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
SIMILARITY: Contains 1 CARD domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0004674; F:protein serine/threonine kinase activity; TAS. GO; GO:0004871; F:signal transducer activity; TAS. GO; GO:0006915; P:signal transducer activity; TAS. GO; GO:0006915; P:apoptosis; TAS. GO; GO:0006915; P:signal transduction; TAS. InterPro; IPR001315; CARD. InterPro; IPR001315; CARD. InterPro; IPR008271; Ser_thr_pkin_AS. InterPro; IPR008271; Ser_thr_pkin_AS. Prot Prof(5); CARD; IPR008271; Prot kinase. Prof(5); Prof(5); TAT_pkinase. Prof(5); Prof(5); TAT_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE, PS50209; CARD; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
PROSITE; PS00109; PROTEIN KINASE_ATP; FALSE_NEG.
TRANSFIE; PS00108; PROTEIN KINASE_ST; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
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ProDom; PD000001; Prot kinase; 1.
SMART; SM00114; CARD; 1.
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EMBL, AF078830; AAC2722.1; --
EMBL, AF068024; AAC25668.1; --
EMBL, AC04003; AAC24561.1; --
EMBL, BF17829; AAD04654.1; --
EMBL, BC004553; AA404553.1; --
Genew, HGNC:10020; RIPK2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phosphorylation; Apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD000001; Protemart: SM00114; CARD;
                                                                                                                                                                                                                                                                                          receptor complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14
22
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74
74
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                                                                                                                                                                                                                                                                                                                      184
                                                                                                                                     64
                                                                                                                                     5 QLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDF
                                                                                                                                                            313 KLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDF
                                                                                                                                                                                                                 65 LSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ
                                                                                                                                                                                                                                                                                             PGIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDINE-201891093; PubMed=11894097; Chin A.I., Dempsey P.W., Bruhn K., Miller J.F., Xu Y., Cheng G.; Involvement of receptor-interacting protein 2 in innate and adaptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TABLE TO STATION ACTIVATES PRO-CASPASE-1 and pro-CASPASE-8. Potentiates CASP-8-mediated apoptosis. Activates NF-kappaB (By similarity).

-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- SUBBUIT: BINGS to CFFAR/CLARP and CASP1 via their CARD domains.
-!- SUBBUIT: BINGS to CFFAR/CLARP and CASP1 via their CARD domains.
-!- RAF6. May be a component of both the TNFRSF1A and TNRFSF5/CD40 receptor complex (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- FUM: Autophosphorylated (By similarity).
-!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
-!- SIMILARITY: Contains 1 CARD domain.
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                            493 TTDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM 540
                                                                                                                                                                                                                                                                                                                                                                           185 TIDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM 232
D->N: ABOLISHES KINASE ACTIVITY
                                                         Length 540;
                                                                                              Indels
                61194 MW; 575A692239505792 CRC64;
                                                       Score 1182; DB 1;
Pred. No. 1.5e-91;
                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001315; CARD.
InterPro; IPR00719; Prot kinase.
InterPro; IPR08271; Ser Thr pkin AS.
InterPro; IPR01245; Tyr pkinase.
Pfam; PF00619; CARD; 1.
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF461040; AAL96436.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
                                                         98.08;
                                                                            99.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 416:190-194(2002).
                                                                                                Matches 227; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:1891456; Ripk2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
146 1
540 AA;
                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immune responses.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIK2 MOUSE
P58801;
                                                                                                                                                                                                                                                                                               125
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                    SEQUENCE
  MUTAGEN
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       313 KIQSSSSTIHLCD-KKMDLSLNIPANHPPQEESCGSSLLSRNTGSPGPSRSLSAPQDKGF 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 PGIAQOMIQSKREDIVNOWTEACLNOSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      432 IGIAQOWIQSKREAIVSQMTEACLNQSLDALLSRDLIMKEDYELISTKPTRTSKVRQLLD 491
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MEDLINE=99265599; PubMed=10129646;
INDHINE=99265599; PubMed=10129646;
INDHINE=10., Kisseki I., Gerebeso L., Hu Y., Yee C., Chen S., Carrio R.,
Merino J., Liu D., Ni J., Nunez G.;
"Nod1, an Apaf-1-like activator of caspase-9 and nuclear factor-
kappaB.";
J. Biol. Chem. 274:14560-14567(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 OLOSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              || ||| :| ||| :| ||||||||| :| |||||| 372 LSGAPQDCSSLKAHHCPGNHSWDGIVSVPPGAAFCDRRASSCSLAVISPFLVEKGSERPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Endothelial cells;

MEDLINE=99240667; PubMed=10224040;

Bertin J., Nir W.-U. Fischer C.M., Tayber O.V., Errada P.R.,

Grant J.R., Keilty J.J., Gosselin M.L., Robison K.E., Wong G.H.W.,

Gluckmann M.A., Distefano P.S.;

"Human CARD4 protein is a novel CED-4/Apaf-1 cell death family member

that activates NF-kappaB.";
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                   69.6%; Score 839.5; DB 1; Length 539; 71.9%; Pred. No. 7.6e-63; ive 20; Mismatches 43; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM 232
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                                                                                                                                                                                                                                                                                                                      42951BF97CA15DFA CRC64;
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09Y239; QBIMFS;
28-FEB-2003 (Rel. 41, Created)
10-OCT-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Caspase recruitment domain protein 4 (Nod1 protein).
CARD4 OR NOD1...
                                                                                                                                                                                                                                                 ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                        60400 MW;
PRINTS; PR00109; TYRKINASE
                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 71.9%
Matches 164; Conservative
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24
47
146 1
539 AA;
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                                                                                                                                                                                                                                                                                            ACT SITE
SEQUENCE
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NP_BIND
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ID CAR4 H

CAR4 H

CAR4 H

DT 28-FEB-
DT 28-FEB-
DT 10-CAR4 C

GN CARD4 (

GN CARD4 (

GN CARD4 (

CO MAMMALI.

CO MAMMALI.

RA MEDLIN

RA Grant Human

RT Human

RT Human

RT Human

RT T HABDEN

RT T RESUGUEN

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Richards The D. Colling F.S., Magner L.S., Schwafer J.G.,

Richards T.D., Colling F.S., Magner L.S., Schwafer J.G.,

Richards T.D., Colling F.S., Magner L.S., Schwafer J.G.,

Richards T.E., Jozdeny H., Moore T., Max S.L., Mang J., Haish F.,

Richards T.E., Jozdeny H., Moore T., Max S.L., Mang J., Haish F.,

Richards T.E., Jozdeny H., Moore T., Mang J., Haish F.,

Richards S., Molly R.E., Jozdeny H., Moore T., Mang J., Haish F.,

Richards S., Molly W. H., Persis J.G., Norman R.D., Milling S.J.,

Richards S., Molly W. M., Markerman K.J., Malky J.A., Galber R.A.,

Richards S., Molly K.C., Hard S., Garcia A.M., Galber R.A.,

Richards S., Molly K.C., Hard S., Garcia A.M., Galber R.A.,

Richards S., Molly D.M., Sodergen E.J., Ju X., Gibbs R.A.,

Richards S., Molly K.C., Hard S., Garcia A.M., Galber R.A.,

Richards S., Molly K.C., Hard S., Garcia A.M., Galber R.A.,

Richards S., Molly D.M., Sodergen E.J., Ju X., Gibbs R.A.,

Richards S., Molly D.M., Sodergen E.J., Ju X., Gibbs R.A.,

Rabey J., Hailon E., Ketteman W., Madha A., Radilus D.B.,

Rabey J., Hailon E., Ketteman W., Madha A., Radilus D.B.,

Rabey J., Hailon M., Wadan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Raber J., Hailon M., Madan A., Young J.A., Shalke J., Sanihez A.,

Raber J., Mallon R., Marker M., Mallon J., Soderson W., Marker M.A.,

Raber J., Mallon A., Young A.C., Shevchenko Y., Boutfard G.G.,

Raber J., Mallon A., Young A.C., Shevchenko Y., Boutfard G.G.,

Raber J., Mallon A., Young A.C., Shevchenko Y., Boutfard G.G.,

Raber J., Mallon A., Young A.C., Chrome S.J., Marker M.A., Manz G. M.A.,

Raber J., Shalker J., Saniha J.E., Shalker J., Saniha R.A.,

Raber J., Shalker J., Shalker J., Saniha R.A.,

Raber J., Shalker J., Shalker J., Saniha R.A.,

Raber J., Shalker J., Shalker J., Shalker J., Saniha R.A.,

Raber J., Shalker J., Shal
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                                                                                                                                                                                                                                       QWIQSKREDIVNQMTEA-CLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDI 188
                                                                                                                                                                                                                                                         Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Comell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Rooper A., Saunders D., Shomkeen R.,
Sims M., Smaldon M., Smith M., Sonnhammer B., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                               V->0: ABOLISHES CASPASE-9 ACTIVATION AND INTERACTION WITH RICK.
K->R: REDUCES CASPASE-9 ACTIVATION.
                                                                                                                                                                    10.2%; Score 122.5; DB 1; Length 953;
37.1%; Pred. No. 0.021;
Live 19; Mismatches 36; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                          189 QGE---EFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNK 230
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107690 MW; 0A9DF5FC6487E21A CRC64;
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01-FEB-1994 (Rel. 28, Last sequence update)
01-CCT-2003 (Rel. 42, Last annotation update)
Hypothetical protein F22B7.5 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 368:32-38(1994).
-!- SIMILARITY: Contains 1 GoLoco domain.
-!- SIMILARITY: Contains 1 J domain.
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HSSP, P00622; IXBL.
INCEMPED; F22B7.5; CE00158.
INTERPRO; IPR002939; DnaJ_C.
InterPro; IPR001305; DnaJ_CXXCXGXG.
LRR 6.
LRR 7.
LRR 8.
LRR 9.
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MEDLINE=94150718; PubMed=7906398;
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                                                                                                                                                                                       Local Similarity 37.1 tes 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
 862
891
918
946
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953 AA;
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CONFLICT
SEQUENCE
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ID YLWS CAI
AC P34408;
                                                                    MUTAGEN
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SEQUENCE FROM N.A.

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SEQUENCE TROWNON, TASSURAWA T., Adachi J., Bono H., Kondo S.,

MEDLINE=22354683; PubMed=12466851;

MEDLINE=22354683; PubMed=12466851;

Nikaido I., Osaton N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Nikaido I., Osaton N., Saito R., Suzuki H., Yamanaka I. Kiyosawa H.,

Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Marapin A., Matsuda H., Batalov S., Beisel K.W.,

Balake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Dalla E., Dragani T.A., Fletcher C.F., Forrest R., Frazer K.S.,

Gasterland T., Gariboldi M., Gissl C., Godzik A., Gough J.,

And Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

Konagaya A., Kurochkin I.V., Lee Y., Lehnard B., Lyons P.A.,

Maglott D.R., Maltais L., Marchionni L., McKenzie I., Miki H.,

Nagashima T., Numata K., Pontius J.U., Ql., Pavan W.J., Pertea G., Pesole G.,

Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 TAG----NSERLQPGIAQQWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVST 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           349 IDVAMNQERSETATDQDVCLAIDSSPDFTSS-----NDMINK-----FVVELEHATNVE 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :|: ::|
398 TWEMIVNGIIDDQKKPVAIEKKENEEPVDMMDLIFSMSSRMDDQRTELPAARFIPPRPVS
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Local Similarity 19.4%; Pred. No. 1.4;
Les 45; Conservative 44; Mismatches
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IPR008971; HSP40_DnaJ_pep
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                                                                                                Fram; PF00226; DnaJ; 1.
Pfam; PF00226; DnaJ; 1.
Pfam; PF00684; DnaJ CXXXXXXXX Pfam; PF00684; DnaJ CXXXXXXX Pfam; PF00685; DnaJ CXXXXXX SMNTT; SM00271; DnaJ; 1.
PROSITE; PS00636; DNAJ 1; 1.
PROSITE; PS50076; DNAJ 2; 1.
PROSITE; PS50077; GOLOCO; 1.
                                        IPR003095; Hsp DnaJ. IPR008941; TPR-like.
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595
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                                            InterPro;
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SEQUENCE
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RN SEQUENCE FROM N.A., AND VARIANT ALA-884.

RY SEQUENCE FROM N.A., AND VARIANT ALA-884.

RY SEQUENCE FROM N.A., AND VARIANT ALA-884.

RY SEQUENCE FROM N.A., AND VARIANT ALA-884.

RY STAINS-CZECH II, and FVB/N. TISSUE-Breast cancer;

RY Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Workernan K.J., Malek J.A., Gunetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., Loquellano N.A., Sodergren E.J., Lu X., Gibbs R.A.,

Ry Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Rodriques S., Sanchez A.,

Rhey J., Helton B., Ketteman M., Madan A., Rodriques S., Sanchez A.,

Rhey J., Helton B., Xoung A.C., Sheychenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.J., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Salaka U., Smailus D.E.,

Ronerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length

Rhuman and mouse cDNA sequences.";

"Generation and initial analysis of more than 15,000 full-length

Rhuman and mouse cDNA sequences.";

"Generation and initial analysis of more than 15,000 full-length

Rhuman and mouse cDNA sequences.";

"Generation and initial analysis of more than 15,000 full-length

Rhuman and mouse cDNA sequences.";

"Generation and initial analysis of more than 15,000 full-length

Rhuman and mouse cDNA sequences.";

"Generation and initial analysis of more than 15,000 full-length

Rhuman and mouse cDNA sequences.";

"Generation an
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Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw Boris A., Yanagisawa M., Yang I., Yang L., Yang L.G., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Komon H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagawa I., Mayazaki A., Sabakino M., Materston R., Lander E.S., Rogers J., Yashino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.; Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.; Materston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.; Materston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.; Materston R., Lander E.S., Rogers J., Mature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Apoptosis; ATP-binding; Repeat; Leucine-rich repeat; Polymorphism. DOMAIN 15 107 CARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interaction (By similarity).
--- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
--- SIMILARITY: Contains 1 CARD domain.
--- SIMILARITY: Contains 1 NACHT domain.
--- SIMILARITY: Contains 9 leucine-rich (LRR) repeats.
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InterPro; IPR007091; LRR RNinh.
InterPro; IPR007111; NACHT_NTPase.
Pfam; PF00619; CARD; 1.
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EMBL, AK089662, BAC40940.1;
EMBL, BC042670, AAH42670.1;
EMBL, BC043670, AAH43670.1;
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PROSITE; PS50209; CARD; 1.
PROSITE; PS50837; NACHT; 1.
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ATP (POTENTIAL). LRR 1. LRR 2.

NP\_BIND REPEAT REPEAT

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'n
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                                                                                                                                                                                                                                                              23 LKINREHLVINIRNIQCL----VDNLLENGYFSAEDAEIVCACPIKPDKVRKILDLVQSKG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G., Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G., "Suppression of apoptosis in mammalian cells by NAIP and a related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V., "The TNFR2-TRAF sign, Henzel Complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins."; Cell 83:1243-1252(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Fetal liver;
MEDLINES $6.09843; PubMed=8643514;
MEDLINES $6.09843; PubMed=8643514;
Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
Uren A.G. and expression of apoptosis inhibitory protein homologs that function to inhibit apoptosis and/or bind tumor necrosis factor receptor-associated factors;
Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978 (1996).
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TISSUE=Testis, and Uterus;

MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
                                                                                                                                                                                                7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               BIR2 HUMAN STANDARD; PRT; 618 AA. (13450; Q16516; Q13450; Q16516; Q1-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Baculoviral IAP repeat-containing protein 2 (Inhibitor of apoptosis protein 2) (HIAP2) (G-IAP1) (TNFR2-TRAF signaling complex BIRC2 OR AP11 OR IAP2 OR MIHB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                            k; Score 96.5; DB 1; Length 953;
k; Pred. No. 3.2;
13; Mismatches 29; Indel8
                                                                                                               884 S -> A (in strain Czech II).
107739 MW; 39C639621CEB1A58 CRC64;
LRR 3.
LRR 4.
LRR 5.
LRR 6.
LRR 7.
LRR 8.
LRR 9.
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MEDLINE=96128127; PubMed=8548810;
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                                                                                                                                                               ch 8.0%;
1 Similarity 35.5%;
27; Conservative 13
                                                                                                                                                                                                                                                                                                  ---EFAKVIVQKLKD 203
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80 EEVSEFFLYVLQQLED 95
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                                                                                                                                                                                                                                                                                                   191
                                                                                                               VARIANT
SEQUENCE
                                                                                                                                                                 Query Match
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                                REPEAT
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Matches
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B., Jones S.J.W., Marra M.A.; Marian A., Schein J.B., Jones S.J.W., Marra M.A.; Thuman and mouse cDNA sequences:", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -I- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS WITH THE RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAFI AND TRAF2) TO FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR NECROSIS FACTOR 2 (TNFR2).
-I- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions inhibit apoptotic suppressor activity.
-I- SUBCELLUAR LOCATION: Cyroplasmic (Potential).
-I- TISSUE SPECIFCITY: PRESENT IN MANY FETAL AND ADULT TISSUES.
MAINLY EXPRESSED IN ADULT SKELETAL MUSCLE, THYMUS, TESTIS, OVARY, AND PANCREAS, LOW OR ABSENT IN BRAIN AND PERIPHERAL BLOOD
                                                                                                                                                                                                                                                                                                                                                                                STRUCTURE BY NMR OF 266-363.
MEDLINE=9932054; PubMed=10404221;
Hinds MG.9., Norton R.S., Vaux D.L., Day C.L.;
"Solution structure of a baculoviral inhibitor of apoptosis (IAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew, HGNC:590, BIRC2.
MIM, 601712; F. apoptosis inhibitor activity, TAS.
GO, GO:0008189; F. apoptosis inhibitor activity, TAS.
GO, GO:0007166; P. cell surface receptor linked signal transdu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to the IAP family.
SIMILARITY: Contains 3 BIR repeats.
MILARITY: Contains 1 CARD domain.
SIMILARITY: Contains 1 RING-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001370; BIR.
InterPro; IPR001370; BIR.
InterPro; IPR001315; CARD.
InterPro; IPR001315; CARD.
InterPro; IPR001315; CARD.
Pfam; PF00619; CARD; 1.
Pfam; PF00619; CARD; 1.
SMART; SM00114; CARD; 1.
SMART; SM00114; CARD; 1.
PR0SITE; PS01282; BIR, 3.
PR0SITE; PS01282; BIR, REPEAT 1; 3.
PR0SITE; PS01282; BIR, REPEAT 2; 3.
PROSITE; PS010518; ER REPEAT 2; 3.
PROSITE; PS010518; ER RING; 1.
PR0SITE; PS010518; ZFRING; 1.
PR0SITE; PS010518; ZFRING; 1.
PR0SITE; PS010518; ZFRING; 1.
PR0SITE; PS01089; ZFRING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BIR 1.
BIR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nat. Struct. Biol. 6:648-651(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U45879; AAC50372.1; -.
EMBL; U37547; AAC50508.1; -.
EMBL; BC016174; AAH16174.1; -.
EMBL; BC028578; AAH28578.1; -.
PIR; S68450; S68450.
PDB; 1QBH; 20-OCT-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L49431; AAC41942.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HGNC:590; BIRC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEUKOCYTES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 IQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIQGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Utatsu I., Sakamoto S., Imura T., Toh-B A.;
"Yeast plasmids resembling 2 micron DNA: regional similarities and diversities at the molecular level.";
J. Bacteriol. 169:537-5545(1987).
-!- FUNCTION: PLASMID PARTITION REQUIRE REP1, REP2, AND A CIS-ACTING DNA SEQUENCE (KNOWN AS STB). REP 1 MAY ACT BY INTERCALATING IN THE YEAST NUCLEAR MATRIX AND BINDING STB BITHER DIRECTLY OR VIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Zygosaccharomyces.
NCBI_TaxID=4954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 EFAKVIVOKLKD------NKOMGLOPYPEILVVSRSPSLNLLONK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                519 AAANIFKNCLKEIDSTLYKNLFVDKNMKYIPTEDVSGLSLEEQLRRLÖEE 568
                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 618;
                                                                                                                                                                                                                                                                                                                                                                             69899 MW; C1778D328063586D CRC64;
                                        . . . .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN'1990 (Rel. 13, Created)
01-JAN'-1990 (Rel. 13, Last sequence update)
01-AUG-1990 (Rel. 15, Last annotation update)
Trans-acting factor B (REP1).
                                                                                                                                                                                                                                                                                                                                                                                                                  7.7%; Score 92.5; DE Local Similarity 24.5%; Pred. No. 3.9; es 27; Conservative 24; Mismatches
                                      RING-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=IFO 1047;
MEDLINE=88058763; PubMed=3680169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR008897; Yeast_TAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M18274; AAA35283.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zygosaccharomyces bailii.
                                                                                                                                                                                                                                                                                                                                                         353
618 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                      Plasmid pSB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
REP1_ZYGBA
ID REP1_ZYGBA
AC P13776;
DOMAIN
ZN FING
CONFLICT
                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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Matches
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STRAND
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HELIX
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CONFLICT
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                                                                                                                                                                                                                                                 144
                                                                                                                                                                                                                                                                                               60 QDNDFL----SRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLS 115
                                                                                                                                                                                                                                                                                                                                                                                                116 TAGNSERLQ---PGIAQOWIQSKREDIVNOMTEACLNOSLDALLSRDLIMKEDYELVSTK 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 QTTTAREESEALDTTSNGLDALNTQINAİETERSFWEAIRALHNE----LRTSPTQLEEC 296
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=22354683; PubMed=12466851;

MEDLINE=22354683; PubMed=12466851;

MEDLINE=22354683; PubMed=12466851;

MEDLINE=22354683; PubMed=12466851;

MEDLINE=22354683; PubMed=12466851;

MEDLINE SAID R., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Maladar I. R., Milli D.P., Bult C., Hume D.A., Quackenbush J., Badarelli R., Hilli D.P., Bult C., Hume D.A., Quackenbush J., Badarelli R., Marapin A., Matsuda H., Batalov S., Beisel R.W., Blake J.A., Fletcher C.F., Forrest A., Frazer K.S., Gasterland T., Gariboldi M., Gissi C., Godzik A., Gousins S., Armain A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Armain A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Anavasi T., Reed D.C., Reigh B.Z., Ringwald M., Schneider C., Senple C.A., Sectou M., Shimada K., Taylor M.S., Teasdale R.D., Tomita M.,
                                                                                                                                                                                                                            173 PTRTSKVR-QLLDTTD-----IQGEEFAKVIVQKLKDNKQMGLQPYPEILVVS
                                                                                                                                                                                                  1 MYSLQLQ-SVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAP
                                                                                                                                                                                                                                                                                                                                               145 IEETFIDATNARKELDEYFRKLQ-----DGTLTGDLEGGLCKVKTLISCKALF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95014147; PubMed=7929068; Starborg M., Brundell B., Gell K., Hoeoeg C.; Starborg M., Brundell B., Gell K., Hoeoeg C.; Movel murine gene encoding a 216-kDa protein is related to a mitotic checkpoint regulator previously identified in Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P53995; QBBP33; QBC772; U-07-1996 (Rel. 34, Created) 01-007-1996 (Rel. 34, Last sequence update) 10-007-1996 (Rel. 34, Last sequence update) 10-007-2003 (Rel. 42, Last annotation update) Anaphase promoting complex subunit 1 (APC1) (Cyclosome subunit 1) (Arotein Tsg24) (Mitotic checkpoint regulator).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                               72;
                                                                                              Score 90; DB 1; Length 357;
Pred. No. 3;
                                                                                                                                                  83; Indels
Pfam; PF05797; Yeast TAF; 1.
Plasmid; Trans-acting factor.
SEQUENCE 357 AA; 40752 MW; 7DF4C06359D4BA35 CRC64;
                                                                                                                                                  43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol. Chem. 269:24133-24137(1994).
                                                                                            7.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CBA; TISSUE=Testis;
                                                                                                                        Best Local Similarity 21.7
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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SUBUNIT: The APC/C is composed of at least 11 subunits (By 66 1404 PC 2. 67 1501 PC 3. 12 112 Q -> A (IN REF. 2). 48 349 GV -> AA (IN REF. 2). 43 643 N -> K (IN REF. 2). 44 AA; 216086 MW; 48FIEEF01053E6C3 CRC64; DB 1; Length 1944; 72; Indels 25; Mismatches 7.4%; Score 89; 5.4%; Pred. No. -!- SIMILARITY: Contains 4 PC repeats. 175 RTSKVRQLLDTTDIQGEEFAKVIVQ 199 426 QASKV---FITTDLCGQKFLCFLVE 447 PIR; A55117; A55117. MGD; MGI.13097; MGDr. LINEMPRO; IPR002015; APC\_proteasome. Pfam; PF01851; PC\_rep; 5. similarity).
TISSUE SPECIFICITY: Abundantly EMBL; X80169; CAAS6450.1; -. EMBL; AX052404; BAC34976.1; -. EMBL; AX077847; BAC37032.1; -. conjugation pathway; Cell 25.4%; 52; Conservative Query Match Best Local Similarity cycle. 1467 1520 112 1944

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genes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 FMKLHHCPGNHSWDSTISGSQRAAFCDHKTTP-----CSSAIIN----PLSTAGN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --LLSRDL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPGKIKPAKEEBGPKGLDEQSESSEESEEBKAEEBEGEEEKKAPTPQDNK--KKKKGD-- 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----SSDESETSEDSDIDGASSSLFMQKKKTPPKKDKKGGSNSSSRGNSRPGTPSPDTGN 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 IPVNHGPQEESCGSSQLHENSGSPETS-----RSLPAPQDNDFLSRKAQDCY 73
                                                                                                                                                                                                                                                                                                                                                       primary structure of Xenopus and human RAP74.";
Nucleic Acids Res. 20:6736-6736 (1992).
-!- FUNCTION: TFIIF IS A GENERAL TRANSCRIPTION INITIATION FACTOR THAT BINDS TO RNA POLYMERASE II AND HELPS TO RECRUIT IT TO THE INITIATION COMPLEX IN COLLABORATION WITH TFIIB. IT PROMOTES
                                                                                                                                                                                                                                                                                                                                       "Elucidation of three putative structural subdomains by comparison of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: Hererodimer of an alpha and a beta subunit. SUBCELLULAR LOCATION: Nuclear. SIMILARITY: TO OTHER TRANSCRIPTION FACTOR IIF, ALPHA SUBUNIT.
                                 01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
Transcription initiation factor IIF, alpha subunit (TFIIF-alpha)
(Transcription initiation factor RAP74).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90;
                                                                                                                                                                                                                                                                                                 Gong D.-W., Hasegawa S., Wada K., Roeder R.G., Nakatani Y.,
Horikoshi M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 IMKED--YELVSTKPTRTSKVRQLLDT--TDIQGEEFAKVIVQKLK 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.3%; Score 88; DB 1; Length 524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S35551; S35551.
TRANGFAC; T02171; -.
InterPro; IPRO08851; TFIIF-alpha.
Pfam; PF05793; TFIIF-alpha; 1.
Transcription regulation; DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    524 AA; 58699 MW; 8CF3A74A3BF77BB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESRI YEAST

ID ESRI YEAST

AC P3811; Q02580;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 01-OCT-1994 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SERLQPGIAQQWIQSKREDIVNQMTEACLNQSLDA.
524 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.9%; Prec. ...
tive 22; Mismatches
                                                                                                                                               Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                  MEDLINE=93126122; PubMed=1480494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSCRIPTION ELONGATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; 217426; CAA78999.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 23.93
54; Conservative
STANDARD;
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                            NCBI_TaxID=8355;
               Q04870;
01-FEB-1994
T2FA XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290
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엄
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Herbert C.J.;
"The sequence of 29.7 kb from the right arm of chromosome II reveals
13 complete open reading frames, of which ten correspond to new
                                                                                                                                                                                                                                                            Kato R., Ogawa H.; "An essential gene, ESR1, is required for mitotic cell growth, DNA repair and meiotic recombination in Saccharomyces cerevisiae."; Nucleic Acids Res. 22:3104-3112(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94378717; PubMed=8091856;
Becam A.-M., Cullin C., Grzybowska E., Lacroute F., Nasr F.,
Ozier-Kalogeropoulos O., Palucha A., Slonimski P.P., Zagulski M.,
ESRI protein.

ESRI OR MECI OR SAD3 OR YBR136W OR YBR1012.

Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO, GO:0005634; C:nucleus; IC.
GO; GO:0000076; P:DNA replication checkpoint; IMP.
GO; GO:0007131; P:maiotic recombination; IMP.
GO; GO:0006139; P:nucleobase, nucleoside, nucleotide and nucl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -! - FUNCTION: Required for cell growth, DNA repair and meiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | InterPro; | IPR008938 | ARM. | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| InterPro; | IPR008938 | ARM. |
| InterPro; | IPR008151; | FAT. |
| InterPro; | IPR008941; | FAT. |
| InterPro; | IPR008941; | TPR-like. |
| InterPro; | IPR008941; | TPR-like. |
| InterPro; | IPR008941; | TPR-like. |
| InterPro; | IPR008941; | TPR-like. |
| InterPro; | IPR008941; | TPR-like. |
| InterPro; | IPR008941; | TPR-like. |
| InterPro; | IPR008941; | TPR-like. |
| InterPro; | IPR008941; | TPR-like. |
| InterPro; | IPR008941; | TPR-like. |
| InterPro; | IPR008941; | INTERPO; | INTERPO; |
| InterPro; | IPR008941; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | INTERPO; | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- DEVELOPMENTAL STAGE: Induced during meiosis.
-!- SIMILARITY: IN THE N-TERMINAL REGION, TO S.POMBE CUT1.
-!- SIMILARITY: Belongs to the PI3/PI4-kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Weinert T.A., Harlow D.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    recombination.
                                                                                                                                                                                                                                   MEDLINE=94344772; PubMed=8065923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X75891; CAA53494.1; -.
EMBL; U31109; AAA74482.1; -.
EMBL; Z36005; CAA85094.1; -.
EMBL; D11088; BAA01860.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S46005; S46005.
GermOnline; 138679; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yeast 10:S1-S11(1994)
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                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                              NCBI_TaxID=4932;
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CONFLICT
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Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

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Baldarelli R., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Dalla E., Dragami T.A., Fletcher C.F., Forrest A., Frazer K.S.,

Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

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Rayashima T., Numara K., Okido T., Pavan W.J., Pertea G., Pesole G.,

Rayashima T., Numara K., Okido T., Reid J., Ring B.Z., Ringwald M.,

Sandelin A., Schneider C., Semple C.A., Sectou M., Shinada K.,

Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

Nerardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

Wallang L.G., Wynabaw-Boris A., Yanagisawa M., Yang L.,

Nilming L.G., Wynabaw-Boris A., Yanagisawa M., Yang L.,

Nilming L.G., Wynabaw-Boris A., Yanagisawa M., Yang I.,

Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

Shiraki T., Waki K., Kawai J., Alzawa K., Arakawa T., Fukuda S.,

Hara A., Hashizume W., Imotani K., Ishiagawa A.,

Namishin A., Yoshiha, Waterston R., Ishiayawa A.,

Hara A., Hashizume W., Imetrston R., Ishiayawa A.,

Namishin A., Yoshiba.
                                                    11;
                                                                                                                                                  535
                                                                                                                                                                                                                                      536 -SESLLSGILFSLHRIFSHFQPPKLTDGNGQINKSFKLVQKCFMNSNRYLRLLSTRIIPL 594
                                                                                                                                                                                                                                                                                                       ---STAGNSERLQPGIAQQWIQSKREDIV-----NQMTEACLNQSLDALLSR--DLI 161
                                                                                                                                                                                                                                                                                                                                                                                                           162 MKEDYELVSTKPTRTSKVRQLLDTTDIQ-GEEFAKVIVQKLKDN---KQMGLQPYPEILV 217
                                                                                                                                                                                                                                                                                                                                                                                                                                        595 FNIŚDSHNSEDEHTATLIKFLOŚOKLPVVKENLVIAWTOLTLTTSNDVFDTLLKLIDIF 654
                                                                                                      64
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"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                     191 HLCDIEKTGNPFVRINPNRP-----EAAGKSEIFRILHSN-----FLSHPNIDEF
                                                                                                                                                                                                       LSRKAQDCYFMKLHH-----CPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPL
                                                                                                      14 HLCDKKK-----MELSLNIPVNHGPQEESCGSSQ----LHENSGSPETSRSLPAPQDNDF
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                    52;
  DB 1; Length 2368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Dorsal root ganglion, Small intestine, and Testis; MEDLINE=22354683; PubMed=12466851;
                                                    38; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOUSE STANKL...
SYAP MOUSE STANKL...
QOD5V6; QOD870;
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
7.3%; Score 88; DB 22.3%; Pred. No. 54;
                                                    56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 VSRSPSLNLLQ 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              715 YSSKTILDIFQ 725
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                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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                                                                                                                                                                                                    65
                                                                                                                                                                                                                                                                                                       115
Query Match
Best Local (
                                                    Matches
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MEDLINE=22388257; PubMed=12477932;
A Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Atlausner R.L., Colline F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A popkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A branecian M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Agy L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Rodingues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Brane D.N., March C., Ghercation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 ISLIKOSAQLTALAAQQQASGKEEKSSNRDDNLPLTEAVRPKTPPVVIKSQLKSQEDEEE 279
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
Asteroidea; Forcipulatacea; Forcipulatida; Asteriidae; Asterias.
NCBI_TaxID=7605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; -> K (IN REF. 1; BAB25643).
7553E79C0C50E96B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 VSTKPTRTSKVRQLLDTTDIQGEEFAKVIVQKLKDNKQ 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280 ISTSPGVSEFVSDAFDTCSLNQEDLRKEMEQLVLDKKQ 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [5-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BSD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:1914293; Syap1.
GO; GO:0005634; C:nucleus; IDA.
InterPro; IPR005607; BSD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AK008390; BAB25643.1; -. EMBL; AK014893; BAB29608.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AK051251; BAC34575.1; -. BC021373; AAH21373.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      365 AA; 41350 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50858; BSD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MYC_ASTVU
Q17103;
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protein 2) (MIAP2) (MIAP-2)
          BIRC2 OR BIRC3 OR IAP2.
                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 26; Conserv
                                                                                                                                         SEQUENCE FROM N.A.
                                                 NCBI_TaxID=10090;
                                                                                                                                                                                            1 and 2 genes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apoptosis;
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZN FING
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                            14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 DLSSAPPIAALIODC--------MWSSIJAEERRKLFMKSEKKHAEERATKKASTP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 KKFELYPTPPLSPSHNPDDKESDRHPRHHQQDGDGSPSRSYQHLMDDDDLPLVNPQVPLL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----SRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHK------TTP 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSSAIINPL---STAGNSERLQP-GIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 SSGVMLPPLVPASEYGTSDCVDPSAVCPYPLSETRLDLFSSGT----NTPSDSEEELDVV 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 MKED-----YELVSTKP--TRTSKVRQLLD------TTDIQGEEFAKVI----VQKLK 202
      KKMELSLNIPV--NHGPQE-ESCGSSQLHENSGSPETSRSLPAPQDNDFL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 42, Last annotation update)
IRP repeat-containing protein 2 (Inhibitor of apoptosis
                                                                                                                                                                                                                                                                                                                        PROSITE; PS50888; HLH; 1.
Nuclear protein; DNA-binding; Transcription regulation; Activator.
                                                                                                                                                                                                                                                                                                                                                                                                                           79;
                                                                                                                                                                                                                                                                                                                                                                                                       7.2%; Score 86.5; DB 1; Length 407; 21.9%; Pred. No. 7.1;
                                                                                                                                                                                                                                                                                                                                                                                                                           91; Indels
                                                                                                                                                                                                                                                                                                                                                               HELIX-LOOP-HELIX MOTIF.
LEUCINE-ZIPPER (POTENTIAL).
F4E52DD01182113A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                1 Similarity 21.9%; Pred. No. 7.1; 59; Conservative 40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 DNKQMGLQPYPEILVVSRSPSLNLLQNKS 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --TEGNLEEVKQILQKS----NLIRSSS 288
                                                                                                                                                                                                                                                                                                                                                      BASIC DOMAIN
MEDLINE=93026376; PubMed=1408141;
                                                                                                                                                                                                                                                 TRANSFAC; T03463; -.
InterPro; IPR001092; HLH_basic.
InterPro; IPR002418; TF_Myc.
                                                                                                                                                                                                                                                                                                                                                                                   45673 MW;
                                                                                                                                                                                                                                                                                Pfam; PF00010; HLH; 1. — Pfam; PP10105; Myc N term; 1. PRINTS; PR00044; LEUZIPPRMYC. SMART; SM00353; HLH; 1.
                                                                                                                                                                                                                     EMBL; M80364; AAA27788.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                          401
                                                                                                                                                                                                                                 PIR; S27774; S27774.
HSSP; P25912; 1HLO.
                                                                                                                                                                                                                                                                                                                                                     321
335
380
407 AA;
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Q62210; O08864;
01-NOV-1997 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997
10-OCT-2003
Baculoviral
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DNA_BIND
DOMAIN
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SEQUENCE
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Best Local
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1D BIR2_MC

AC 062210.

DT 01-NOV.

DT 10-OCT.

DE Baculor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomics 46:495-503(1997).

Genomics 46:495-503(1997).

-:-FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS

WITH TWE RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR

NECROSIS FACTOR RECEPTOR 2 (TWRE2).

-:-SUBGNUT: Interacts with SMAC and with PRSS25; these interactions
inhibit apoptotic suppressor activity (By similarity).

-:-SUBCELLULAR LOCATION: Cycoplasmic (Potential).

-:-SUBCELLULAR LOCATION: Cycoplasmic (Potential).

-:-TISSUE SPECIFICITY: Expressed in heart, brain, spleen, lung,
liver, skeletal muscle, kidney and testis.

-:-SIMILARITY: Contains 3 BIR repeats.

-:-SIMILARITY: Contains 1 CARD domain.
                                                                                                                                                        SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=96128127; PubMed=8548810;
Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
"The TNFR2-TRF4 signaling complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins.";
Cell 83:1243-1252(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Skeletal muscle; MEDLINES91: PubMed=9441758; Liston P., Lefebyre C., Fong W.G., Xuan J.Y., Korneluk R.G.; Liston P., Lefebyre C., Fong W.G., Xuan J.Y., Korneluk R.G.; Genomic characterization of the mouse inhibitor of apoptosis protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Eukaryota.io (Modose).
Fukaryota: Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E -> K (IN REF. 2).
E08969D93C6C610D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.2%; Score 86.5; I
llarity 23.6%; Pred. No. 12;
Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00518; ZF_RING 1; FALSE_NEG.
PROSITE; PS50089; ZF_RING 2; 1.
Apoptosis; Zinc-finger; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RING-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BIR 1.
BIR 2.
BIR 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00238; BIR; 3.
SMART; SM00114; CARD; 1.
SMART; SM00184; RING; 1.
PROSITE; PS01282; BIR_REPEAT_1; 3.
PROSITE; PS50143; BIR_REPEAT_2; 3.
PROSITE; PS50209; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1197009; Birc3.
ThterPro; IPR001370; BIR.
InterPro; IPR001315; CARD.
InterPro; IPR001841; Znf_ring.
Pfam; PF00653; BIR; 3.
Pfam; PF006519; CARD; 1.
Pfam; PF00697; zf-C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69676 MW;
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Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Altschul S.F., Zeeberg B., Bonaldo M.F., Casvant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toobliyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzartne P.H.,

A Richards S., Worley K.C., Hale S., Garcycan A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rachards S., Worley K.C., Hale S., Garcychenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalsu D.E.,

Beneration and initial analysis of more than 15,000 full-length human
                     132 IQSKREDIVNOMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIQGE 191
                                                  |: |: |: | : || :: | :: | 455 IRKNRMALFQQLTHVL--PILDINLLEASVITKQEHDIIRQKTQIPLQARELIDTVLVKGN 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arita M., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K., Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R., Ofsuki T., Sato H., Ota T., Wakamatsu A., Ishihi S., Yamamoto J., Isono Y., Kawai-Hio Y., Satto K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; "NEDO human cDNA sequencing project.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The complete sequences of unidentified human genes. XV.
The complete sequences of 100 new cDNA clones from brain which code
for large procedus in vitro.";
DNA Res. 6:337-345(1999).
-!- FUNCTION: Poor transcriptional factor which uses the canonical
single or multiple CARG boxes DNA sequence. Acts as a cofactor of
serum response factor (SRP) with the potential to modulate SRF
target genes (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                         -----NKQMGLQPYPEILVVSRSPSLNLLQNK 230
                                                                                                                                                                         513 AAANIFKNSLKEIDSTLYENLFVEKNMKYIPTEDVSGLSLEEQLRRLQEE 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nagase T., Ishikawa K.-I., Kikuno R., Hirosawa M., Nomura N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                           Q9ULH7; Q86WW2; Q8N226;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Myocardin-related transcription factor B (MRTF-B).
                                                                                                                                                                                                                                                                                                        PRT; 1088 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 261-1088 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20039619; PubMed=10574462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Medulla oblongata;
                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                         192 EFAKVIVQKLKD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MRTFB OR KIAA1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rissum=Brain;
                                                                                                                                                                                                                                                                                                        MRTB HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         monse
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NSTRCSEKSYSIIPEINS (in isoform 2).

/FITd=VSP 007654.

/FITd=VSP 007654.

PLIDEAUSP 007655.

PLADKNSNSGNSALNNATPRTPRONTSTPVRKFGPLPSSLD DLKVSELKTPLKRGLPSGLAAGGIVANSSALTSNPEVTALN. -> YGGAHAI LNAGFSVVFRNNYKLPKVECCHLFVLSNDFHFFVIRAYHTV
                                                                                                                                                                                                                                                                                           Note=No experimental confirmation available;
DOMAIN: The N-terminal region is required for nuclear localization
and the C-terminal region mediates transcriptional activity (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLNDKNSNSGNSALNNATPNTPRONTSTPVRKPGPLPSSLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLKVSELKTELKLRGLPVSGTKPDLIER -> AYHTVSEVH
MVRVACIPFQFLSSKIGSEFLQVRNAFSQLFIQICLLLLEHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIDSSKKQQQGFPEILTAGDFEPLKEKECLEGSNQKSLKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEVHMVRVACI PFQFLSSKIGSEFLQVRNAFSQLFIQICLL
                                                                  Event=Alternative splicing; Named isoforms=3; Comment=Full isoforms so far detected are isoform 2 and isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59; Indels 41; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEHQNSTRCSEKSVSSIIPGINS (in isoform 3)
                                                                                                                                                                                                          VSP_007654, VSP_007655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nuclear protein; Coiled coil; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 1088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OCA4A52A115C0C83 CRC64;
                                                                                                                                                                                                                                                                             IsoId=Q9ULH7-3; Sequence=VSP 007656, VSP 007657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /FTId=VSP 007656.
Missing (in isoform 3).
/FTId=VSP 007657.
SUBUNIT: Interacts with SRF (By similarity). SUBCELLULAR LOCATION: Nuclear (By similarity). ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -> M (in isoform 2).
/FTId=VSP 007653.
                                                                                                                                                                                                                             Note=No experimental confirmation availble;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> R (IN REF
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22.4%; Pred. No. 26;
tive 32; Mismatches
                                                                                                                                                                                                          IsoId=Q9ULH7-2; Sequence=VSP_007653,
                                                                                                                                                           IsoId=Q9ULH7-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                 similarity).
SIMILARITY: Contains 3 RPEL repeats.
SIMILARITY: Contains 1 SAP domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPEL 1.
RPEL 2.
RPEL 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLN-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR004018; RPEL repeat.
InterPro; IPR003034; SAP.
Pfam; PF02755; RPEL; 3.
Pfam; PF02037; SAP; 1.
SMART; SM00707; RPEL; 3.
SMART; SM00513; SAP; 1.
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Transcription regulation;
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REPEAT 40 6
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                                                                                                                                          Name=1;
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QWI------QSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVR 180
                                                                                                                                                   665 KAVVIKQEVPVGQAEQQSVVSQFYVSSQGQPPPAVVAQ-------PQALLTTQTA 712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein from Saccharomyces cerevisiae.";
Oncogene 16:121-130(1998).
-!- FUNCTION: Potential methyltransferase (By similarity). Binds Fractin and shows weak Fractin crosslinking activity.
-!- SUBCELLULAR LOCATION: Cytoplasmic and cortical cytoskeleton.
-!- MISCELLANEOUS: A ribosomal frameshift occurs between the codons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98127445; PubMed=9467951;
Asakura T., Sasaki T., Nagano F., Satoh A., Obaishi H., Nishioka H.,
Ilmamura H., Hotta K., Tanaka K., Nakanishi H., Takai Y.,
"Isolation and characterization of a novel actin filament-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97127829; PubMed=8972580;
Boyer J., Michaux G., Fairhead C., Gaillon L., Dujon B.;
Sequence and analysis of a 26.9 kb fragment from chromosome XV of
the yeast Saccharomyces cerevisiae.";
Yeast 12:1575-1586(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for Leu-276 and Gly-277. SIMILARITY: Belongs to the methyltransferase superfamily. METL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                   QLLDTTDIQGEEFAKVIVQ----KLKDNKQMGLQPYPEILVVSRSPSLNL 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                              ABPX YEAST STANDARD; PRT; 627 AA. 008641; 008644; [6-CGT-2001 (Rel. 40, Created) 16-CGT-2001 (Rel. 40, Last sequence update) 10-CGT-2003 (Rel. 42, Last annotation update) Actin-binding protein ABP140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97313270; PubMed=9169874;
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STRAIN=S288c / FY1679;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 KREDIVNQMTEACLNQSL-DALLSRDLIMKEDYELVSTKPTRTSK------VRQLLDTT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81
                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005884; C:actin filament; IDA.
GO; GO:0003780; F:actin cross-linking activity; IDA.
GO; GO:00303780; F:actin cross-linking activity; IDA.
InterPro; IPR001601; Methyltransf.
InterPro; IPR000051; SAM_blind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 ELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDFLSRKAQDCYFMKLHHCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transferase; Methyltransferase; Cytoskeleton; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         627 AA; 71354 MW; D4E55F9485412F39 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 DI------QGEEFAKVIVQKLKDNKQMGLQPYPE 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.0%; Score 85; 18.8%; Pred. No.
                                                                                                                                                                                                                                                                                          EMBL; Z75147; CAA99460.1; ALT SEQ
EMBL; Z75147; CAA99461.1; ALT SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41; Conservative
                                                                                                                                                                                                                                                                                                                                                     GermOnline; 143827; -. SGD; S0005765; ABP140.
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family
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Q86169 yersinia pe Q966fm caenorhabdi Q90zt7 xenopus lae Q9xxr3 caenorhabdi Q22081 caenorhabdi Q7xbn6 antirrhinum Q922pg homo sapien Q91x4 caenorhabdi Q81y4 caenorhabdi Q81y4 caenorhabdi Q81y5 methanosarc Q9yms2 drosophila Q91x61 neisseria m Q91x61 neisseria m Q91x61 neisseria m Q81y15 homo sapien Q91x61 phomo sapien Q9xw80 caenorhabdi Q8n53 homo sapien Q9xw80 caenorhabdi Q9n2b6 bos taurus Q8n2b6 bos taurus Q81yp9 vibrio para Q87q93 arabidopsis Q8231 arabidopsis Q8531 human herpe Q56513 human herpe Q50510 human herpe Q950510 homo sapien Q22831 arabidopsis Q8513 human herpe Q56513 human herpe Q56513 human herpe Q50510 human herpe Q50510 human herpe Q50510 human herpe

Perfect score:

Sequence:

OM protein -

Run on:

Scoring table:

Database

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SECUENCE FROM N.A.
MEDLINE=98241596; PubMed=9575181;
Inohara N., del Peso L., Koseki T., Chen S., Nunez G.;
"RICK, a novel protein kinase containing a caspase recruitment domain, interacts with CLARP and regulates CD95-mediated apoptosis.";
J. Biol. Chem. 273:12296-12300(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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Q9XHR9
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Q8LLR0
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Q9P2P8
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Q8JGL7
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Q7XBM3
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Q9XW80
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GO; GO:0006915; P:apoptosis; IEA.
GO; GO:0006468; P:protein amino a
InterPro; IPR001315; CARD.
InterPro; IPR000719; Prot_kinase.
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                                                                                                                                                         March 29, 2004, 14:03:30 ; Search time 45 Seconds (without alignments) 1626.672 Million cell updates/sec
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- 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                    protein search, using sw model
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sp_nodent:*
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Copyright (c) 1993
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sp_bacteriap:*
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sp_bacteria:*
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Maximum DB seq length: 200000000
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Match Length DB
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Q91XI0 Q87L04

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51; Conservative
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Matches
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                                                                                                                                                                                                                                                                                                                           QWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIQ 189
                                                                                                                                                                                                                               21 MELSIALPVAHGPQEESCGSSQLHENSGSPE----TSRSLP----APPQDNDFLSRKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. 1JAel W.F.J., Weldens J.G.M., Broer R., Zuidema Goldbach R.W., Vlak J.M., Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20036646; PubMed=10567663;
IJkel W.F., van Strien E.A., Heldens J.G., Broer R., Zuidema D.,
Goldbach R.W., Vlak J.M.;
"Sequence and organization of the spodoptera exigua multicapsid
                                                                                                                                                                                                       26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44;
                                                                                                                                                                                Length 584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.2%; Score 99; DB 12; Length 461;
.larity 22.3%; Pred. No. 1.3;
Conservative 37; Mismatches 79; Indels 4
                                                                                                     PROSITE; PSS0209; CRED; 1.
PROSITE; PSS011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE_ST; 1.
ATP-binding; Kinase; Transferase.
SEQUENCE 584 AA; 66124 MW; 7A4EFFCB65DEB9C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50089; ZF RING 2; 1.
Metal-binding; Zinc; Zinc-finger.
SEQUENCE 461 AA; 50820 MW; 6C062A3B43DD5D06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spodoptěra exigua nucleopolyhedrovirus.
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SIMILARITY: CONTAINS I RING-TYPE ZINC FINGER
EMBL, ARF38023, ARF33605.1, -.
InterPro; IPROU3841, Znf ring.
Pfam; PP00097; zf-C3HC4; I.
                                                                                                                                                                                 DB 13;
                                                                                                                                                                                                                                                                                                    QP---LTLHPHPQDFV-----TAFDDQ----
                                                                                                                                                                                                                                                                                                                                                                                          GEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSP 222
                                                                                                                                                                                27.8%; Score 335; DB 1:
39.4%; Pred. No. 4e-22;
cive 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              461
            InterPro; IPR008271; Ser_thr_pkin_AS.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
                               Pfam; PF00619; CARD; 1.
Pfam; PF00619; CARD; 1.
Pfam; PF00109; TYRKINASE.
ProDom; PD000001; Prot kinase; 1.
SWART; SM00220; S TKC; 1.
SWART; SM00219; TYRC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleopolyhedrovirus genome.";
J. Gen. Virol. 80:3289-3304(1999).
                                                                                                                                                                                           Local Similarity 39.4 tes 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10454;
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                                                                                                     ---ERLQPGIAQQWIQS 134
                                                                                                                                                                                                              135 KREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIQGEEFA 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---LDALLSRDLIMKEDY------ELVSTKPTRTSKVRQLL 183
90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "OCSYN, A novel syntaxin-interacting protein enriched in the subapical region of inner hair cells.";
MAI. Cell. Neurosci. -0:0-0(2002).
EMBL, AF4942296; AAM14616.1;
SEQUENCE 537 AA, 58735 MW; EA9DFFD9AADDECD4 CRC64;
                                 -HCPGNHSWDSTI
                                                                                                                                                       214 AGPSTSAGPSTSA--GPSTSAGPSTSAEYQNNDDDDDLEKQRLDAAIELSRIQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 NHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDFLSRKAQDCYF-MKLHHCPGNHSWDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89 TISGSQRAAFCDHKTTPCSSAIINP--LSTAGNSERLQPGIAQQWIQS-KREDIVNQMTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Safieddine S., Ly D., Wang Y.-X., Wang C.-Y., Kachar B., Petralia R., Wenthold R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cávia porcellus (Guínea pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleosto
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.2%; Score 98.5; DB 11; Length 537; 22.0%; Pred. No. 1.8;
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last annotation update)
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                                                                                                   SGSQRAAFCDHKTTPCSSAIINPLSTAGNS------
SPETSRSLPAPQDNDFLSRKA-----QDCYFMKLH--
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                                                                                                                                                                                                                                                                                                                       195 KVIV---QKLKDNKQMGLQPYPEILV 217
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Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                     SEQUENCE FROM N.A.
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                                                                                    RAW BEDUINGE FROM N.A.

RAM REDLINES-219-6006; Pubmed=10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RAM Gans M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,

Baradon R.C., Rogers Y.H., Blazel R.G., Change M., Pfeiffer B.D.,

RAM R.H., Doyle C., Bazer E.G., Helt G., Nelson C.R., Gabor G.L.,

RAM Antil J.F., Adpayani A., An H.J., Andrews-Frankoch C., Baldwin D.,

Ballew R.M., Baros P.V., Berman B.P., Bhandari D., Bolshakov S.,

RAM Ballew R.M., Gaver B. Bouck J., Broketen P., Brottier P.,

Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Clandra I.,

RAM Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Clandra I.,

RAM CHETY J.M., Cawley S., Dahle C., Daw P., Dew I., Dietz S.M.,

Burtis K.C., Busam D.A., Deng Z., Mays A.D., Dew II., Dietz S.M.,

RAM CHETY J.M., Cawley S., Daller R., Deng Z., Gans P., Burtis R.,

RAM CHETY J.M., Cawley S., Daller R., Deng Z., Gans P., Burtis R.,

RAM CHETY J.M., Cawley S., Deller R., Deng Z., Gans P., Harris M.,

RAM Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RAM Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RAM Harris N.L., Harvey D., Heiman T.J., Mernandez J.R., Houck J.,

RAM Harris N.L., Marvey D., Meimel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RAM Lasko P., Lei Y., Leviteky A.A., Li J., Wei M., Nelson D.L.,

RAM Martis M., May M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RAM Merulov G., Milahina N.V., Mochary C., Morris J., Month S., Martel B. M., Marchy B., Murphy L., Muzny D.M., Nelson D.L.,

RAM Balazon D.R., Nelson K.A., Nixon K., Nusskern D.R., Parl R.,

RAM Beiter K., Spradling A.C., Stapleton M., Stupsk M., San E.,

RAM Beiter K., Spradling A.C., Turner R., Venter E., Shen H.,

RAM RAM G. Milams S.M., Rodder E., Stapleton M., Shorng H.,

RAM RAM G. Milams S.M., Rodder E., Stapleton B., San R.,

RAM R., Spier E., Spradling A.C., Stapleton M., Shorng R., San H.,

RAM R., Spier E., Spradli
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By Bans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

A Ferriers S., Frise E., Galle R.F., Garg N.S., George R.A.,

Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A Pacleb J., Paragas V., Park S., Patel S., Ffeiffer B.,

Pacleb J., Paragas V., Park S., Puri V., Richards S., Scheeler F.,

Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

Sequencing of Drosophila melanogaster genome ";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,

Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,

Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,

Clamp M., Drysdale R., Emmert D., Prise B., de Grey A., Harris N.,

Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,

Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,

"Annotation of Drosophila melanogaster genome.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
   Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.

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72 CYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQPGIAQQW 131
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
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Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
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Bukaryota, Metazoa, Arthropoda, Hexapoda; Insecta, Pterygota,
Neoptera, Endopterygota; Diptera, Brachycera, Muscomorpha;
Ephydroides, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 8.1%; Score 98; DB 5; Length 799; 1 Similarity 21.3%; Pred. No. 3.3; 44; Conservative 39; Mismatches 78; Indels
                                  Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
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EMBL; BT004903; AAO47881.1; -.
FlyBase; FBgn0021776; mira.
GO; GO:0045180; C:basal cortex; NAS.
GO; GO:0006105; P:saymmetric protein localization; IGI.
SEQUENCE 799 AA; 89816 MW; AE00B9F2C7F65486 CRC64;
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211 HKAL------NEQMG-QEHADLL 226
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MEDLINE=20196006; PubMed=10731132;
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        de Pablos B., Deficher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

A de Pablos B., Deficher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

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Cherry J.M., Cawley S., Dahlke C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda; Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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Shen C.P., Jan L.Y., Jan Y.N.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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211 HKAL--------NEQMG-QEHADLL 226
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Cell 90:449-458(1997).
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RESULT 044224

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46;

78; Indels

Pred. No. 3.5; 39; Mismatches

Conservative

Best Loca Matches

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(TrEMBLrel. 22,
                                                           54; Conservative
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PROSITE; PS50200; RA; 1.
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                 Query Match
Best Local Similarity
Matches 54; Conservat
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68; Conserv
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 CYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQPGIAQQW 131
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                             directs Prospero to a daughter cell during Drosophila
                                                                                                                                       Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Bhydroidea, Drosophilidae, Drosophila.
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                                                                                                                                                                                                                                                                                       STRAIN=CANTON-S;
MEDLINE=98065952; PubMed=9403694;
Ikeshima-Kataoka H., Skeath J.B., Nabeshima Y., Doe C.Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone:P0407B12.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP002843; BAB17189.1; -
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GO; GO:0045180; C:basal cortex; NAS.
GO; GO:0008105; P:asymmetric protein localization; IGI
SEQUENCE 830 AA; 93171 MW; F7AD159AA58F178A CRC64;
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                                                             Last sequence update)
Last annotation update)
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830 AA
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HKAL------NEOMG-OEHADLL 226
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Sasaki T., Matsumoto T., Yamamoto K.;
                                           Created)
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Nature 390:625-629(1997).
EMBL; AB005661; BAA24111.1; -.
PIR; T00029; T00029.
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PRELIMINARY;
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P0407B12.26 protein.
P0407B12.26.
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SEQUENCE FROM N.A.
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                                                                                                                          MIRA OR CG12249
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                                                                                                                                                                                                                                                                    422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 NOMTEACLNOSLD--ALLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIQGEEFA--- 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99
                                                                                                             24 SLNIPVNHGPQEESCGSS---QLHENSG---SPETSRSLPAPQDNDFLSRKAQDCYFMKL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 PET-----HCPGNHSWD 87
                                                                                                                                                                                                                                                    S DVNCKGEHKVNDDDDGSLSMGSEQKRKECDEDSLVDESMCKTHEQKSKDDHSSPEDVSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||:|
LQIQ------DEKQIFSNESSVKSPDPISPLGNKRGMTRWGEFDNLHNIAELEEAGS
                                                                                                                                                                                                                                                                                                                        130 QWIQSKREDIVNQMTEACLNQSL-----DALLSRDLI-----MKED-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 LQLQSVSSAIHLCDKKKM---ELSLNIPVNHGPQEESCGSSQ-----LH-----ENSGS
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                 166 -YELVSTKPTRTSKV------RQLLDTTDIQGEEFAKVIVQKLKDNKQMGLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  483 THEFDSTKDNISSAVDGNEKHEFESKKDDTNSLEGESLNKEHEOKSKEDENSGLE
                                                         75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84;
     Length 869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 QYLNLEMPILKVILQKLEEQENLEIQRIKAKYQKERSLLLQCLRKK 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----KVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 285;
                                                         71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kimberley A.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL603786; CAD49437.1; -.
GO; GO:0007218; Pineuropeptide signaling pathway; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 285 AA; 33269 MW; D757B6A7D1046693 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
8.1%; Score 97.5; DB 10;
23.0%; Pred. No. 4.1;
tive 35; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.0%; Score 97; DB 13;
23.8%; Pred. No. 1.1;
cive 41; Mismatches 93,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, Last sequence U-UNA-2003 (TrEMBLrel. 24, Last annotati SI:257F23.2 (Novel protein) (Fragment) SI:DZ57F23.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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83; Gaps

503

-VNHGPQEESCG 39

92

563

610 201 648

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93 SQRAAFCDHKTTPCSSAIINPLSTAG----NSERL----QPGIAQQWIQSKREDIVN 141
Chiang H.C., Hooper L.V., Gordon J.I.; "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis."; Science 299:2074-2076(2003).
                                                                                                                                                                                                                                                                                                504 SLLTSTEASSVSTARNODYGHFDDILCKAFEHELISSSYKINGRHPLKVEYPSLSAFLTG
                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22579291; PubMed=12693553; Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S., Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S., Nakajima D., Nagase T., Ohara O., Koga H.; Prediction of the coding sequences of mouse homologues of KIAA gene: II. The complete nucleotide sequences of 400 mouse KIAA-homologous cDNAs identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries.";
                                                                                                                                                                                                                                           452 YTLSLQAI -----RKKNTAATNIPDEPEEPKLAFPLIPADISRAQLITHLINNQSCS
                                                                                                                                                                                                                                                                             40 SSQLHENSGSPETSRSLPAPQDNDFLSRKAQDCYFMKLHHCPGNH-----SWDSTISG
                                                                                                                                                                                                                                                                                                                                                                                                          142 OMTEACLNOSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIQGEEFAKVIVQKL
                                                                                                                                                                                                                                                                                                                                                                                                                                         ----FLKDSPTE-----VKLTDTQKKEFNRVFTQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 LNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDFLSRKAQDCYFMKLHHCPGNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AK122531; BAC65813.1; -.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003575; P:regulation of transcription, DNA-dependent;
InterPro; IPR001095; Myb_DNA_binding.
InterPro; IPR003822; PAH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2063;
                                                                                                                                            Length 791;
                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2063 AA; 227819 MW; 8AA6E1AA113B3899 CRC64;
                                                                            Probom; PD000225; Hemaggluth; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 791 AA; 88443 MW; 7C72011D0CD93232 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) MKIAA1606 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84;
                                                                                                                                                                              80;
                                                                                                                                          DB 16;
                                                                                                                                            7.9%; Score 95.5; DE 19.4%; Pred. No. 5.6; ative 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.9%; Score 95.5; D
21.2%; Pred. No. 19;
cive 35; Mismatches
                                                                                                                                                                                                              2 YSLQLQSVSSAIHLCDKKKMELSLNIP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                              InterPro; IPR001364; Hemagglutn.
                                               EMBL; AE016928; AAO75816.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50090; MYB 3; 1.
                                                                                                                                            Query Match
Best Local Similarity 19.45
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Res. 10:35-48(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                            611 ELSMRFAQMAL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KDNKQMG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           649 KDTDQLG 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
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                                                                                                                                                                                                                                                                                                                                                                             564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               619 HDWNSSSDEHVYETPSKQQDEQIQKLQDDFHFENANHAKINNSNETGNQSNISHSKRSQY 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---IAQQWIQSKREDI- 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STNESKNIDTQTSNSSTSNQNFQRIRKGPNIKLPSYQLLEAPEPHEKDQDWIDNKKQELN 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DALYYFNVPAEVKNVTEGPSVTRFELSVEKGVKVSRITALQDDIKMALAAKDIRIEAPIP 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----YELVSTKPTRTSKVRQLLDTTDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVS 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTSLVGIEVPNQNPTKVN-LRSIIESPKFKNTESKLTVAMGYRINNE-----PLLMDIA 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DKKRMMDONHKKVSVPELKPEKOANANHRKDSESNKSEEFKQINTNRETDSNSYESNGIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---NSGSPETSRSLPAPQDNDFLSRKAQDCYFMKLHHCPGNHSWD----STISGSQRAAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                              STRAIN=ATCC 12228;
Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
Chen Z., Wen Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           93; Indels 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteroides thetaiotaomicron.
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
                                                                                                                                                                                                                                                                                                                                                                                                                           8.0%; Score 96; DB 16; Length 1169;
16.2%; Pred. No. 8.3;
ive 57; Mismatches 93; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-BYD15-5482 / ATCC 29148;
MEDLINE=22550889; PubWed=12663928;
Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DKKKM----ELSLNIP-----VNHGPQEESCGSSQLHE----
                                                                                                                                                                                                                                                                                                                                                                                             1169 AA; 133548 MW; 320DC7EDAA48E2C8 CRC64;
                                                                                                                                                                                                                                                                                              Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------VNQMTEAC----LNQSLDALLSRDLIMKED
                                                                               01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DNA translocase stage III sporulation prot.
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Last annotation update)
                                                                                                                                                               Staphylococcus epidermidis.
Bacteria, Firmicutes, Bacillales, Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDHKTTPCSSAIINPLSTAGNSERLQPG-----
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                                                 1169 AA
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                                                 PRT;
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InterPro; IPR002543; FtsK_SpoiliE.
Pfam; PF01580; FtsK_SpoiliE; 1.
PROSITE; PS50901; FTSK_SPOIIIE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24,
24,
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                                                 PRELIMINARY;
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BT0709.
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                             Complete proteome
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KTP 854
                                                                                                                                                                                             NCBI_TaxID=1282;
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01-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                 Q7ZAJ1
                RESULT 10
07ZAJ1
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091XI0
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                                                             1136 NLQDSLSSPSKDLLNMVKMEAEDCMVEISSNLPKQDIGEEVKEECSMELDSESPQEKPSR 1195
SWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ-------PG 126
                                                                                                127 IAQQWIQSKREDIVNQM---TEACL-----NQSLDALLSRDLIMKEDYELVSTKPTR 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 IQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIQGE 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |: |: |: || : |: || 432 IRKNRMALFQQLT---CVIPILDDLLEASVLTKEEHDIIRQKTQIPLQARELIDTILVKGN 489
                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      PEQUENCE FROM N.A.

CTISSUE=Kidney;

A Dong Z., Denton M., Gu S.M., Saikumar P., Venkatachalam M.A.;

CTISSUE=Kidney;

A Dong Z., Denton M., Gu S.M., Saikumar P., Venkatachalam M.A.;

CTISSUE=Light for rat inhibitor of apoptosis protein 2.";

CL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

C. !- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

R EMBL; AF190020; AAF04585.1; -..

R GO; GO:0005622; C:intracellular; IEA.

R GO; GO:000189; F:apoptosis inhibitor activity; IEA.

R GO; GO:0006189; F:apoptosis; IEA.

R GO; GO:0006916; P:anti-apoptosis; IEA.

R InterPro; IPR001370; BIR.

R InterPro; IPR001315; CARD.

DR PRAM: FF00651; EC3HC4; 1.

BR SWART; SM00144; CARD; 1.

BR SWART; SM00144; CARD; 1.

BR SWART; SM00144; CARD; 1.

BR SWART; SM00144; CARD; 1.

BR SWART; SM00144; CARD; 1.

BR PROSITE; PS50189; BIR REPEAT_1; 3.

BR PROSITE; PS50189; ER RING; 1.

BR PROSITE; PS50189; ZF RING; 2; 1.

BR PROSITE; PS50189; ZF RING; 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192 EFAKVIVOKLKD------NKOMGLOPYPEILVVSRSPSLNLLONK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           490 AAASVFKNSLKEVDSTLYEHLFVEKTMKYIPTEDVSGLSLEEQLRRLQEE 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.8%; Score 94.5; DB 11; Length 589; 25.5%; Pred. No. 4.7; ive 21; Mismatches 48; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Zinc-finger.
66777 MW; E6812FFB3EA34142 CRC64;
                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Inhibitor of apoptosis protein 2.
                                                                                                                                                                                   1196 ASEMSKQTVLQREDTQAAKSPSV 1218
                                                                                                                                                        176 TSKV--RQLLDTTDIQGEEFAKV 196
                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 25.5
Matches 28; Conservative
                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat)
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SEOUENCE 589 AA; 6
                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
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PRELIMINARY;

Q9ESE8

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132 IQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIQGE 191
                                                                                                                                                                                                                                                                                                                                                                                                                      Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
"Cloning and Characterization of the Rat Homologs of the Inhibitor of Apotocoais Protein 1, 2, and 3 Genes."
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
EMBL; AF183431; AAG22971.1; -..
HSSP; Q13490; 1QBH.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
GO; GO:000916; P:anti-apoptosis; IEA.
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Inhibitor of apoptosis protein 2.
Rattus norvegicus (Rat).
Elbaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 EFAKVIVOKLKD------NKOMGLOPYPEILVVSRSPSLNLLQNK 230
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Pred. No. 8.1;
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STRAIN=BALB/C; TISSUB=Heart;
Leu M., Ehler E., Perriard J.-C.;
"Cloning of an unknown protein.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AX040842, AAK84686.1;
Hypothetical protein.
SEQUENCE 896 AA; 97422 MW; 7F2DFFD53500B5A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01282; BIR REPEAT 1; 3.
PROSITE; PS50143; BIR REPEAT 2; 3.
PROSITE; PS50209; CARD; 1.
PROSITE; PS50209; Zinc 2; Zinc 2; Zinc 2; Zinc 2; Zinc 2; Zinc 2; Zinc 2; Zinc 2; Zinc 2; Zinc 2; Zinc 2; Zinc 2; Zinc 2; Zinc 2; Zinc 2; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zinc 3; Zin
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001315; BIR.
InterPro; IPR001315; CARD.
InterPro; IPR001315; CARD.
InterPro; IPR001841; Znf_ring.
Pfam; PP00653; BIR; 3.
Pfam; PP00097; Zf_C3HC4; 1.
SMART; SM00238; BIR; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 25.55
Matches 28; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
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Matches	43;	Matches 43; Conservative 35; Mismatches 84; Indels 41; Gaps 7;	35;	Mismatches	84;	Indels	41;	Gaps	7;	
λō	25 L	25 LNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDFLSRKAQDCYFMKLHHCPGNH 84	SOLHEN	SGSPETSRSLPAP	QDNDF1	SRKAQDCY	FMKLH	HCPGNH 8	34	
ор	436 L	436 LTLPVTSIPEDKAQVKLDVAEGKNAPQNPESKLKPQELTPLCTTVFPKEEPK 487	DVAEG	KNAPQNPESKLKF	OELTPI	CT	TVFPK	EEPK	187	
ολ	85 S	85 SWDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ	KTTPC	SSAIINPLSTAGN	SERLO		1	PG 126	126	
qq	488 S	488 SWHSSADIGSQEAFSESSACSWAVVKIESQEGSSEKSACGWIVVKIEDGGHAVEPLPQ 545	SSAC	SWAVVKTESQEGS	SEKSA(	CGWTVVKTE	DGGHA	VEPLPQ :	545	
ζŏ	127 I	127 IAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTR 175	1TE	ACLNC	SLDALI	NOSLDALLSRDLIMKEDYELVSTKPTR	DYELV	STKPTR :	175	
qa	546 N	546 NLÓDSLSSPSKDLINMVKMEAEDCMVEISSNLPKQDIGBEVKEECSMELDSBSPQEKPSR 605	KMEAE	DCMVEISSNLPKÇ	DIGEE	Keecsmed	DSESP	QEKPSR (	505	
δ	176 T	176 TSKVROLLDTTDIOGEEFAKV 196	SEEFAK	y 196						
Ę	A 20.5	AND ASEMSKOTUTOREDITOAAKSPSV 628	AKSPS	V 628						

Search completed: March 29, 2004, 14:09:37 Job time : 47 secs

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Title: Perfect score:

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1224 AACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCATGAA 1283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1284 AATAGTGGTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTTTTA 1343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 LeuGlnSerValSerSerAlaIleHiBLeuCysAspLysLysLysMetGluLeuSerLeu
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   Sequence
Sequence
Sequence
                                                                                                                                                                                                                               APPLICANT: Donna T. Ward
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF RIP2 EXPRESSION
FILE REFERENCE: RTS-0233
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Mismatches:
Indels:
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US-09-207-359B-1
US-09-340-620A-1
US-09-865-364-1
US-09-748-537-2
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Matches:
                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/920,663
CURRENT FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                             Sequence 3, Application US/09920663
Patent No. 6426221
GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
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; LOCATION: (225)
US-09-920-663-3
                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
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                                                                                                                                           RESULT 1
US-09-920-663-3
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-MODBL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/USO9771161/runat_29032004_124852_19881/app_query.fasta_1.391
-Q=/cgn2_1/USPTO_spool/USO9771161/runat_29032004_124852_19881/app_query.fasta_1.391
-Q=/cgn2_1/USPTO_spool/USO9771161/runat_29032004_124852_19881/app_query.fasta_1.391
-UCOPCL=0 -LOOPEXT=0 -UNITS=bits -STRAT=1 -ENN=-1 -MATRIX=01150
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -TRR SCORE=quality -THR MIN=20
-MAXLEN=200000000 -USER=USO9771161 @CGN 1 1 56 @runat_29032004 124852_19881
-NCPGL=6 -ICCDP MAAPL -LARGEQUERY -NGS GCORES=0 -WAIT -DSPBLOCK=100
-NGPLOS -DEV TIMEOTT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELEXT=7
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Sequence 2, Appli
                                                                                                                     April 1, 2004, 12:09:03 ; Search time 105 Seconds (without alignments) 1226.177 Million cell updates/sec
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Sequence 3, App
Sequence 3, App
Sequence 3, App
Sequence 3, App
Sequence 2, App
Sequence 1, App
Sequence 1, App
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232
1 MYSLQLQSVSSAIHLCDKKK......PEILVVSRSPSLNLLQNKSM
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11. /Ggn2_6/prodata/2/ina/5A_COMB.seq:*
12. /Ggn2_6/prodata/2/ina/5B_COMB.seq:*
31. /Ggn2_6/prodata/2/ina/6A_COMB.seq:*
41. /Ggn2_6/prodata/2/ina/6B_COMB.seq:*
42. /Ggn2_6/prodata/2/ina/FDCTUS_COMB.seq:*
63. /Ggn2_6/prodata/2/ina/PCTUS_COMB.seq:*
64. /Ggn2_6/prodata/2/ina/PCTUS_COMB.seq:*
65. /Ggn2_6/prodata/2/ina/Packfiles1.seq:*
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                  version 5.1.6
- 2004 Compugen Ltd.
                                                                                     nucleic search, using frame_plus_p2n model
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US-09-069-023-2
US-09-023-65-684
US-09-245-281-3
US-09-340-6208-3
US-09-340-6208-3
US-09-340-6208-3
US-09-0110-942-2
US-09-0110-942-2
US-09-0410-1
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560.0 , Ygapext 60.0
6.0 , Fgapext 7.0
6.0 , Delext 7.0
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                  GenCore (c) 1993
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Maximum DB seq length: 200000000
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105

Score

Result No.

Database

1704

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; Sequence 684, Application US/09023655
; Sequence 684, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CONTRY: USA
                                                                                                                                                                                                                                                                           1705 ACTGACATCCAAGGAGAAGAATTTGCCAAAGTTATAGTACAAAATTGAAAGATAACAAA 1764
146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp
                                                                                                           186 ThrAspileGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys
                                                                                                                                                                                                                                                     206 GlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsn
                        166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr
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APPLICATION NUMBER: US/09/023,655
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Matches:
Conservative:
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REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMUNICATION INFORMATION:
TELEPANE: (650) 845-0555
INFORMATION FOR SEQ ID NO: 684:
SEQUENCE CHARACTERISTICS:
LENGTH: 1060 base pairs
                                                                                                                                                                                                                                                                                                                                                                                1825 TTACTTCAAAATAAAGCATG 1845
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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98.69%
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: single
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                                                                                     1704 ACTGACATCCAAGGAGAAGTTTTGCCAAAGTTATAGTACAAAATTGAAAGATAACAAA 1763
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                                                                                                                                 206 GlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsn 225
                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09069023A

Sequence 2, Application US/09069023A

Sequence 2, Application US/09069023A

GENERAL INFORMATION:

APPLICANT: Nunez, Gabriel

APPLICANT: Nunez, Gabriel

APPLICANT: Nonez, Takeyoshi

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS

TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS

FILE REPERBENCE: UM-03333

CURRENT PILING DATE: 1998-04-27

NUMBER OF SEQ ID NOS: 38

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 2502
                                                186 ThrAspileGlnGlyGluGluPheAlaLysVallleValGlnLysLeuLysAspAsnLys 205
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Mismatches:
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Matches:
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ORGANISM: Homo sapiens
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Pred. No.:
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US-09-069-023-2
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Patent No. 6340576

GENERAL INFORMATION:
APPLICANT: BERTIN, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
FILE REFRENCE: 07334-07601

CURRENT APPLICATION NUMBER: US/09/099,041A

CURRENT FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-02-06
                                            US-09-771-161A-93 (1-232) x US-09-023-655-684 (1-1060)
 Mismatches:
Indels:
Gaps:
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SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 1620
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Best Local Similarity:
Query Match:
DB:
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US-09-245-281-3

US-09-245-281

S Equence 3, Application US/09245281

Patent No. 6369196

GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY

TITLE OF INVENTION: NOWEL MOJEST THEREOF

FILE REFERENCE: 07334/118001

CURRENT APPLICATION UNDHER: US/09/245, 281

CURRENT FILING DATE: 1999-02-05

EARLIER APPLICATION NUMBER: US 09/207, 359

EARLIER PILING DATE: 1998-12-08
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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EARLIER APPLICATION NUMBER: US 09/099,041
EARLIER FILING DATE: 1998-06-17
EARLIER APPLICATION NUMBER: US 09/019,942
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1620
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US-09-245-281-3
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US-09-207-359B-3; Sequence 3, Application US/09207359B

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GENERAL INFORMATION:
APPLICANT: Bartin, John
TITLE OF INVENTION:
FILE REPERENCE: 07334-112001
CURRENT APPLICATION NUMBER: US/09/207,359B
CURRENT APPLICATION NUMBER: US/09/207,359B
CURRENT APPLICATION NUMBER: US/09/09,041
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR PILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Homo sapiens
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Best Local Similarit
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Pred. No.:
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165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh
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US-01.0
Sequence 3, Application US/09865364.
Sequence 3, Application US/09865364.
Sequence 3, Application US/09865364.
Fatch No. 661321
TITLE OF INVENTION: NOVEL MOLECULES OF THE CATTLE OF INVENTION: PROPER: US/09/865,364
CURRENT APPLICATION NUMBER: US 09/207,359
PRIOR FILING DATE: 1998-12-08
PRIOR FILING DATE: 1998-12-08
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 4.0
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CORGANISM: Homo sapiens
US-09-865-364-3
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Best Local Similarity:
Query Match:
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Sequence 3, Application US/09340620A

Sequence 3, Application US/09340620A

Sequence 3, Application US/09340620A

GENERAL INFORMATION:
APPLICAMY: Bertin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
FILE REFERENCE: 07334-124001

CURRENT APPLICATION NUMBER: US 09/245,281

PRIOR FILING DATE: 1999-06-28

PRIOR FILING DATE: 1999-06-06

PRIOR FILING DATE: 1999-06-10

PRIOR FILING DATE: 1998-0-17

PRIOR PRILING DATE: 1998-0-17

PRIOR PRILING DATE: 1998-0-06

PRIOR FILING DATE: 1998-0-06

PRIOR FILING DATE: 1998-0-06

NUMBER OF SEQ ID NOS: 71

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CENTWARE: FastSEQ for Windows Version 4.0
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1000 AACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCATGAA 1059
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                                           1599 TTTACTTCAAAATAAAAGCATG 1620
                      nLeuLeuGlnAsnLysSerMet 232
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US-09-340-620A-3
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Query Match:
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1239 ATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAGCG 1298
                                                              TGGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAAATGACAGA 1358
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                                                                                          uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs
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                                oGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGl
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Patent No. 6033855

GENERAL INFORMATION:
TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
TITLE OF INVENTION: DOMAIN POLYPEPTIDES

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
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226
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Fast-SEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,942
FILING ADPLICATION DATA:
APPLICATION NUMBER:
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NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/0680
TELECHMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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EDNESS: single
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ZIP: 02110-2804
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STATE: MA
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US-09-019-942-2
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Sequence 1, Application US/0909041A

Patent No. 6346576

GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-07601)
CURRENT APPLICATION NUMBER: US/09/099,041A
CURRENT FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
TYPE: DNA
TYPE: DNA
   0440
Conservative:
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                           Mismatches:
Indels:
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, LOCATION: (214)...(1833)
US-09-245-281-1
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TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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Patent No. 6369196
BAPLICANT: Bestin, John
TITLE OF INVENTION: NOVEL MOLECULES C
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 07334/118001
                                                                       2.78e-126
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  ; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-09-091041A-1
ORGANISM: Homo sapiens
FEATURE:
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CURRENT APPLICATION NUMBER: US/09/245,281
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: US 09/207,359
EARLIER FILING DATE: 1998-12-08
EARLIER PILING DATE: 1998-06-17
EARLIER APPLICATION NUMBER: US 09/099,041
EARLIER APPLICATION NUMBER: US 09/019,942
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 1
SEQ ID NO 1
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APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL MOLECULES OF THEREOF
FILE REFERENCE: 07334-112001
CURRENT PEPLICATION NUMBER: US 09/099,041
PRIOR PELICATION NUMBER: US 09/099,041
PRIOR PELICATION NUMBER: US 09/019,942
PRIOR PELICATION NUMBER: US 09/019,942
PRIOR PELICATION NUMBER: US 09/019,942
NUMBER OF SEQ ID NOS: 47
SOFTWARE PASESEQ for Windows Version 4.0
SEQ ID NO:
LENGTH: 1931
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US-09-207-359B-1
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TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
TITLE OF INVENTION: DOMAIN POLYPEPTIDES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER REDABLE FORM:
MEDIUM TYPE: Diskette
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APPLICATION NUMBER: 09/019,942
FILING DATE:
ATOMES MARE: MANE:                                                      1812 TTTACTTCAAATTAAAAGCATG 1833
232
                                                                                                                                            Sequence 2, Application US/09470271; Sequence 2, Application US/09470271; Patent No. 6410689; GENERAL INFORMATION:
nLeuLeuGlnAsnLysSerMet
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TELEX: 200154
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1931 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
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APPLICANT: Bertin, John
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
TITLE REFERENCE: 07334-112001
CURRENT PALICATION NUMBER: US/09/865,364
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/207,359
PRIOR APPLICATION NUMBER: US 09/207,359
PRIOR APPLICATION NUMBER: US 09/207,359
PRIOR FILING DATE: 1998-12-08
PRIOR FILING DATE: 1998-06-17
                                            Conservative:
Mismatches:
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ORGANISM: Homo
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Matches:
Conservative:
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Indels:
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PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 47
SUTTARRE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1931
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; LOCATION: (214)...(1833)
US-09-865-364-1
                                                                                               TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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Pred. No.:
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Job time : 116 secs

GenCore (c) 1993

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Run on:

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Sequence 13, Appl
Sequence 173, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
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Sequence 1, Appli
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Sequence 20565,
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US-10-105-931-1
US-10-118-984-1
US-10-255-981-1
US-09-918-995-20565
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Matches:
Conservative:
Mismatches:
Indels:
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TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
SOFTWARE: PALCATION NUMBER: 135619
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PALCHIN VERSION 3.0
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                                                       US-09-925-301-173

US-09-728-721-3

US-10-105-931-3

US-10-118-984-3

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US-09-748-537-2

US-09-728-721-1
                     US-10-342-887-957
US-09-981-397A-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09771161A Patent No. US20020110811A1
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ORGANISM: Homo sapiens
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OTHER INFORMATION: "n
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Alignment Scores:
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-MODEL-frame+ D2n.model -DEV=xlh
-Q=CGGY2_1VGFTO_SODO_IVGOS71161/runat_29032004_124852_19907/app_query.fasta_1.391
-Q=CGGY2_1VGFTO_SODO_IVGOS771161/runat_29032004_124852_19907/app_query.fasta_1.391
-DB=Published Applications NA -QFMT=fastap -SUFFTX=0120p2n.rmpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=0130
-TRAMS=human40.cdi -LIST=45 -DOCALLGN=200 -THR SCORES=qualty -THR MIN=20
-MAXLEN=2000000000 -USER=US09771161_@CGN 1 1.57 @runat_29032004_124852_19907
-NCFUS=6 -LOOP MAAP -LARGEQUERY -NGG_SCORES=0 -WAIT -DSPEDCCK=100
-LONGLOG -DEV THREOTT=120 -WANT TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELEXT=7
                                                                                                                                         April 1, 2004, 12:50:59; Search time 417 Seconds (without alignments) 2080.611 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/USO7 PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq:*
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5: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
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                     version 5.1.6
- 2004 Compugen Ltd.
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Total number of hits satisfying chosen

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Word size:

Searched:

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Scoring table:

Title: Perfect score:

Sequence:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Listing first 45

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dai, Hongyue
APPLICANT: Dai, Hongyue
APPLICANT: Dai, Hongyue
APPLICANT: Linsley, Peter S.
APPLICANT: Mao, Mao
APPLICANT: Roberts, Christopher J.
APPLICANT: Non't Veer, Laura Johanna
APPLICANT: Van't Veer, Laura Johanna
APPLICANT: Van't Veer, Marc J.
APPLICANT: Van't Weer, Laura Johanna
APPLICANT: Van't Weer, Laura Johanna
APPLICANT: Van't Weer, Laura Johanna
APPLICANT: Van't Weer, Laura Johanna
APPLICANT: Van't Weer, Laura Johanna
APPLICANT: Van't Weer
TITLE OF INVERTION DIABER: US/10/342,887
CURRENT APPLICATION NUMBER: 60/298,918
PRIOR APPLICATION NUMBER: 60/298,918
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
SEGO ID NO 957
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                                                                                     CACAAGACCACTCCCATGCTCTTCAGCAATAAATACAACTCTCTCAACTGCAGGAAACTCA
                                                                                                                                                                                                                                    740 AACCAAATGACAGAAGCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTG
ProGlyAsnHisSerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAsp
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                                                               HisLysThrThrProCysSerSerAlallelleAsnProLeuSerThrAlaGlyAsnSer
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ORGANISM: Homo sapiens
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Best Local Similarity:
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US-10-342-887-957
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APPLICANT: Axxima Pharmaceuticals AG
APPLICANT: Axxima Pharmaceuticals AG
APPLICANT: Schubart, Daniel
APPLICANT: Schubart, Daniel
APPLICANT: Stein-Gerlach, Matthias
APPLICANT: Stein-Gerlach, Matthias
APPLICANT: Stein-Gerlach, Matthias
APPLICANT: Stein-Gerlach, Matthias
APPLICANT: Stein-Gerlach, Matthias
APPLICANT: Stein-Gerlach, Matthias
APPLICANT: Stein-Gerlach
TITLE OF INVENTION: Callular Kinases Involved in Cytomegalovirus Infection and their
TITLE OF INVENTION: Inhibition
FILE REPERENCE: AXM-004.1 US
CURRENT APPLICATION NUMBER: 60/240,750
PRIOR FILING DATE: 2000-10-16
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SOFTWARE: Patentin version 3.1
SEQ ID NO 13
LENGTH: 2501
TYPE: DNA
ORGANISM: Homo sapiens
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Matches:
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SEQ ID NO 173

LENGTH: 2709

TYPE DNA
ORCANISM: Home sapiens
FEATURE:
NAME/KEY: misc feature
LCCATION: (2595)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LCCATION: (2625)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LCCATION: (2659)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
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LCCATION: (2659)
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Query Match:
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Sequence 173, Application US/09925301

GENERAL INFORMATION:

TILLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

TILLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA106

CURRENT APPLICATION NUMBER: US/09/925,301

CURRENT PILING DATE: 2001-08-10

PRIOR PPLICATION NUMBER: 60/124,270

PRIOR PILING DATE: 2000-03-08

PRIOR FILING DATE: 1009-03-08

PRIOR FILING DATE: 1000-03-08

PRIOR FILING DATE: 1000-03-08

SPRIOR FILING DATE: 2000-03-08

SPRIOR FILING DATE: 1000-03-08

SOFTWARE: PatentIN Ver. 2.0
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    Length:
Matches:
Conservative:
Mismatches:
Gaps:
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Best Local Similarity:
Query Match:
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1419 CTATGAACTTGTTACTACCAAGCCTACAAGGACCTCAAAAGTCAGAACAATTACTAGACAC 1478
                                                                                      1479 TACTGACATCCAAGGAGAAGTTTGCCAAAGTTATAGTACAAAATTGAAAGATAACAA 1538
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                                                    rThrAsp1leGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLy
                                                                                                                                                                                                                                                                                   Sequence 3, Application US/10105931
; Sequence 3, Application US/10105931
; Publication No. US20020150987A1
; GENERAL INFORMATION:
    APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-07601
; CURRENT APPLICATION NUMBER: 09/099,041
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR FILING DATE: 1998-06-17
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LEAGTH: 1620
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CRGANISM: Homo sapiens
US-10-105-931-3
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                                                                                                                                                     TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE FILE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE FILE REPERENCE: 07334-12401.

CURRENT PELLOATION NUMBER: US/09/728,721

CURRENT FILING DATE: 1909-06-28

PRIOR FILING DATE: 1999-06-28

PRIOR FILING DATE: 1998-12-08

PRIOR FILING DATE: 1998-12-08

PRIOR FILING DATE: 1998-10-08

PRIOR APPLICATION NUMBER: US 09/099,041

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-07-06

NUMBER OF SEQ ID NOS: 71
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                                                                                                      ; Sequence 3, Application US/09728721; Patent No. US20020061845A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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APPLICANT: BERTIN, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREC
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREC
CURRENT APPLICATION NUMBER: US/10/295,981
CURRENT FILING DATE: 1999-06-28
PRIOR FILING DATE: 1999-02-05
PRIOR FILING DATE: 1999-02-05
PRIOR PAPLICATION NUMBER: US 09/245,281
PRIOR APPLICATION NUMBER: US 09/207,359
PRIOR PRIJOR DATE: 1998-12-08
PRIOR PRIJOR DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 71
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TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY

TITLE OF INVENTION: AND USES THEREOF

FILE REPERBNCE: 07334/118001

CURRENT APPLICATION NUMBER: US/10/118,984

CURRENT FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/207,359

PRIOR PILING DATE: EARLIER FILING DATE: 1998-02-05

PRIOR PPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/099,041

PRIOR PILING DATE: EARLIER FILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/019,942

PRIOR PILING DATE: EARLIER FILING DATE: 1998-06-17

PRIOR PLING DATE: EARLIER FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 44

SOFTWARE: FASTSEQ for Windows Version 4.0

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US-10-118-984-3
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Score:       128.00       Matches:       226         Percent Similarity:       99.12%       Conservative:       0         Best Local Similarity:       99.12%       Mismatches:       1         Query Match:       55.17%       Indels:       2         DB:       9       Gaps:       0         US-09-771-161A-93 (1-232) x US-09-748-537-2 (1-1931)       0	Qy 6 LeuGlnSerValSerSerAlaileHisLeuCysAspLysLysLysMetGluLeuSerLeu 25 	Oy 26 AsnileProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHisGlu 45	Qy 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaBroGlnAspAsnAspPheLeu 65	Oy 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85 	Oy 86 TrpAspSerThrlleSerGlySerGlnArgAlaAlaPheCySASpHisLySThrThr-Pr 105 	OY 105 OCYSSERSEALAILEILEABNPYOLEUSETTHRALAGIYASNSERGIUARGLEUGINPR 125	Oy 125 oGlylleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGl 145	Oy 145 ualaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeulleMetLysGluAs 165	Oy 165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185 	Oy         185 rThrasp1leGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLy         205	Oy 205 sGlnWetGlyLeuGlnProTyrProGlulleLeuValValSerArgSerProSerLeuas 225	Oy 225 nLeujeuGlnAsnLysSerWet 232 	RESULT 10 US-09-728-721-1 ; Sequence 1, Application US/09728721 ; Patent No. US20020061845A1 ; GENERAL INFORMATION: ; APPLICANT: Bertin, John ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREC; ; FILE REFERENCE: 07344-124001	; CURRENT APPLICATION NUMBER: US/09/728,721 ; CURRENT FILING DATE: 2000-12-01 ; PRIOR APPLICATION NUMBER: 09/340,620 ; PRIOR FILING DATE: 1999-06-28 ; PRIOR APPLICATION NUMBER: US 09/207,359 ; PRIOR FILING DATE: 1998-12-08	; PRIOR APPLICATION NUMBER: US 09/099,041 ; PRIOR FILING DATE: 1998-06-17 ; PRIOR APPLICATION NUMBER: US 09/019,942
Oy 6 LeuGhnSerValSerSerAlaileHisLeuCysAspLysLysEysMetGluLeuSerLeu 25	Qy 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65	Qy 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85	Qy     86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr-Pr 105       Db     1180 TGGGATAGCACCATTTCTGGATCTCAAAGGCTGCATTCTGTGATCACAAGACCAT-TCC 1238	Qy 105 oCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125	Qy         125 oGly1leAlaGlnGhTrp1leGlnSerLySargGluAsp51eValAsnGlnMetThrG1 145           L	Qy       145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165         Db       1359 AGCCTGCCTTAACCAGTGGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGGA 1418	Qy 165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185	Oy 185 rThraspiledinglyGluGluPhealaLysValileValGlnLysLeuLysaspasnLy 205	Oy 205 sGlnWetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAs 225	Oy 225 nLeuLeuGlnAsnLysSerMet 232	RESULT 9 US-09-748-537-2 ; Sequence 2, Application US/09748537	; FACENT NO USZUDZUOLZUOLZUOLZUOLZUOLZUOLZUOLZUOLZUOLZUOL		SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2 LENGTH: 1931 TYPE: DNA TYPE: DNA US-09-748-537-2	1. 1.

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Alignment Scores:
Pred. No.:
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Matches:
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Mismatches:
Indels:
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PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 71
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1
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US-10-133-780-2
; Sequence 2, Application US/10133780
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128.00
99.12$
99.12$
                                                                                                          FEATURE:
NAME/KEY: CDS
LOCATION: (214)...(1833)
                                                           LENGTH: 1931
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
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US-09-728-721-1
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Publication No. US20020123115A1
GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION
DOMAIN POLYPEPTIDES
                                                                                                                                                                                                                                                    COMPUTER: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows Version 2.0b

SOFTWARE: FastSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION UNBER: US/10/133,780

FILING DATE: 26-Apr-2002

PRIOR APPLICATION DATA:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE! COCKET NUMBER: 07334/068001
TELECOMMUNICORATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/019,942
FILING DATE: 06-FEB-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                              ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-133-780-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1931 base pairs
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128.00
99.12%
99.12%
55.17%
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                                                                                                                     NUMBER OF SEQUENCES:
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Best Local Similarity:
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165

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1751
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; Sequence 1, Application US/10118984
; Publication No. US20020197693A1
; GENERAL INFORMATION:
APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/10/118,984
; CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/207,359
; PRIOR PILING DATE: EARLIER FILING DATE: 1998-02-05
; PRIOR PELING DATE: EARLIER FILING DATE: 1998-02-06
; PRIOR PELING DATE: EARLIER FILING DATE: 1998-06-17
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 1
: LENGTH:: 1931
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1273 AATAGTGGTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTTTA 1332
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                                                 1333 İCTAGAAAAGCICAAGACTGITATITATGAAGCTGCATCACTGTCCTGGAAATCACAGT
                                                                                                   TrpAspSerThr11eSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr-Pr
                                                                                                                       oCysserSerAlallelleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr
                                                                                                                                                                                           uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs
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                                 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer
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Matches:
Conservative:
Mismatches:
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ORGANISM: Homo sapiens
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Best Local Similarity:
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 RESULT 12

US-10-105-931-1

Sequence 1, Application US/10105931

Sequence 1, Application US/2002015098741

GENERAL INFORMATION:

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

FILE REFERENCE: 07334-076001

CURRENT APPLICATION NUMBER: US/10/105,931

CURRENT APPLICATION NUMBER: 09/099,041

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

NUMBER OF SEQ ID NOS: 37

SEQ ID NO 1

LENGTH: 1931
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US-10-105-931-1
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NUMBER OF SEQ ID NOS: 71
SOFTWARE: FastSEQ for Windows
SEQ ID NO:
LENGTH: 1931
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US-10-295-981-1
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US-09-918-995-20565
                                                                      TYPE: DNA
ORGANISM: Homo
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Pred. No.:
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Publication No. US20030120055A1

GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
FILE REPERENCE: 0734-12401

CURRENT APPLICATION NUMBER: US/09/340,620

PRIOR APPLICATION NUMBER: US/09/340,620

PRIOR APPLICATION NUMBER: US 09/245,281

PRIOR PILING DATE: 1999-06-28

PRIOR PILING DATE: 1999-06-05

PRIOR FILING DATE: 1999-06-05

PRIOR FILING DATE: 1998-12-08

PRIOR FILING DATE: 1998-12-08

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

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TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrPro 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 AATAGTGGTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACATGATTTTTA 310
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APPLICANT: Hypeq, Inc.

APPLICANT: Hypeq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES;
FILE REPERENCE: 20411-756

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 20565

LENGTH: 491
                                                                                                                                                                                                                                                                                                                                                                                          US-09-771-161A-93 (1-232) x US-09-918-995-20565 (1-491)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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100.00$
51.72$
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; ORGANISM: Homo sapiens
US-09-918-995-20565
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Best Local Similarity:
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Search completed: April 1, 2004, 14:59:43 Job time : 426 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - nuclei	OM protein - nucleic search, using frame plus p2n model		ಹ
Run on: Apr	April 1, 2004, 12:07:21 ; Search time 2694 Seconds (without alignments) 2571.650 Million cell updates/sec	Res	Result No.
Title: US- Perfect score: 232 Sequence: 1 M	US-09-771-161A-93 232 1 MYSLQLQSVSSAIHLCDKKKPEILVVSRSPSLNLLQNKSM 232	i o	1 4 6 6 .
Scoring table: OLIGO Xgapog Ygapog Fgapog	OLIGO Xgapop 60.0 , Xgapext 60.0 Ygapop 60.0 , Ygapext 60.0 Fgapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0		4 N O C B O C
Searched: 275	27513289 segs, 14931090276 residues	U	112
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Total number of hit	Total number of hits satisfying chosen parameters: 108	טט	15
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Post-processing: Li	Post-processing: Listing first 45 summaries	υ	285
Command line parameters:	eters:		22

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## 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Location/Qualifiers
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Seg primer: M13 FORWARD
POLYA=Yes.
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                                                Email: cgapD8-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMNO471 row: e column: 12
High quality sequence stop: 767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCAATAATAAATCACTCTCAACTGCAGGAAACTCAGAACGTCTGGCAGCCTGGTATAGCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Matches:
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/tissue trype="Human Lung Epithelial cells"
/lab host="DHIOB (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-FN0"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequenoring by: Dr. M. Bento Soares, University of Iowa
DNA Sequenoring by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
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TAG_SEQ=None found"
                                                                                              228
                                     541
                                                                                                                          542 CTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAAATTTACTTCAA 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 683)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene.
209 LeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsnLeuLeuGln
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Genome Res. 6 (9), 791-806 (1996)
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124 361

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DEFINITION

RESULT 3 BQ670832

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

AUTHORS TITLE JOURNAL COMMENT

REFERENCE

source

FEATURES

164

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/note="organ: salivary gland, Vector: potB7; Site_1: Xho1;
Site_2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/Xho1 sites using the
following 5' adaptor: GGGACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M: Rubin
(University of California, Berkeley) using ZAP-CDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
E 1 (bases 1 to 938)
NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC.Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2410 row: k column: 04
High quality sequence stop: 659.
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2 Homo sapiens cDNA clone IMAGE:6257019
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                             (1-683)
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AGENCOUR 8191703 NIH_MGC_102 .
5', mRNA sequence.
BQ670832
                           x CB852764
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EST.
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                             US-09-771-161A-93
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506

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446

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148

168 266 146

86

SOURCE ORGANISM

KEYWORDS

REFERENCE AUTHORS TITLE

JOURNAL MEDLINE PUBMED COMMENT

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BM840808 660 bp mRNA linear EST 06-MAR-2002
K-EST0117952 S12SNU216 Homo sapiens CDNA clone S12SNU216-38-G08 5',
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Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

S. Ecoun-Gong Yuseong-gu, Daejeon 305-333, South Korea

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Plate: 38 row: G column: 08
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Unpublished (2002)
Contact: Kim YS
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                                                                                                                                                                                                                                                                                                                               Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com)
Seq primer: M13 FORWARD
POLYA=Yes.
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                                                                                                                                                                                                                                                             University of Iowa 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA Feat: 319 356 7147 Eas: 319 356 7147 Eas: 319 356 7147 Eas: 319 367 7147
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                       sapiens (human)
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                                            Homo sapiens
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Query Match:
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source

FEATURES

Pred. No.:

ORIGIN

Score:

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/tissue type="Human Lung Epithelial cells"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone lib="UU-cF-FNO"
/note="Organ: Lung; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR 1; Site 2: Not 1; Ur-cF-FNO is a subtracted cDNA library derived from two normalized Human lung epithelial cell libraries (EN1 and DU1) The library was subtracted according to according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact:
DAG_SEQ=None found"
                                                                                                                                                                                                                                                                                                                                   McCray Lab
University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@ulowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 715)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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UI-CF-FN0-aem-0-20-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetics (www.resgen.com) or from Open Blosystems (www.openbiosystems.com).
The following repetitive elements were found in this cDNA sequence: 1-24, AT rich#Low_complexity (matched compliment) FORWARD POLYA=Yes.
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208
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/db_xref="taxon:9606"
/clone="UI-CF-FN0-aem-o-20-0-UI"
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Matches:
Conservative:
Mismatches:
Indels:
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/organism="Homo sapiens"
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                                                           CB851847.1 GI:30046667
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AUTHORS
TITLE
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MEDLINE
PUBMED
COMMENT
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KEYWORDS
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                            /cloud ill EcoRI; /cloud ill EcoRI; /cloud ill EcoRI; /cloud ill EcoRI; /cloud ill EdoRI; Site_2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intect mRNA was ligated with DNA-RNA linker including EcoR is site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The cDNA vector was adjusted to have about 60nt. The cDNA vector was circularized with B. coll DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli ToplOF' by electroporation method. The CDNA libraries constructed by this method are full-length enriched cDNA library."
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/lab_host="Top10F'"
/clone lib="S12SNU216"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-remail.nib.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
POLYA-Yes.
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                                                                       CAGCCTGGTATAGCCCCAGCAGTAGATCCAGAGCAAAAGGGAAAGACATTGTGAACCAAATG
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                      TTTTTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCCTGGAAAT
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/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_ED1"
/note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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(Pharmacia) with a modified polylinker; Site 1: ECOR I; Site 2: Not I; NCI CGAP_ED1 is a normalized cDNA library contraining the following tissue(s): Chondrosarcoma cell line CS5. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded CDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence that got this library is GCTCAAGGCT.

TAG_INSUE-Chondrosarcoma
TAG_LIB-UI-H-ED1
TAG_SEQ-CGTCAAGGCT"
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Qy         132 IleGlnSerLysArgGluAspIleValAsnGlnMetThrGluAlaCysLeuAsnGlnSer 151           Db         352 ATCCAGAGCAAAGGGAAGCATTGTGAACCAAATGACAGAGCTGCTTGACCTGCTTGACCAGTCG 293           Qy         152 LeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAspTyrGluLeuValSerThr 171           Db         292 CTAGATGCCTTCTGTCCAGGGACTTGATCAAAGAGGACTTGATGATTGAT	RESULT 9 BG757422 LOCUS BG757422 BG757422 BG757422 BG7711061F1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4851542 5', mRNA sequence. ACCESSION BG757422.1 GI:14068075 KEYWORDS BG757422.1 GI:14068075 KEYWORDS BG757422.1 GI:14068075 FEFERENCE ORGANISM Homo sapiens (human) ORGANISM FEFERENCE I (bases 1 to 852) AUTHORS II (bases 1 to 852) AUTH	Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  CNA Sequencing by: Incyte Genomics, Inc.  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  http://image.llnl.gov  Plate: LLCM1654 row: i column: 15  High quality sequence stop: 814.  Plate: LLCM1654 row: i column: 16  High quality sequence stop: 814.  Acation/Qualifiers  source /organism='WHMO sapiens"  //do_xref="taxon:9606" //clone="taxon:9606" //clone="taxon:9606" //clone="taxon:9606" //clone="taxon:9606" //clone="taxon:9606"	/tissue type="primary B-cells from tonsils (cell line)" /lab hose="primary B-cells from tonsils (cell line)" /clone_lib="NIH_MGC_48" /clone_lib="NIH_MGC_48" /force="Organ: B-cells; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGAGA(G). Size=selected >SOODp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II R (Life Technologies).  ORIGIN Alignment Scores: 1.85e-167 Length: 852
ACCESSION AI745575. GI:5113863 KEYWORDS SOURCE ORGANISM Homo sapiens (human) ELKATYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Homo sapiens ELKATYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Homamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  I (bases 1 to 592) AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), TUMOR Gene Index JOURNAL Unpublished (1997) COMMENT CONTACT: Robert Strausberg, Ph.D. Email: Cgapbs-r@mail.nih.gov Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/Link at: www-bio.llnl.gov/bbrp/image.html	Insert Length: 673 Std Error: 0.00 Seq primer: -40UP from Gibco. High quality sequence stop: 459.  Location/Qualifiers Location/Qualifiers  1592 Anol type="makna" Anol = "mana" Adv zetg="makna" Adv zetg="mana" Adv zetg="mana" Adv zetag="mana" Adv zetage="mana" Adv zetage Adv zetage Adv zetage Adv zetage Adv zetage Adv zetage Adv zetage Adv zetage Adv zetage Adv zetage Adv zetage Adv zetage Adv zetage Adv zetage Adv zetage Adv zetage Adv zetage Adv zetage	IGIN ignment Scores: ed. No.: ore: creet Similarity st Local Simila ery Match: :	Oy 52 Intseragistral arrodina spannas pheleuser aggly shall all and the season of the

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BQ773811 667 bp mRNA linear EST 26-JUL-2002 UI-H-EZI-bbz-f-10-0-UI.s1 NCI CGAP_Ch2 Homo sapiens cDNA clone UI-H-EZI-bbz-f-10-0-UI 3', mRNA sequence.
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Homo sapiens
Homo sapiens
Bukaryotas, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Bukaryotas, Metazoa, Primates; Catarrhini, Hominidae, Homo.
1 (bases 1 to 667)
                                                         /tissue type="hypernephroma, cell line"
/lab host-"DH10B (phage-resistant)"
/clome_lib="NIH MGC_8"
/inche="lorgan: kidney, Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 AsnileProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHisGlu
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
'organism="Homo sapiens'
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               /mol_type="mRNA"
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/clone="IMAGE:4426016"
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I (bases 1 to 811)

NH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapba-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                              240
                                                                                                                                                                                                                                                                                            300
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10172 row: g column: 09
High quality sequence stop: 721.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuleu 183
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                  Conservative:
Mismatches:
Indels:
      Matches:
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BG170405.1 GI:12677108
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Homo sapiens
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100.00%
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76.72%
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                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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RESULT 10 BG170405 LOCUS DEFINITION

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

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347

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/tissue_type="Adult"
//lab_host="Philips (Life Technologies)"
//lab_host="DHIOB (Life Technologies)"
//lab_host="DHIOB (Life Technologies)"
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//note="Torgan: Bone; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR 1; Site 2: Not 1;
NCI_CGAP FHO is a cDNA library containing the following tissue(s): Human Grade 1 Chondrosarcoma Cell Line The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I dagsted with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGAATCCGGC. The cell line was provided by Dr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGAP_FHO Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbe-remail.nib.gov
Tissue Procurement: James Martin
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@ulowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-22, AT rich#Low_complexity (matched compliment)
POLYA-Yes.
                                                                                                                                                                     206 GlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsn 225
                                                                                                                                                                                                                                                                       210 CAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGGTTTCTAGATCACCATCTTTAAAT 151
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 721)
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TAG TISSUE=Human Chondrosarcoma Cell Line CS8 - Grade 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                          ThraspileGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys
                            TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'tissue_type="Human Chondrosarcoma Cell Line"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UI-H-FH0-bcd-1-20-0-UI.81 NCI CGAP FH0 Ho
UI-H-FH0-bcd-1-20-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
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1. .721
/organism="Homo sapiens"
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Chondrosarcoma
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Homo sapiens
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BQ774940/c
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VERSION
KEYWORDS
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AUTHORS
TITLE
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/dav stage="Adult"
/lab_host="DH10B (Life Technologies)"
/dloon lib="NCI CGAP CL2"
/dloon lib="NCI CGAP CL2"
/note="Organ: Left Pelvis' Vector: pT7T3-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP CL2 is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma crade II. The library
was constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dr prime containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligomucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
Orthoapedics
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
BouyAs-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                390 GCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGGAC 331
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   570 regearaccaccarrrcregarcreaaaeeecrecarrcrereacaaccacreca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="UI-H-EZ1-bbz-f-10-0-UI"
/tissue_type="Chondrosarcoma Grade II"
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TAG_LIB=UI-H-E21
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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/db_xref="taxon:9606"
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                                                     Tumor Gene Index
Unpublished (1997)
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Query Match:
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UI-H-FT2-bjj-h-03-0-UI.81 NCI CGAP_FT2 Homo sapiens CDNA clone
UI-H-FT2-bjj-h-03-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Context: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
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                                                                                                                                                                                                                                                                                                                                                                    AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeulleMetLysGluAsp 165
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                                                                                                                                                                                                                                                                      CysSerSerAlallelleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125
                                                                                                                                                                                                                                                                                  313
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                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. T. (Dases 1 to 744)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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TAG_LIB=UI-H-FH0
TAG_SEQ=AGAATCCGGC"
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/ Organism="now" sapiens
/ moi type="mRNA"
/ db xref="taxon:966"
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/ tissue type="Aveolar Macrophage"
/ dev stage="Adult"
/ tissue type="Aveolar Macrophage"
/ dev stage="Adult"
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/ clone lib="NOI CGAP FT2"
/ clone lib="NOI CGAP FT2"
/ clone lib="NOI CGAP FT2"
/ clone lib="NOI CGAP FT2"
/ clone lib="Noi Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: Son i; Site_2: NOt I;
/ NOI CGAP FT2 is a subtracted cDNA library constructed a pool of F RNA samples from Alveolar Macrophages challenged with different treatments. The library was subtracted according to Bonaldo, Lennon and Soares, Gary W. Hunninghake of the University of Iowa.

TAG_IIS-Human Lung Aveolar Macrophage
TAG_LIB-UI-H-FT2
TAG_SEQ=GGCCATGCCG"
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  can be found
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Clone Distribution: Distribution information http://genome.uiowa.edu/distribution/cgap.html Seq primer: M13 FORWARD POLYA-Yes.
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Mismatches:
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Matches:
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/organism="Homo sapiens"
                                                                                    Location/Qualifiers
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UI-H-EZO-bau-f-07-0-UI.sl NCI_CGAP_Chl Homo sapiens cDNA clone CA413941
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Emall: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
Orthoapedics
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                                                                                                                                                                                                                                                                                                                                                                                           128 AlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGluAlaCys 147
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                    from Dr. M. Bento Soares, bento-soares@ulowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-64, AT rich#Low_complexity (matched compliment)
Seq primer: M13 FORWARD
POLYA=Yes.
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/organism="Homo sapiens"
     US-09-771-161A-93 (1-232) x CA314123 (1-672)
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CA413941.1 GI:24776592
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University of Iowa Med Labs, Iowa City, IA 52242, USA
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation. Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
Seq primer: M13 FORWARD
POLYA=Yes.
                                                                                                                                                                                                                                                UI-CF-FNO-aez-o-11-0-UI.sl UI-CF-FNO Homo sapiens cDNA clone CA314123
        223
203 pAsnLysGlnMetGlyLeuGlnFroTyrProGlulleLeuValValSerArgSerProSe 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 672)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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TAG TISSUE=Lung Epithelial Cells Tissue nos 359-368
TAG LIB=UI-CF-FN0
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Search completed: April 1, 2004, 14:50:52 Job time : 2712 secs

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April 1, 2004, 08:35:52 ; Search time 4002 Seconds (without alignments) 2512.640 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Perfect score:
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Sequence:

Run on:

Total number of hits satisfying chosen parameters: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

6940544

3470272 segs, 21671516995 residues

Searched:

Command line parameters:
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-MODEL=frame+ p2n.model -DEV=xlh
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	530 Ното вар	5645 Synt	3813 F	1553 Homo	824	1808 Phosp	583	13	7 Seguence	658	453	AX429236 Sequence		AR194318 Sequence			ñ				Seque	BD123999 Novel mol		Sequenc			Sequenc		Seque	BD123998 Novel mol	Seque		9 Mus	HOMO	Homo sa	Rattus	9 Mouse	Primer	21 Homo s	540 Danio r	645	1247 Sequenc	263 Sequenc	31610 S	AX082238 Sequence
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ALIGNMENTS

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Park, J., Rolfs, A., Hu, Y., Shen, B., Vannberg, F., Moreira, D., Kelley, T., Zuo, D., Raphael, J., Baqui, M., Jepson, D., Harlow, E., IaBaer, J. and Brizuela, L.

Direct Submission

Submitted (102-UIL-2003) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141-2023, USA

This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics.

Each CDS has been cloned without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TW) cloning system between the Sall and HindlII sites of the pDNR-Dual vector. Additional sequences in the clone: 'ACC' after Sall site and before 'ATG' to provide Kozak consensus
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                                                                                                              AGTTGGGACAGCACTTTCTGGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCACT
                                                                                                                                                                                                                                                                                                1297 CCTGGTATAGCCCAGCAGTGGATCCAGAGCAAAAAGGGAAGACATTGTGAACCAAATGACA
65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis
                                                                                       85 SerTrpAspSerThr11eSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr
                                                                                                                                                                               ProCysSerSerAlallelleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln
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                                                                                                                                                                                                                                                                                                                                                          145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu
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1 (bases 1 to 1623)
Park, J., Pale, B., Vannberg, F., Moreira, D., Park, J., Rolfs, A., Hu, Y., Shen, B., Vannberg, F., Moreira, D., Kelley, T., Zuo, D., Raphael, J., Baqui, M., Jepson, D., Harlow, E., LaBaer, J. and Brizuela, L.
Cloning of human full-length CDS FLEXGene kinases in recombinational vector system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AY335645 1inear SY Synthetic construct Homo sapiens receptor-interacting serine-threonine kinase 2 (RIFK2) .mRNA, partial cds.
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1 (Dases 1 to 1623)
McCarthy,J.V., Ni,J. and Dixit,V.M.
RIP2 is a novel NF-kappaB-activating and cell death-inducing kinase J. Biol. Chem. 273 (27), 16968-16975 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/product="receptor interacting protein 2"
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AVKHJHITHPLIDSBRKDVYLRABEILHKARFSYILPIIGICNEPELGIVTEYWPNGS
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KIADFGLSKWRMMSLSQSRSSKSAPEGGTIIYMPPENYEPGGKSRASIKHDIYSYAVI
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PDERPSFLKCLIELEPVLRTFEEITFLEAVIQLKKTKLQSVSSAIHCDKKKMELSIN
PUNGOPEESCGSSQLHENSGSPETSRSLPARDDNPLSKRAQDCYFWKLHHCPGNH
SWDYTISGSQRAAFCDHKTPCSSAIINPLSTAGNSERLQPGIAQQMIQSKREDIVNQ
MTBACLNQSLDALLSRDLIMKEDYELVSTKFTSKVRQLLDTTDIQGEEFAKVIVQK
LKDNKQMGLQPYPEILVVSRSPSINLLQNKSM"
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Homo sapiens receptor interacting protein 2 (RIP2) mRNA, complete
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Submitted (15-JUL-1998) Molecular Oncology, Genentech Inc, 1
Way, South San Francisco, CA 94080, USA
Location/Qualifiers
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Mismatches:
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function="activtes NF-kappaB"
function="induces cell death"
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McCarthy,J.V., Ni,J. and Dixit,V.M.
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Best Local Similarity:
Query Match:
DB:
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Homo sapiens clone DNA43306 RIPK2 (UNO277) mRNA, complete cds.
AY358813.
AY358813.1 GI:37182743
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GSPETSRSLPAPQDNDFLSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTP
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EDSELVSTKETRTSKVRQLLDTTDIQGEBFAKVIVQKLKDNKQMGLQPYPEILVVSRS
PSLNLLQNKSM"
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KSAPEGGTIIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIM
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  1417 GACTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGAC 1476
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CA 94080, USA
                                                   205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu
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227
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Inc., 1 DNA Way, South San Francisco,
Location/Qualifiers
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/db_xref="G1:37182744"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DNA43306"
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TWEVLSKKQPEDVTNPLQIMYSVSQCHRPVIRESLEYDIPHRARMISLIESGMAQN
PDERPSFLKCLIELEPVLRTFEEITFLEAVIQLKGTKLQSVSSAIHCDKKKWELSLN
IPVNHGPQEESCGSSQLHENSGSPETTFLEAVIQLKGTKLQSVSSAIHCDKKKWELSLN
SWDSTISGSQRAAFCHKTTPCSSAIINPLSTRANBUSELQPGTAQOGTQKREDIVNQ
WDSTISGSQRAAFCHKTTPCSSAIINDLSTRANBUSELQPGTAQOGTQKREDIVNQ
MARACLMQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIQGEEFAKVIVQK
LKDNKQMGLQPYPEILVYSRSPSLNLLQNKSML"
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AVKHLHIHTPLLDSERKDVLREAEILHKARFSYILPILGICNEPEFLGIVTEYMPNGS
LNELLHRKTEYPDVAWPLRFRILHEIALGVNYLHNWTPPLLHHDLKTQNILLDNEFHV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 TTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCCTGGAAATCAC 1176
                                                                                                                                                                                                                                                                                                                                                                                  producE="receptor-interacting serine-threonine kinase 2"
protein_id="AAQ02472.1"
db_xref="GI:33303917"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProGlylleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProCysSerSerAlallelleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1057 GAAAATAGTGGTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1623
227
1
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                                                                               /clone="FLH000128.01L"
Clone lib="MGC clone templates"
(lab host="DH5alpha T1 resistant"
/note="Vector: pDNR-Dual"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
organism="synthetic construct"
                                                                                                                                                                                                                                                                                                     note="Mutations: Stop->Leu"
codon start=1
transI table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (1-1623)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                               mol_type="mRNA"
db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-771-161A-93 (1-232) x AY335645
                                                                                                                                                                                                                                                  . .>1623
gene="RIPK2"
                                                                                                                                                                                                                        gene="RIPK2"
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1182.00
100.00%
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scores:
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Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Frange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McEwan, P.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Vilalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Modan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y. Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D. Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E., Schnerch, A., Schein, J.B., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: nisc_mgc@nhgri.nih.gov
Akhter.N., Ayele.K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="receptor-interacting serine-threonine kinase 2"
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/tb xref="Locus10:8767"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 15 Row: n Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 20127435.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (14-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replaced gi:13528713.
Contact: MGC help desh.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 22388257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="synonyms: RICK, RIP2, CARDIAK, CARD3"
/db xref="LocusID:8767"
/db xref="MIM:603455"
203 .1825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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/clone="MAGC:10684 IMAGE:4026156"
/tissue_type="Skin, melanotic melanoma."
/clone_lib="NIH MGC 20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 1889)
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUBMED
REFERENCE
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
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1 (Bases I to 1889)

2 (Rauserg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heish, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1487
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                                                                                                                                                                                                                                                                     1068 CTGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1188 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCCTGGAAATCAC 1247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1308 CCATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAG 1367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          488 GACTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGAAATTACTAGAC 1547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1548 ACTACTGACATCCAAGGAGAAGATTTGCCAAAGTTATAGTACAAAAATTGAAAGATAAC 1607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProCysSerSerAlallelleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64
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                                                                                                                                                                                                                                                                                                                                                      LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProGly11eAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThrThrAspIleGlnGlyGluGluPheAlaLysVallleValGlnLysLeuLysAspAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis
                        4000
                        Conservative:
                                              Mismatches:
Indels:
                                                                                                                                                                        US-09-771-161A-93 (1-232) x AY358813 (1-1886)
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                     100.00%
99.56%
98.01%
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                                                    Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDERPSFLKCLIELEPVLRTFEEITFLEAVIOLKKTKLOSVSSAIHLCDKKKMELSLN
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                                                                                                                AF064824 1902 bp mRNA linear PRI 07-JUL-1998
Homo sapiens CARD-containing ICE associated kinase mRNA, complete
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1 (Dases 1 to 1902)
Thome, M., Hofmann, C. Burns, K., Martinon, F., Bodmer, J.-L., Mattmann, C. and Tschop, J.
Identification of CARDIAK, a RIP-like kinase that associates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/cell type="pancreatic adenocarcinoma"
/clobe=lib="Stratagene library, catalog number 937208"
243. 1865
/note="CARDIAK; RIP-like kinase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product="CARD-containing ICE associated kinase"
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Lausanne, Chemin des Boveresses, 155, Epalinges, CH 1066,
Switzerland
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/noce="encodes intermediate domain"
1545. .1811
/noce="encodes CARD motif"
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2 (bases 1 to 1902)
Thome, M., Hoffmann, K., Burns, K., Maktmann, C. and Tschopp, J.
Direct Submission
Submitted (12-MAY-1998) Institute
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225 AsnLeuLeuGlnAsnLysSerMet 232
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KEYWORDS
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              INBLLHRKTEYPDVAWPLRFRILHEIALGVNYLHNMTPPLLHHDLKTONILLDNEFHY
KIADFGLSKRRMSLSQSRSSKSAPEGGTIYMPEPENYEFGGKSRSASTKHDYSYAVI
WEYLSRKQPFEDVYNPFLGJUNSVSQGRRPVINBESLPYDIPHRARMISLIESGWAQN
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                                                                                                                                                                        763. ..1063
7. hote="pkinase; Region: Protein kinase domain"
7. db xref="CDD:pfam00069"
1508. .1774
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Fredicted to possess a DEATH (pfam00531) domain-like fold"
7. db_xref="CDD:pfam00619"
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MTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIQGEEFAKVIVQK
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  AVKHLHIHTPLLDSERKDVLREAEILHKARFSYILPILGICNEPEFLGIVTEYMPNGS
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A61P5/14,A61P5/38,
PC A61P7/100,A61P9/10,A61P11/00,A61P17/00,A61P19/02,A61P19/06, PC
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PC C12Q1/68,G01N33/50,G01N33/566,C12N15/00,C12N5/00,A61K37/02 CC
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FH Key
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                                    GINA A GORGONE, HENRY YUE, YALDA AZIMZAI, ROOPA REDDY, DYUNG AINA
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GUEGLER,
MARIAH R BAUGHN, CHANDRA PATTERSON, OLGA BANDWAN, JANICE
                                                                                                                                                                                                                                                                         ce 1. 2024 / Organism='Homo sapiens (human)'.
Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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I. (bases I to 2024)
Hillman,J.L., Lal,P., Tang,T.Y., Corley,N.C., Guegler,K.J., Baughn,M.R., Patterson,C., Bandman,O., Young,J.A., Gorgone,G.A., Fue,H., Azimzai,Y., Reddy,R., Lu,D.A.M. and Shih,L.L. Phosphorylation effectors
Phosphorylation effectors
Patent: JP 2002526035-6 20-AUG-2002;
 1179 AAGTTACAGAGTGTTTCAAGTGCCATTCACCTATGTGACAAGAAGAAAATGGAATTATCT 123
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Oy         185 ThrThrAspIleGInGlyGluGluPheAlaLysValIleValGInLysLeuLysAspAsn 204           Db         1679 ACTACTCACATCCAAGGAAGAATTTGCCAAAGTTATAGTACAAAATTGAAAAATTGAAAGTTAACTACAAAATTGAAAAATTGAAAGTTAACTACAAAATTGAAAAATAC 1738           Oy         205 LysGlnMetGlyLeuGlnProTyrProGlulleleuValValSerEncoSerLeu 224           Db         1739 AAACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTA 1798           Oy         225 AsnLeuLeuGlnAsnLysSerMet 232           Db         1799 AATTTACTTCAAAATAAAAGCATG 1822	RESULT 7 BD127583 COCUS DEFINITION Primer for synthesizing full-length cDNA and use thereof. ACCESSION BD127583 DEFINITION Primer for synthesizing full-length cDNA and use thereof. ACCESSION BD127583 ACCESSION BD127583 BD127583.1 GI:2322528 KEYWORDS UPROJON DP127583.1 GI:2322528 HOMO sapiens (human) ORGANISM HOMO sapiens EUKaryote, Metaca, Crondata, Craniata, Vertebrata, Buteleostomi, Bukaryote, Metaca, Craniata, Vertebrata, Buteleostomi, Rammania; Eutheria; Primates, Catarrhini, Hominidae, Homo. REFERENCE 1 (bases 1 to 2033) AUTHORS OLA,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamateu,A., Suqivama,T., Nadai,K., Kolima,S., Otsuki,T. and	Koga,H.  TITLE Primer for synthesizing full-length cDNA and use thereof JOURNAL Patient for synthesizing full-length cDNA and use thereof JOURNAL HELIX RESEARCH INSTITUTE COMMENT OS Home sapiens (human) PN JP 2002017375-A/3014 PD 22-JAN-2002 PF 07-JUL-2000 JP 200253172 PF 07-JUL-2000 JP 200253172 PI TOSHIG OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO PI TOSHIG OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO PI TOSHIK, PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI SHINICHI KOJIKM, PI TERSUJI OTASIKT, HISASHI KOGA	ZN15/09, CO7K14/47, CO7K16/7.  o, C12P21/02, C12Q1/68//C1.  rimer for synthesizing fur Location/Qualifier 1. 2033 //mol_type="genomic /db_xrefe="taxon:96"	Alignment Scores: 6.57e-104 Length: 2033  Pred. No.: 1182.00 Matches: 227 Score: 100.00\$ Conservative: 1 Best Local Similarity: 99.56\$ Mismatches: 0 Query Match: 68.01\$ Gaps: 0 US-09-771-161A-93 (1-232) x BD127583 (1-2033)	5 GlnLeuGlnServalSerserAl :::

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boldin,M. and Wallach,D.
MODULATORS OF INTRACELLULAR INFLAMMATION, CE
SURVIYAL PATHWAYS.
PATHWAYS.
PATHWAYS.
PATHWAYS.
BOLDIN MARK (IL); WALLACH DAVID (IL)
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
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                                               GlualaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu
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Ward, D. T. and Cowsert, L. M.
Antisense modulation of RIP2 expression
Patent: US 6426221-A 3 30-JUL-2002;
Location/Qualifiers
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Sequence 3 from patent US 6426221.
AR221453
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Modulators of intracellular inflammation, cell death and cell
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JP 200250228-A/1.
Switheric construct
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Latent. JP 200250228-A 1 22-JAN-2002;
YEDA RESEARCH AND DEVELOPMENT CO LTD
PN JP 2002502258-A/1
PP 22-JAN-2002
PF 01-JUN-1998 JP 1999501993
PR 05-JUN-1997 IL 121746
PI DAVID WALLACH, WARK BOLDIN, NIKOLAI MALININ
PP CINIS/12, CONTA/4/7, CONTA/6/18, C1201/68, A61K38/17, G01N33/68 CC
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DAVID WALLACH, MARK BOLDIN, NIKOLAI MALININ
C12N15/12, C07K14/47, C07K16/18, C12Q1/68, A61K38/17, G01N33/68
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                   1856 AATTTACTTCAAAATAAAAGCATG 1879
225 AsnLeuLeuGlnAsnLysSerMet 232
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CC Topology: Linear;
FH Key Lo
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BD106658
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9575181
2 (bases 1 to 2501)
1 Inohara,N., Koseki,T., Chen,S., del Peso,L. and Nunez,G.
Direct Submission
Direct Submission (01-OCT-1997) Dept. Pathlogy, Comprehensive Cancer &
Submitted (01-OCT-1997) Dept. Pathlogy, Comprehensive Cancer &
Geriatrics Center, 4-131 CCGC 1500 E. Medical Center Dr, Ann Arbor,
MI 48109, "...erion/Onalifiers
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Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete
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1 (bases 1 to 2501)

Inohara,N., del Peso,L., Koseki,T., Chen,S. and Nunez,G.
RICK, a novel protein kinase containing a caspase recruitment domain, interacts with CLARP and regulates CD95-mediated apoptosis 98241596
                                                                                                                                              165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
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225. .1847
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Cellular kinases involved in cytomegalovirus infection and their
Inhibition
Axxima Pharmaceuticals Aktiengesellschaft (DE)
Axxima Pharmaceuticals Aktiengesellschaft (DE)

1. 2501

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Sequence 13 from Patent EP1201765.
AX429236.1 GI:21540548
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Nunez, G., Inohara, N. and Koseki, T.
Compositions and methods for identifying apoptosis signaling pathway inhibitors and activators Patent: 18 6348573-A 2 19-PEB-2002,
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LKDNKQWGLQPYPEILVVSRSPSLNLLQNKSM"
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phosphorylated protein; apoptosis regulator"
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  function="regulates apoptosis"
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AVKHLHIHTPLLDSBRKDVLABABILHKARFSYILPILGICNEPEFICAIVTEYMRNGS
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PVHIGPOEBGCGSOLHENGSSPFRTSRLPAPONDFLSKRADDCYRMKLHHCPENH
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                                                                                                                                                                                                                                                                                                                                                                                                                      AX358814 2521 bp mRNA linear PRI 03-OCT-2003
Homo sapiens clone DNA43305 RIPKZ (UNQ277) mRNA, complete cds.
AX358814
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CA 94080, USA
                                                                    AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp
                                                                                                                                 ThrThrAspileGlnGlyGluGluPheAlaLysValileValGlnLysLeuLysAspAsn
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Submitted (01-AUG-2003) Department of
Inc., 1 DNA Way, South San Francisco,
Location/Qualifiers
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Genome Res. 13 (10), 2265-2270 (2003)
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'db_xref="GI:37182746"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                            AsnLeuLeuGlnAsnLysSerMet 232
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/locus_tag="UNQ277"
252. .1874
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note="PRO314"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
product="RIPK2"
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Homo sapiens (human)
Homo sapiens
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Clark,H.F.
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                                               165
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUBMED
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
AY358814
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AUTHORS
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## CKDNKOMGLOPYPEILVVSRSPSLNLLQNKSM"

2521 227 1 0 0

Length:
Matches:
Conservative:
Mismatches:
Indels:

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1727
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                                                        44
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                                                                                                                                                                         84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 GluhlaCygLeudsnGlnSerLeudspAlaLeuLeuSerArgAspLeulleMetLysGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu
                 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis
                                                                                                                                                                                                                                                    ProGly1leAlaGlnGlnTrplleGlnSerlysArgGluAsplleValAsnGlnMetThr
                                                        25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis
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5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer
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1, 2004, 11:22:01

Human CAR Human CAR Human cDN

Human cDN Human cas DNA of hu Human KPP

CDNA of h

Human col Human CAR Human CAR Human CAR Human CON Human CON Human CAR Human CAR Human CAR Human CAR Human CAR Human CAR

Human cDN Human nuc

Apoptosis DNA of th

Human

Human nuc

Human pc DNA of 1

Нитап Сав Apoptosis

cDNA of h

OM protein

Run on:

Sequence:

Searched:

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Aak52606
Aal40755
Abx75872
Aaa95798
Aah34994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA sequence encoding a human phosphorylation effector PHSP-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; phosphorylation effector; PHSP; proliferative disorder; immune disorder; neuronal disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
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                                                                                                                                                                       ABK89281
AAL40754
                                                                                                                         ABK89283
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203. .1825
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98US-0155196P.
98US-0155239P.
98US-0106889P.
98US-0109093P.
                                                                                                                                                                                                                                                                                                                                                                                                              AAZ46143 standard; cDNA; 2024
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1931
1931
1931
1931
1931
1619
1959
97.5
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985.3
985.2
985.3
94.6
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14-SEP-1998;
14-OCT-1998;
03-NOV-1998;
19-NOV-1998;
22-DEC-1998;
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                  AAZ46143;
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1
AAZ46143
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                                                                                                                                                                                                                                                                                                    Command line parameters:
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Aax02558 Human B1
Abx51169 CDNA enco
Aad45172 Human rec
Aaz4862 Human RIC
Aac7779 Human Can
Abx75870 Human Can
                                                               April 1, 2004, 06:43:21; Search time 473 Seconds (without alignments) 2083.683 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                        MYSLQLQSVSSAIHLCDKKK.....PEILVVSRSPSLNLLQNKSM
          version 5.1.6
- 2004 Compugen Ltd.
                                              nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                  3373863 segs, 2124099041 residues
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Maximum Match 100%
Listing first 45 summaries
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AAX92558
AAX62558
ABK51169
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AAZ48762
AAC77779
                                                                                                                                                    , Xgapext
, Ygapext
, Fgapext
, Delext
         GenCore
Copyright (c) 1993
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geneseqn2001as:*
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and is derived by analysis of
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1206
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Match Length DB
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Ygapop 10.0,
Fgapop 6.0,
Delop 6.0,
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Database

Result Š

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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful been determined. Primers for synthesising the full length cDNA are useful length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers anable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly
1619 GACTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGAC 1678
                                                                   1679 ACTACTGACATCCAAGGAGGAATTTGCCAAAGTTATAGTACAAAAATTGAAAGATAAC 1738
                                                                                                                         1739 AAACAAATGGGTCTTCAGCCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTA 1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        synthesizing full length cDNA clones and their use
                                    ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn
                                                                                                        LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; SEQ ID NO 3453; 1380pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2033 BP; 612 A; 447 C; 438 G; 536 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                           full length cDNA; cDNA synthesis; oligo-capping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ishii S, I
S, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Nagai K, Kojima S,
                                                                                                                                                                                                                                                                                                                                                                                            Human full-length cDNA, SEQ ID NO: 3453.
                                                                                                                                                                                                      1799 AATTTACTTCAAAATAAAAGCATG 1822
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                                                                                                                                                                                                                                                                                       BP.
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                                                                                                                                                                                                                                                                                       AAK94554 standard; cDNA; 2033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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98.01%
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Wakamatsu A, Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                           (first entry)
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P-PSDB; AAM93621.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP1130094-A2
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProCysSerSerAlallelleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
                                                                                                                                                                                                                                                                                     AAZ46138-Z46168 encode human phosphorylation effectors (PHSP), designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not given in the specification). The sequences were isolated from cDNA libraries prepared from various human tissues. The PHSP proteins are useful for the disgnosis, treatment and prevention of proliferative disorders, immune disorders and neuronal disorders. The PHSP proteins form pharmaceutical compositions which useful for treating or preventing disorders associated with decreased PHSP expression/activity. PHSP antagonists are useful for treating or preventing disorders associated with increased PHSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerTrpAspSerThr1leSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24
                                                                                                                                                                                                      human phosphorylation effectors useful for the diagnosis, treatment prevention of proliferative, immune and neuronal disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu
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                                                                                Tang YT, Corley NC, Guegler KJ, Baughn MR;
n O, Au-Young J, Gorgone GA, Yue H, Azimzai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2024 BP; 612 A; 445 C; 434 G; 533 T; 0 U; 0 Other;
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Matches:
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                                                                                                                                                                                                                                                             Claim 9; Page 121-122; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.79e-108
1182.00
100.00$
99.56$
              99US-0155233P
                                                                                Hillman JL, Lal P, Tang YJ
Patterson C, Bandman O, Av
Reddy R, Lu DAM, Shih LL;
                                                   (INCY-) INCYTE PHARM INC.
                                                                                                                                                          WPI; 2000-183125/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression/activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity:
                                                                                                                                                                        P-P$DB; AAY68774.
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                  12-JAN-1999;
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                                                                                                                                                                                                                                               This invention describes the isolation of a novel human B1 protein which can interact with, intracellular mediators or modulators of inflammation, cell death and/or cell survival pathways, directly or indirectly. Cells can be modulated or mediated in inflammation, cell death or cell survival pathways or another intracellular signalling activity using B1. Conditions such as AIDS and cancer can be treated using B1. Antibodies, oligonucleotides and ribozymes can also be used to regulate the above
                                                                                                                                                      New B1 protein regulates cell death and cell survival pathways -
derivatives, DNA and antibodies, also regulate intracellular inflammation
; for treating AIDS, cancer.
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            US-09-771-161A-93 (1-232) x ABK51169 (1-2501)
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                                                                                  The present invention relates to a new method for identifying compounds for treating and/or preventing cytomegalovirus (CMV) infection and/or related diseases. The method of the invention comprises contacting a test compound with at least one of the cellular kinases RICK, RIP, Nck-Interacting kinase, MKK3 and SRPK-2 and detecting any change in kinase activity. The method of the invention can be used to treat and/or prevent CMV infections and related diseases. Oligonucleotides that can detect the specified kinases can also be used for diagnosis of infection. The present nucleic acid sequence encodes the human cellular kinase RICK
                            1736 ACTACTGACATCCAAGGAGAAGATTTGCCAAAGTTATAGTACAAAATTGAAAGATAAC 1795
                                                               224
                                                                                                                                                                                                                                                                                                                                                                  Human; virucide; cytomegalovirus infection; CMV; cellular kinase; RICK; RIP; Nck-Interacting kinase; MKK3; SRPK-2; gene; ss.
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ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn
                                                            LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying agents for treatment or prevention of cytomegalovirus infection, comprises contacting test compound with cellular kinase detecting change in cellular kinase activity.
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/product= "Human cellular kinase RICK"
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                                                                                                                                                                                                                                                                                                                                      cDNA encoding human cellular kinase RICK protein.
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                                                                                                                                                      AATTTACTTCAAAATAAAAGCATG 1879
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                                                                                                                                  AsnLeuLeuGlnAsnLysSerMet 232
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185 ThrThrAspIleGlnGlyGluGluPheAlaLysVallleValGlnLysLeuLysAspAsn 204
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                                                                                                                                                                                                                                                             The invention relates to antisense compounds targetted to a nucleic acid encoding human receptor interacting protein (RIP)2 to inhibit its expression. Antisense compounds are used for treating diseases associated with RIP2 expression. They are also useful in antisense gene therapy. The present sequence is human RIP2 DNA
                                                                                                                                                                            New antisense oligonucleotide that targets regions of a nucleic acid encoding human receptor interacting protein (RIP)2, for treating diseases associated with RIP2 expression.
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                                                                                (ISIS-) ISIS PHARM INC
                                                                                                           Cowsert LM;
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This sequence encodes the human RICK (RIP-like interacting CLARP kinase)

Co fapoptosis, potentiating apoptosis induced by caspase-8 and caspase-10

cduring CD95 signalling. The invention provides methods for identifying

apoptosis signalling pathway inhibitors and activators, and methods and

compositions for screening compounds which will modulate the interactions

of the various compositions identified: ARC, RICK, and the CIDE family of

activators (CIDE-A, CIDE-B and DREF-1). RICK is useful in screening

cativators (COMP-A, CIDE-B and DREF-1). RICK is useful in screening

assays for agents, useful in the diagnosis, prognosis or treatment of

disease associated with excess cell growth and dysregulation of

capoptosis. Complexes containing RICK and CLARP can be used in drug

screening assays to identify inhibitor molecules blocking CD95-mediated

capoptosis. Overspression of ARC in an in vitro cell system can be used

cto identify inhibitors of the enzymatic activity of caspase-8.

Cto identify inhibitors of the enzymatic activity of caspase-8.

Cto identify inhibitors of the enzymatic activity of caspase-8.

Cto identify inhibitors of the enzymatic activity of caspase-8.

Cto identify inhibitors of the enzymatic activity of caspase-8.

Cto identify inhibitors of the enzymatic activity of caspase-8.

Cto identify inhibitors of the propatential set in muscle tissue

and candiac disorders. Therapoutic compositions of CIDEs can be used to

Ctreat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia,

ctreat e.g. cancer, AIDS, neurodegenerative disorders, aplastic annemia,

ctreat e.g. cancer, AIDS, neurodegenerative disorders, aplastic inhibitor

cof an essential step in the proparation or affinity chromatography

media, and for diagnostically measuring RICK levels. A specific inhibitor

of an essential step in the biochemialstry of apoptosis is needed. RICK

interaction with intracellular factors such as CLARP and FADD appears to
                1760
                                                                                                     1761 AAACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCCATCTTA 1820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC; caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway; CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation; gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS; aplastic anaemia; ischaemic injury; toxin-induced liver disease; ss.
LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu
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inhibitors of RICK binding to intracellular
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Matches:
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Mismatches:
              apoptosis factors are potential drug candidates
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 essential for apoptosis,
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AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and calls the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antidathmatic; antirheumatic; antibarthritic; antidiahmatory; antihyorid; antiallergic; antibacterial; antiviral; dermatological; neuroprotective; cardiant; thrombolytic; cagulant; nootropic; vasotropic; antipsoriatic and antianglogenic. The polynuclectides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynuclectides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune calls, to treat disorders of hematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of
               diagnosis, cytostatic; proliferative, vulnerary; immunomodulator; antidiabetic; antiarchmatic; antiarchritic; antiviral; antidiflammatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoletic cell disorder; attoimmune disorder; allergic cell disorder; attoimmune disorder; allergic caction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening; ss.
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cancer associated gene; cancer antigen; detection; cancer;
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                                        1683 GACTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGAC 1742
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1263 CTGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1322
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contiguous amino acids of a human caspase recruitment domain (CARD)-4Y, muan CARD-4Z or murine CARD-1 (all splice variants of CARD-4).

CC human CARD-4Z or murine CARD-14 (all splice variants of CARD-4)

polypeptide. Also included is an isolated fusion protein, comprising the card polypeptide covalently linked by a peptide bond to a heterologous CC detection assays, e.g. chromosomal mapping, tissue typing and forensic CC biology), predictive medicine (e.g. diagnostic assays, prognostic assays, contioning clinical trials and pharmacogenomics), and in therapeutic and CC prophylactic treatments (in diseases associated with apoptotic cell death cc g. cancers, autoimmune disorders (e.g. systemic lupus erythematosus and immunodeficiency syndrome), neurological diseases (e.g. Alzhahmer's cimmunodeficiency syndrome), neurological diseases (e.g. Alzhahmer's disease, amyotrophic lateral sclerosis, retinitis confisease, spinal muscular atrophy and cerebellar degeneration), confisease, parkinson's disease, amyotrophic lateral sclerosis, retinitis confisease, spinal muscular atrophy and cerebellar degeneration).

CC pigmentosa, spinal muscular atrophy and cerebellar degeneration).

CC syndromes), myocardial infarction and stroke). The CARD polypeptide is useful as bait protein in a two-hybrid assay or three hybrid assay to confidentify other proteins, which bind to or interact with other CARD crocked are CARD-3 proteins and cDNAS. The gene for chaman CARD-4 is located on chromosome 7. The present sequence is a human card con CDNA.
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                                                                                                                                          Novel isolated human caspase recruitment domain (CARD)-4Y or CARD-4Z polypeptide, or murine CARD-4L polypeptide, useful in screening assays, detection assays, predictive medicine, and in therapeutic applications.
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(MILL-) MILLENNIUM PHARM INC.
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ACTACTGACATCCAAGGAGAAGATTTGCCAAAGTTATAGTACAAAAATTGAAAGATAAC 1536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARD-1; caspase recruitment domain, CARD-4; regulation; detection; caspase activation; detection; screening; therapy; diagnosis; disease; apoptotic cell death; Fas/APO-1 receptor complex; cancer; follicular lymphoma; carcinoma; p53 mutation; viral infection; hormone-dependent tumour; autoimmune disorder; Alzheimer's disease; systemic lupus erythematosis; immune-mediated glomerulonephritis; stroke; parkingon's disease; amyotrophic lateral sclerosis; retinitis pigmentosa; spinal muscular dystrophy; cerebellar degeneration; anaemia; drug; myelodysplastic syndrome; mycardial infarction; cell proliferation; cell differentiation; cell survival; CARD-41; CARD-42; CARD-41; CARD-42;
                                                                                                                                                                                                                                                                                                                   204
                                                                                                                                                                                                                                                                                                                                                                                                                             LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
                                                                                     GlualaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
                                                                                                                                                                                                     AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
                                                                                                                                                                                                                                                                                                                Thr Thr Aspile GlnGlyGluGluPhe AlaLysValIle ValGlnLysLeuLysAspAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 214. .1836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "CARD-3"
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17-JUN-1998;
08-DEC-1998;
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This invention describes the isolation of novel human caspase recruitment domain, CARD-3 and CARD-4 polynucleotides and proteins and a partial comain, CARD-1 protein and genes. The genes and proteins of the invention are involved in the regulation of caspase activation. The caspase crectuitment domain (CARD) polynucleotides, polypeptides, homologues and recruitment domain (CARD) polynucleotides, polypeptides, homologues and antibodies can be used in screening assays, detection assays, predictive methods may be used to diagnose and treat patients which are suffering from a disorder associated with abnormal level or rate of apoptotic cell death, abnormal activity of the TMF receptor complex, or abnormal activity of the TMF receptor complex, or abnormal activity of the TMF receptor complex, or abnormal activity of a caspase. Complex associated with mutations in p53 and hormone—corrupted associated with mutations in p53 and hormone—corrupted associated with mutations in p53 and hormone—corrupted associated with mutations in p53 and hormone—corrupted associated with mutations in p53 and hormone—corrupted associated with mutations in p53 and hormone—corrupted associated with muscular dystrophy, cerebellar degeneration, anaemia, myelodysplastic syndrome, mycoradial infarction, and stroke—corruption interacts with other cellular proteins, and so can be used for regulation of cellular proliferation and differentiation and cell survival. The CARD proteins may also be used to for screen drugs or compounds which modulate their activity. The CARD-4 gene can express a campound which modulate their activity. The CARD-4 gene can express a compound which modulate their activity. The CARD-4 gene can express a campound which modulate their activity. The CARD-4 gene can express a compound which modulate their activity. The CARD-4 gene can express a campound which modulation described by a sport transcript that encodes CARD-4, a short transcript that encodes CARD-4 as short transcript that encodes CARD-4 as short transcript that en
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domain 3 (CARD-3, see AAB20079). The CDNA was isolated following a database search using known CARD sequences. Plasmid pXE17A containing cARD-3 cancer in the protein product of an arracellular protein predicted to be involved in regulating caspase activation. It is useful as a modulating agent in regulating cellular processes include cell growth and cell death. Methods of diagnosing and treating patients suffering from a disorder associated with an abnormal level or rate of apoptotic cell death, abnormal activity of the tumour necrosis factor receptor complex, abnormal activity of the tumour necrosis factor receptor or abnormal activity of a caspase involve administering a compound that modulates the expression or activity of CARD-3, CARD-4, CARD-5 or CARD-6 e.g. a small molecule, antisense nucleic acid, ribozyme or polypeptide.
                                  204
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                                                                                                                                                                                                                                                                                                          CARD-3; caspase recruitment domain; human; cancer; infection; autofimmune disease; neurological disease; haematological disease; inflammation; antitumour; antiseptic; immunomodulator; antiinflammatory; apoptosis; diagnosis; gene therapy; ss.
                                                                               LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu
           GACTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGAC
                                  ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn
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Such disorders include cancer, viral infection, autoimmune disorders, neurological diseases, haematological disorders, inflammatory disorders and immune disorders. CARD nucleic acids can be used to express CARD proteins in a host cell e.g. for gene therapy applications, to detect a genetic lesion and to modulate CARD activity
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Mismatches:
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Best Local Similarity:
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Sequence 1931 BP; 613 A; 429 C; 416 G; 473 T; 0 U; 0 Other;
                                                             WPI; 2002-583627/62
                                                               P-PSDB; ABG31075
                                      WO200253765-A1
                         Homo sapiens
                                          11-JUL-2002
                                                         Bertin J,
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LysglnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
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Mismatches:
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Co human or murine caspase recruitment domain (CARD)-4L (long form)

Co polypeptide with a by contacting the polypeptide with a test compound and determining the effect of the test compound on the activity of the compound which modulates the polypeptide. The polypeptide compound which modulates the polypeptide. The method may be adapted for identifying a compound which binds to the LRR (leucine rich repeat) domain of CARD-4. Also included is a method of identifying a candidate compound for modulating LPS, exposing the cell for modulating LPS, exposing the cell for modulating the LRR domain of CARD-4 and cativation, where altered NF-kB activation polypeptide in the presence of the test compound indicates that the test compound is a candidate compound for compound indicates that the test compound is a candidate compound for modulating LPS-mediated activation of NF-kB. Modulators identified by computed to treating a disorder characterised by aberrant CARD-4 creating LPS-mediated activation of NF-kB. Modulators identified by computed to treat or diagnose disorders such as cancer, viral confidence activity of CARD-4L creating, autofimmune disorders eng. systemic lupus erythematosus.

CC infections, autofimmune disorders eng. systemic lupus erythematosus, nuch as multiple sclerosis, Hashimoto's thyroiditis, atopic conditions such as multiple sclerosis, Hashimoto's thyroiditis, atopic conditions such as multiple sclerosis, and lepromatous leprosy, disorders of cell signalling and characters of tissues. The present sequence is the human cDNA encoding characters.
                                                                                 Human; ss; gene; caspase recruitment domain; CARD-3; CARD-4; LRR; leucine rich repeat; LPS; lipopolysaccharide; NF-kB; nuclear factor-kappa B; cancer; Viral infection; autoimmune disorder; systemic lupus erythematosus; immune-mediated glomerulonephritis; arthritis; immune disorder; multiple sclerosis; Hashimoto's thyroiditis; atopic condition; asthma; allergy; psoriasis; contact dermatitis; gastrointestinal allergy; insulin-dependent diabetes; bacterial infection; tuberculosis; lepromatous leprosy; cell signalling disorder; tissue disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying modulators of long form of caspase recruitment domain, (4L useful for treating cancer, infections, and immune disorders, by contacting test compound with CARD-4L and determining effect of the
                                      Human cDNA encoding caspase recruitment domain protein CARD-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sansonetti P, Girardin
                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
214. .1836
/*tag= a
/product= "CARD-3"
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144

184

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204

cerebroprotective; antiparkinsonian; antisclerotic; ophthalmological; nootropic; antianaemic; Caspase Recruitment Domain; CARD; GARD-4L; p53; cancer; CARD-4S; follicular lymphoma; carcinoma; autoimmune disorder; hormone-dependent tumour; breast cancer; prostate cancer; ovarian cancer; systemic lupus; herpes virus; poxvirus; adenovirus; neurological disease; Cytostatic; virucide; immunomodulatory; neuroprotective; antialzheimers; anaemia; neutropenia; myelodysplastic syndrome; human; gene; ss

Length:

6.72e-108

Alignment Scores: Pred. No.:

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1390 AGTIGGGAIAGCACCATTICTGGATCTCAAAGGGCTGCATICTGTGATCACAAGACCATT 1449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated human caspase recruitment domain (CARD)-4Y or CARD-4Z polypeptide, or murine CARD-4L polypeptide, useful in screening assays, detection assays, predictive medicine, and in therapeutic applications.
                                                                                                                                                                                                             GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu
                                                                                                                                                                                                                                                                                               165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp
                                                                                                                                                  CCATGCTCTTCAGCAATAAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAG
                                          ProCysSerSerAlallelleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln
                                                                                                                           ProGly11eAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr
                                                                                                                                                                                                                                                                                                                                                                                 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cDNA encoding Caspase recruitment domain protein, CARD-3.
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98US-00099041.
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stroke; chromosome 7,
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                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated Caspase Recruitment Domain (CARD) polypeptides (CARD-4L and CARD-4S) useful for diagnosing and treating e.g. Parkinson's and Alzheimer's disease, cancers and viral infections.
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N-PSDB; AAO22107, AAO22108, AAO22109, AAO22110.
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98US-00099041.
98US-00207359.
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Best Local Similarity:
                      Homo sapiens
                                                             US6369196-B1
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CARD CDNA 

613 A; 430 C; 416 G; 472 T; 0 U; 0 Other; Sequence 1931 BP;

1630 GACTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGAC 1689 GAAGCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAGAG 1629 creaacaraccreraaarcareerccacaaeaeaarcarereercrerereer 1269 1390 AGTIGGGATAGCACCATITICTGGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCATT 1449 ccargeretreageaaraaraarecaerereaaergeaggaaaereagaaegeredeag 1509 GAAAATAGTGGTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCTCAAGACAATGATTTT 1329 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164 SerTrpAspSerThr11eSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104 ProCysSerSerAlallelleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe -00 Conservative: Mismatches: Indels: Matches: Length: US-09-771-161A-93 (1-232) x ABX75869 (1-1931) 6.72e-108 1176.00 99.56% 99.12% 97.51% Percent Similarity: Best Local Similarity: Alignment Scores: 1270 105 1450 145 1570 ß 1210 125 1510 25 45 65 85 Query Match: DB: 유 g ò QQ g q 엄 ò g ð g ò g à ò ò ò ò

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ACTACTGACATCCAAGGAGAAGTTTGCCAAAGTTATAGTACAAAAATTGAAAGATAAC 1749 224 human; ss; gene; CARD-1; CARD-4; caspase recruitment domain; apoptosis; p75; tumour necrosis factor; TWF; neutrophin receptor; cancer; autoimnume disorder; systemic lupus; immune mediated glomerulonephritis; viral infection; neurological; retinitis pigmentosa; haematologic; chronic neutropenia; myocardial infarction; stroke; RIP; RICK; CARDIAK. LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu Human caspase recruitement domain 3 (CARD-3) cDNA. /product= "CARD-3 protein" 1810 AATTTACTTCAAAATAAAGCATG 1833 225 AsnLeuLeuGlnAsnLysSerMet 232 Location/Qualifiers 214. .1836 ADB81363 standard; cDNA; 1931 BP 26-DEC-2000; 2000US-00748537 98US-00019942 98US-00099041 04-DEC-2003 (first entry) ø /\*tag= WPI; 2003-657125/62 Bertin J, Chao MV; BERTIN J. CHAO M V. P-PSDB; ADB81362 US2002061833-A1 06-FEB-1998; 17-JUN-1998; sapiens 23-MAY-2002 1690 205 (BERT/) CHAO/) Ношо 

This invention relates to two novel genes CARD-3 and CARD-4 (caspase recruitment domains), which are mediators of apoptosis and are useful in the identification of compounds that modulate apoptosis. Specifically, CARD-3 (also known as RIP2, RICK and CARDIAK) is known to be a mediator of p75 (a member of the tumour necrosis factor (TNF) family), and is believed to provide the switch for cell survival and cell death decisions mediated by this p75 neutrophin receptor. Accordingly these genes, and the nincreased number of cells surviving and proliferating when expected is inhibited. These include acncer, autoimmune disorders associated with an increased number of cells surviving and proliferating when systemic lupus and immune mediated glomerulonephritis, viral infections such as those caused by the herpesvirus, neurological disorders such as those caused by the herpesvirus, neurological disorders such as retinitis pigmentosa, haematologic diseases including chronic retinitis pigmentes a novel method for determining whether a test compound alters the binding of CARD-3 to p75, which comprises measuring Detecting compounds which alter binding of the caspase recruitment domain (CARD) of CARD-3 polypeptide to the neurotrophin receptor p75 is useful to provide compounds for treating CARD-3 mediated disorders. Disclosure; Fig 2; 40pp; English.

185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204

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the binding of a polypeptide containing the CARD domain of CARD-3 to a polypeptide comprising the death domain of p75 in the presence and absence of the test compound, and determining if binding is altered. This polymucleotide is the human CARD-3 cDNA sequence of the invention.
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                                                                 Sequence 1931 BP; 613 A; 430 C; 416 G; 472 T; 0 U; 0 Other;
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The invention relates to novel isolated Caspase Recruitment Domain (CARD)

polypeptides, CARD-4L and CARD-4S. The CARD proteins of the invention may

be used to treat disorders associated with decreased CARD expression by

supplementing the patient's own production of CARD. Disorders associated

with the expression and activity of CARD include cancers (particularly

collicular lymphomas, carcinomas associated with mutations in p53, and

hormone-dependent tumours such as breast cancer, prostate cancer, and

covarian cancer), autoimmune disorders (such as systemic lupus

crythematosus, immune-mediated glomerulonephritis), viral infections

crythematosus, immune-mediated glomerulonephritis), viral infections

crythematosus at those caused by herpes viruses, poxviruses, and adenoviruses,

cerythematophic lateral sclerosis (ALS) retinitis pigmentosa, spinal

muscular atrophy, and various forms of cerebellar degeneration), anaemia

associated with chronic disease, aplastic anaemia, chronic neutropenia,

and the myelodysplastic syndromes. This polynucleotide sequence

cerpresents the DNA of a human CARD relating to the invention
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                                                      cerebroprotective; antiparkinsonian; antisclerotic; ophthalmological; nootropic; antianaemic; Caspase Recruitment Domain; CARD; CARD-4L; p53; cancer; CARD-4S; follicular lymphoma; carctinoma; autoimmune disorder; hormone-dependent tumour; breast cancer; prostate cancer; ovarian cancer; systemic lupus; herpes virus; poxvirus; adenovirus; neurological disease; anaemia; neutropenia; myelodysplastic syndrome; human; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated Caspase Recruitment Domain (CARD) polypeptides (CARD-4L and CARD-4S) useful for diagnosing and treating e.g. Parkinson's and Alzheimer's disease, cancers and viral infections.
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                                   neuroprotective; antialzheimers;
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                                     Cytostatic; virucide; immunomodulatory;
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DNA of human CARD-3 SEQ ID No 3.
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Squence 3, Application US/09920663;
Patent No. 642621;
GENERAL INFORMATION:
APPLICANT: Donna T. Ward;
TITLE OF INVENTION: ANTISENSE MODULATION OF RIP2 EXPRESSION
FILE REPERENCE: RTS-023;
CURRENT APPLICATION NUMBER: US/09/920,663
CURRENT APPLICATION NUMBER: 2001-08-01;
NUMBER OF SEQ ID NOS: 49
LENGTH: 2501
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US-09-865-364-1

US-09-023-655-684

US-09-245-281-40

US-09-240-3598-40

US-09-245-281-40

US-09-365-364-40

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US-09-245-281-3

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-MODBL=frame+ p2n:model -DEV=xlh
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-DB=Issued_Patents_NA -QFWT=fastap -SUFFTX=p2n.rni -MINMATCH=0.1 -LOOPCX=0
-LOOPEXT=0 -UNITS=bits -STRART=1 -ENN=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGH=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODB=LOCAL -OUTFMT=pto -NOFM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09771161 @CGN 1 1 56 @runat_29032004 124820 19519 -NCPU=6 -ICPU=3
-NO MAAP -LARGEQUERY -NGG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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APPLICANT: Nunez, Gabriel
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS; CURRENT APPLICATION NUMBER: US/09/069,023A; CURRENT FILING DATE: 1998-04-27; NUMBER OF SEQ. ID NOS: 38 SOFTWARE: Patentin Ver. 2.0
SEQ. ID NO 2
IENGTH: 2502
TYPE: DNA
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                  LeuserarglysalaglnaspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis
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US-09-099-041A-3
US-09-099-041A-3
Sequence 3, Application US/09099041A
Sequence 3, Application US/09099041A
Sequence 3. Application
TOTALE NEW BATION:
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-0760D,
CURRENT APPLICATION NUMBER: US/09/099,041A
CURRENT PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
NUMBER OF SEQ ID NOS: 37
SOFUMARE: FRASEEQ for Windows Version 4.0
SEQ ID NOS: 37
LENGTH: 1620
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Patent No. 6469140
GENERAL INFORMATION:
APPLICANT: BERTIN, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELAT
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
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                                                                                                      GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGlnLeuSer
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 Conservative:
Mismatches:
Indels:
                                                                          US-09-771-161A-93 (1-232) x US-09-099-041A-3 (1-1620)
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Squence 3, Application US/09245281
Parent No. 6169196
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL MOLECULES OF THE CY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 07334/118001
CURRENT APPLICATION NUMBER: US/09/245,281
CURRENT FILING DATE: 1999-02-05
BARLIER APPLICATION NUMBER: US 09/207,359
EARLIER FILING DATE: 1998-12-08
BARLIER FILING DATE: 1998-06-17
EARLIER FILING DATE: 1998-06-17
BARLIER FILING DATE: 1998-06-17

EARLIER FILING DATE: 1998-06-17

SARLIER FILING DATE: 1998-06-17

BARLIER FILING DATE: 1998-06-17

WHOBER OF SEQ ID NOS: 44
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99.56%
99.12%
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Mismatches:
Indels:
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FILE REFERENCE: 07334-112001
CURRENT APPLICATION WUMBER: 1909/207,359B
CURRENT FILING DATE: 1908-12-08
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: 1620
                                                                                                                                                            Length:
Matches:
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1176.00
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97.51%
                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                    Alignment Scores:
                                                                                                                                US-09-207-359B-3
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CARD-RELATED PROTEIN FAMILY AND USES THEREC
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Matches:
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Mismatches:
Indels:
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                                                GENERAL INFUGENTION: JOHN
TITLE OF INVENTION: NOVEL MOLECULES OF THE CAL
TITLE OF INVENTION: NOVEL MOLECULES OF THE CAL
FILE REFERENCE: 07344-124001.
CURRENT APPLICATION NUMBER: US 09/245,281
PRIOR APPLICATION NUMBER: US 09/245,281
PRIOR APPLICATION NUMBER: US 09/207,359
PRIOR FILING DATE: 1999-02-05
PRIOR FILING DATE: 1998-12-08
PRIOR FILING DATE: 1998-12-08
PRIOR FILING DATE: 1998-12-08
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-02-06
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR FILING DATE: 1998-02-06
PRIOR SEQ ID NOS: 71
SOFTWARE: FRASES FOR WINDOWS Version 4.0
                  Sequence 3, Application US/09340620A Patent No. 6482933
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Best Local Similarity:
Query Match:
                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                          TYPE: DNA
CRGANISM: Homo
US-09-340-620A-3
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Pred. No.:
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LENGTH: 1620
RESULT 6
US-09-340-620A-3
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                                                                                                          AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
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                             GlualaCysLeuasnGlnSerLeuaspalaLeuLeuSerargaspLeuIleMetLysGlu
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APPLICANT: Bertin, John
TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
TITLE OF INVENTION: DOMAIN POLYPEPTIDES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: ADDRESS: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FESTESEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,942
FILING APPLICATION DATA:
APPLICATION NUMBER:
FILING APPLICATION DATA:
APPLICATION NUMBER:
FILING MAPHICATION PRICE:
ATTORNEY ABTE:
ATTORNEY ABTE:
NAME: Meiklejohn, Ph.D., Anita L.
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Conservative:
Mismatches:
Indels:
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3R: 07334/068001
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REFERENCE/DOCKET NUMBER: 0793
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
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TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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Query Match:
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US-09-019-942-2
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                                                                                                                                                                                                                                                          Sequence 3, Application US/09865364

Patent No. 6613521

GENERAL INPORMATION:
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-112001
CURRENT APPLICATION NUMBER: US/09/865,364
CURRENT FILING DATE: 2001-05-25
PRIOR FILING DATE: 1998-12-08
PRIOR FILING DATE: 1998-12-08
PRIOR PLILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR PRILING DATE: 1998-06-06
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FESSEQ for Windows Version 4.0
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ORGANISM: Homo sapiens
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Sequence 1, Application US/09245281

Patent No. 6369196

GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: AND USES THEREOF

TITLE OF INVENTION: AND USES THEREOF

TITLE OF INVENTION: AND USES THEREOF

GURRENT APPLICATION UNMER: US/09/245,281

CURRENT FILING DATE: 1999-02-05

EARLIER APPLICATION NUMBER: US 09/207,359

EARLIER PILING DATE: 1998-12-08

EARLIER PLING DATE: 1998-12-08

EARLIER PPLICATION NUMBER: US 09/099,041
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EARLIER FILING DATE: 1998-06-17
EARLIER APPLICATION NUMBER: US 09/019,942
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1931
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ORGANISM: Homo sapiens
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1330 TTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCCTGGAAATCAC 1389
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                                                  APPLICANT: BELLIA.

JOHN
TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
TITLE OF INVENTION: DOMAIN POLYPEPTIDES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIA
SOFTWARE: FastESQ for Windows 95
SOFTWARE: FastESQ for Windows 95
SUSTWARE: FastESQ for Windows 105
CURRENT APPLICATION DATA:
PILING DATE:
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/019,942
FILING DATE:
ATTONIEY/AGENT INFORMATION:
NAME: Meaiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERNEK/DOCKET NUMBER: 07334/06800
TELECOMMUNICATION 17542-5070
TELEFAX: 617/542-8906
Sequence 2, Application US/09470271
Patent No. 6410689
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1931 base pairs TYPE: nucleic acid STRANDEDNESS: single
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1176.00
99.56%
99.12%
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Sequence 1, Application US/09340620A

Sequence 1, Application US/09340620A

Patent No. 6482933

GENERAL INFORMATION:

APPLICANT: Bertih, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREC, PILE REPERENCE: 07334-124001

CURRENT APPLICATION NUMBER: US/09/340,620A

CURRENT APPLICATION NUMBER: US 09/245,281

PRIOR PELING DATE: 1999-02-05

PRIOR APPLICATION NUMBER: US 09/207,359

PRIOR APPLICATION NUMBER: US 09/207,359

PRIOR APPLICATION NUMBER: US 09/019,942

PRIOR APPLICATION NUMBER: US 09/019,942

PRIOR APPLICATION NUMBER: US 09/019,942

PRIOR APPLICATION NUMBER: US 09/019,942

PRIOR APPLICATION NUMBER: US 09/019,942

PRIOR APPLICATION NUMBER: US 09/019,942

NUMBER OF SEQ ID NOS: 71

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO:

LEMACHAL. 100-1

LEMACHAL. 100-1
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                                                                                                                  SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
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                                                   LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis
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Matches:
Conservative:
Mismatches:
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; LOCATION: (214)...(1833)
US-09-340-620A-1
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ORGANISM: Homo sapiens
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Best Local Similarity:
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               ProcysserSerAlaileIlelleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
                                  ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr
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; Batent No. 6469140.
; GENERAL INFORMATION:
; APPLICANT: BETLIA, John
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL: 1909-12-08
CURRENT APPLICATION NUMBER: US/09/207,359B
CURRENT APPLICATION NUMBER: US 09/099,041
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1.
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Matches:
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US-09-207-359B-1
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TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
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US-09-748-537-2
US-09-748-537-2
; Patent No. 6680167
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Chao, Moses V.
                                                                                                                                                                    1.11e-133
1176.00
99.56%
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97.51%
; LENGTH: 1931
; TYBE: DNA
; CNGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-09-865-364-1
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                                                                                           GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09865364

Sequence 10. 6613521

GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
CURRENT APPLICATION NUMBER: US/09/865,364
CURRENT APPLICATION NUMBER: US 09/207,359
PRIOR FILING DATE: 1998-12-08
PRIOR FILING DATE: 1998-06-17
PRIOR PELICATION NUMBER: US 09/019,942
PRIOR FILING DATE: 1998-06-17
SPRIOR FILING DATE: 1998-06-17
                                                      US-09-771-161A-93 (1-232) x US-09-340-620A-1 (1-1931)
Indels:
Gaps:
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US-09-865-364-1
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Query Match:
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TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILE AND USES THERE FILE REFERENCE: 07334-31601
CURRENT APPLICATION NUMBER: US/09/748,537
CURRENT FILING DATE: 2000-12-26
PRIOR PAPLICATION NUMBER: US 09/099,041
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thr Thr Aspile GlnGlyGluGluPhe Alarys Valile ValGlnLysLeutys AspAsn 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProCysSerSerAlallelleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProGlyIleAlaGlnGlnTrpIleGlnSeriysArgGluAspIleValAsnGlnMetThr 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 GlualaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuSerargiysalaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84
                                                                                                                                                                                                                                                                                                                                                                                                                           25 LeuAsnileProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64
                                                                                                                                                                                                                                                                                                                                                                       GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe
                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                            US-09-771-161A-93 (1-232) x US-09-748-537-2 (1-1931)
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1176.00
99.56%
99.12%
97.51%
                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                     Alignment Scores
                                                                                                                                                                                                        US-09-748-537-2
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Search completed: April 1, 2004, 12:08:55 Job time : 117 secs

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Scoring table:

Searched:

Perfect score:

Run on:

Sequence:

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Sequence 27, Appl
Sequence 27, Appl
Sequence 27, Appl
                 2 US-10-342-887-957

US-09-9581-397A-13

US-09-95-301-173

US-09-95-301-173

US-09-728-721-3

US-10-105-991-3

US-10-118-984-3

US-10-118-984-1

US-10-118-984-1

US-10-118-984-1

US-10-118-984-1

US-10-118-984-1

US-10-118-984-7

US-10-118-984-7

US-10-105-991-7

US-10-118-984-7

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US-10-105-991-9

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Facent No. US20020110811A1
GENERAL INFORMATION:
APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/711,161A
CURRENT APPLICATION NUMBER: US/09/711,161A
CURRENT FILING DATE: 2000-11-26
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 13576
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
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US-10-118-984-27
US-10-295-981-27
US-09-728-721-25
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US-09-728-721-27
    13
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: -
US-09-771-161A-2
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-MODEL=frame+ p2n.model -DEV=xlh
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                   version 5.1.6
- 2004 Compugen Ltd.
                                                                                                                OM protein - nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Alignment Scores:
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Matches:
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       "n" can be any nucleotide 'a',
                                                                                       US-09-771-161A-93 (1-232) x US-09-771-161A-2 (1-1669)
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APPLICANT: He, Yudong
APPLICANT: Linsley, Peter S.
APPLICANT: Mao, Mao
APPLICANT: Roberts, Christopher J.
APPLICANT: Van 't Veer, Laura Johanna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 957, Application US/10342887; Publication No. US20040058340Al; GENERAL INFORMATION: APPLICANT: Dai, Hongyue
                                   5.45e-140
1206.00
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; LOCATION: (1)..(1669)
; OTHER INFORMATION: "n
US-09-771-161A-2
                                                   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-10-342-887-957
                              Alignment Scores:
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Matches:
Conservative:
Mismatches:
Indels:
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of
FILE REFERENCE: 9301-188-999
CURRENT APPLICATION NUMBER: US/10/342,887
CURRENT APPLICATION NUMBER: 60/298,918
PRIOR APPLICATION NUMBER: 60/380,710
PRIOR PILING DATE: 2001-06-18
PRIOR PILING DATE: 2002-05-14
PRIOR PILING DATE: 2002-06-14
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US-10-342-887-957
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Best Local Similarity:
Query Match:
DB:
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AsnLeuLeuGlnAsnLysSerMet	1641
DD 1597 AATTTACTTCAAAATAAAAGCATG 1620 RESULT 3	OY 185 THITTRABABABH COUNTY OF THE COUNTY OF
	Qy 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
APPLICANT: Axxima Pharmaceuticals AG APPLICANT: Schubart, Daniel APPLICANT: Habenberger, Peter APPLICANT: Stein-Gerlach, Matthias	Oy 225 AsnLeuLeuGlnAsnLysSerMet 232 
APPINCANT: Bevec, Dorian TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and their TITLE OF INVENTION: Inhibition FILE REFREENCE: AXM-004.1 US CURRENT APPLICATION NUMBER: US/09/981,397A CURRENT FILING DATE: 2002-06-28	RESULT 4 US-09-925-301-173 ; Sequence 173, Application US/09925301 ; Patent No. US20020052308A1 ; GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: 60/240,750 PRIOR FILING DATE: 2000-10-16 NUMBER OF SEQ ID NOS: 22 SOFTWARE: Patentin version 3.1 SEQ ID NO 13 LENGTH: 2501 TYPE: DNA	; APPLICANT: Rosen et al. ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies ; FILE REFERENCE: PA106 ; CURRENT APPLICATION NUMBER: US/09/925,301 ; CURRENT FILING DATE: 2001-08-10 ; PRIOR PILING DATE: 2000-03-08 ; PRIOR PILING DATE: 2000-03-08 ; PRIOR PILING DATE: 2000-03-08
	; PRIOR FILING DATE: 1999-03-12 ; NUMBER OF SEQ ID NOS: 1694
9.87e-137 Length: 1182.00 Matches:	; SOFTWARE: PatentIn Ver. 2.0 ; SEQ ID NO 173 ; LENGTH: 2709
0.00% .56% .01%	TYPE: DNA CORGANISM: Homo sapiens FEATURE:
DB: US-09-771-161A-93 (1-232) x US-09-981-397A-13 (1-2501)	; NAME, KEY: miss ceature ; LOCATION: (2595) ; OTHER INFORMATION: n equals a,t,g, or c
5 GlnLeuGlnSerValSerSerAlaileHisLeuCysAspLysLysMetGluLeuSer 24 :::[	; NAME/KBY: misc feature ; LOCATION: (2622) ; OTHER INFORMATION: n equals a,t,g, or c ; NAME/KBY: misc feature
LeuAsnileProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis 44 	; LOCATION: (2659) ; OTHER INFORMATION: n equals a,t,g, or c ; NAME/KXY: misc feature
nAspPhe 64	; LOCALION: (28.0); ; OTHER INFORMATION: n equals a,t,g, or c US-09-925-301-173
1281 GAAAATAGTGGTTCTCCTGAAACTTCAAGGTCCTGCCAGCTCCTCAAGACAATGATTT 1340 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84 [	ores: 1.11e-136 1182.00 1arity: 100.00\$ imilarity: 99.56\$
85 SerTrpAspSerThr11eSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104	Indels: Gaps: . -925-301-173 (1-2709)
105 ProCysSerSeralaileileasnProLeuSerThralaGlyasnSerGluargLeuGln 124 	Qy         5 GlnLeuGlnSerValSerSeralaileHisLeuCysAspLysLysLysMetGluLeuSer 24           :::
125 ProGlylleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144	Qy 25 LeuasnIleProValasnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis 44
145 GlualaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164 	Oy 45 GludenSerGlySerProGluThrSerArgSerLeuProdlaProGlndepAsnAepPhe 64
165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184	Oy 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84

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       LeuAsnileProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis
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Sequence 3, Application US/10105931

Publication No. US20020150987A1

GENERAL INFORMATION:

APPLICANT BETLIA.

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

FILE REFERENCE: 07334-07601

CURRENT APPLICATION NUMBER: US/10/105,931

CURRENT FILING DATE: 2002-03-25.

PRIOR PILING DATE: 1998-06-17

PRIOR PILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

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SEQ ID NO 3

LENGTH: 1620

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US-10-105-931-3
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US-10-105-931-3
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PRICE REPERENCE: 07334-12401

CURRENT APPLICATION NUMBER: 08/340,620

PRICE FILING DATE: 1998-06-28

PRICE FILING DATE: 1998-06-12-08

PRICE FILING DATE: 1998-06-17

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                                                             LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
                                                                                                                                                                                                                                                                                                                                  ASDIYKGlubeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
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                                        SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr
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Patent No. US20020061845A1
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US-09-728-721-3
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Sequence 3, Application US/10295981
; Publication No. US20030120055A1
; GENERAL INFORMATION:
; APPLICANTS Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREC
; FILE REFERENCE: 07334-124001
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Matches:
Conservative:
Mismatches:
Indels:
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  FastSEQ for Windows Version 4.0
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Best Local Similarity:
Query Match:
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; SOFTWARE: FastSEQ; SEQ ID NO 3; LENGTH: 1620; TYPE: DNA; ORGANISM: Homo 8: US-10-118-984-3
                                                                                                                                     Alignment Scores
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Publication No. US20020197693A1

GENERAL INFORMATION:

APPLICAUT: Bertin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: 07334/118001

CURRENT PELICATION NUMBER: US/10/118,984

CURRENT PELING DATE: EARLIER FILING DATE: 1999-02-05

PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/207,359

PRIOR PELING DATE: EARLIER FILING DATE: 1998-12-08

PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-05

PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-05

PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06

PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06

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PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06

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NUMBER OF SEQ ID NOS: 44
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                                                        US-09-771-161A-93 (1-232) x US-10-105-931-3 (1-1620)
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Query Match:
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Percent Similarity:
Best Local Similarity:
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Matches:
Conservative:
Mismatches:
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CURRENT APPLICATION NUMBER: US/10/295,981
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: US/09/340,620
PRIOR FILING DATE: 1999-06-28
PRIOR FILING DATE: 1999-06-26
PRIOR FLING DATE: 1999-02-05
PRIOR PLING DATE: 1999-02-05
PRIOR PLING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: US 09/0207,359
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR FILING DATE: 1998-02-07
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR PILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 71
SOFTWARE: FRAESE FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER F
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1176.00
99.56%
99.12%
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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APPLICANT: Bertin, John
APPLICANT: Chao, Moses V.
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILE AND USES THERE
FILE REFERENCE: 07334-31601
CURRENT APPLICATION NUMBER: US/09/748,537
CURRENT FILING DATE: 2000-12-20
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1931
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Matches:
Conservative:
Mismatches:
Indels:
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225 AsnleuLeuGlnAsnLysSerMet
              RESULT 9
US-09-748-537-2
Sequence 2, Application US/09748537
Patent No. US20020061833A1
GENERAL INFORMATION:
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1176.00
99.56%
99.12%
97.51%
                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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                                                                    ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr
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Publication No. US20020123115A1
GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION:
DOMAIN POLYPEPTIDES
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COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBW Compatible

COMPUTER: IBW Compatible

OPERATING SYSTEM: Windows Version 2.0b

SOFTWARE: FastSEQ for Windows Version 2.0b

SOFTWARE: 26-Apr-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/10/133,780

FILING DATE: 26-Apr-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/019,942

FILING DATE: 06-FEB-198

ATORNEY/AGENT INFORMATION:

NAME: Meixle-John, Ph. D., Amita 'L.

REGISTRATION NUMBER: 35,283

TELEPROMUNICATION INFORMATION:

TELEPROMUNICATION INFORMATION:

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ADDRESSEB: Fish & Richardson P.C.
STREET: 225 Franklin Street
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MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Sequence 1, Application US/09728721

Sequence 1, Application US/09728721

GENERAL INFORMATION:

APPLICANT: BEATIN, John

TILLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE

FILE REFERENCE: 07334-124001

CURRENT APPLICATION NUMBER: US/09/728,721

CURRENT FILING DATE: 1999-06-28

PRIOR PILING DATE: 1999-06-28

PRIOR PELICATION NUMBER: US 09/207,359

PRIOR APPLICATION NUMBER: US 09/207,359

PRIOR PELING DATE: 1998-06-17

PRIOR PELING DATE: 1998-06-17

PRIOR PELING DATE: 1998-06-17

NUMBER OF SEQ ID NOS: 71

SOFTWARE: FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANKS FRANK
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                                                              1690 ACTACTGACATCCAAGGAGAATTTGCCAAAGTTATAGTACAAAATTGAAAGATAAC 1749
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                                                                                                                         205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu
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Mismatches:
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Matches:
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1176.00
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; LOCATION: (214)...(1833)
US-09-728-721-1
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ORGANISM: Homo sapiens
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US-09-728-721-1
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; SOFTWARE: FastSEQ for Windows Version
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
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                                        ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-10-105-931-1
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US-10-118-984-1
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US-10-105-931-1
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US-10-295-981-1

Squence 1, Application US/10295981

Publication No. US20330120055A1

GENERAL INFORMATION:

TTILE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREC

FILE REPERENCE: 07334-124001

CURRENT APPLICATION NUMBER: US/10/295, 981

CURRENT APPLICATION NUMBER: US/09/340, 620

PRIOR APPLICATION NUMBER: US 09/245, 281

PRIOR FILING DATE: 1999-02-05

PRIOR FILING DATE: 1999-02-05

PRIOR FILING DATE: 1999-02-06

PRIOR FILING DATE: 1998-04-18

PRIOR FILING DATE: 1998-06-18

PRIOR FILING DATE: 1998-06-16

PRIOR FILING DATE: 1998-06-16

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-16

PRIOR FILING DATE: 1998-06-17

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; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-10-295-981-1
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ORGANISM: Homo sapiens
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                                 CARD-RELATED PROTEIN FAMILY
                                                                                                                                                        US/09/245,281
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TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PRITILE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 07334/118001
CURRENT PILING DATE: 07334/118001
CURRENT PILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/PRIOR PILING DATE: EARLIER FILING DATE: 1999-02-05
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-07
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-07
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17
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PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 44
SOSTWARE: FASELSE FILING DATE: 1998-02-06
SOSTWARE: FASELSE FILING DATE: 1998-02-06
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Matches:
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1176.00
99.56%
99.12%
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; LOCATION: (214)...(1833)
US-10-118-984-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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                                                                                                                                                                       AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
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                                 ProGly1leAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr
                                                                                                   GlualaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-918-995-20565

Sequence 20565, Application US/09918995

Publication No. US20030073623A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

PRIOR PILING DATE: 1999-01-20
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Matches:
Conservative:
Mismatches:
Indels:
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 20565
LENGTH: 491
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US-09-918-995-20565
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Query Match:
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        Qy
        85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCySAspHisLySThrThr 104

        Db
        368 AGTTGGGAIAGCACTTTCTGGATCTCTAAGGGCTGCATTCTTGTGATCCACT 427

        Qy
        105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124

        Db
        428 CCTTCTCAGCAATAATAATAATCCACTCTCAACTGCAGGAAACTCTGCAGAACGTCTGCAG 487

        Qy
        125 Pro

        Db
        488 CCT 490

        Search completed: April 1, 2004, 12:50:49
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 1, 2004, 09:53:45; Search time 2693 Seconds (without alignments)
2572.605 Million cell updates/sec
Title: US-09-771-161A-93
Perfect score: 1206
Sequence: 1 MYSLQLQSVSSAIHLCDKKK......PEILVVSRSPSLNLLQNKSM 232
Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Xgapext 0.5
Ygapop 6.0, Fgapext 7.0
Pelop 6.0, Delext 7.0
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Total number of hits satisfying chosen parameters: 55026578
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Listing first 45 summaries

27513289 seqs, 14931090276 residues

Searched:

rost-processing: minimum match 100%
Listing first 45 summaries

Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2\_1/USPTO\_spool/USO9771161/runat\_29032004\_124819\_19503/app\_query.fasta\_1.391
-DB=EST\_-QFWT=fasta\_PSUFTT=p2n.rst -MINMATCH=0.1\_LOFOFCL=0.LOFOFTC=0.DFSTX=0.
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -TRR SCORE=pct -TRR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NORM=ext -HEAPSIZE=550 -MINLEN=0 -MAXLEN=200000000
-USER-USO9771161\_@GGN\_1 1 1996\_@runat\_29032004\_124819\_19503 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV\_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:\*

1: em estba:\*
2: em\_estin:\*
4: em estin:\*
5: em\_estin:\*
6: em\_estpl:\*
7: em\_estpl:\*
7: em\_estpl:\*
10: gb\_est1:\*
11: gb\_est1:\*
12: gb\_est3:\*
13: gb\_est4:\*
14: gb\_est4:\*
15: em\_gss\_ln:\*
16: em\_estcom:\*
17: em\_gss\_ln:\*
18: em\_gss\_ln:\*
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22: em\_gss\_ln:\*
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27: em\_gss\_ln:\*
28: gb\_gs]:\*
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## 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

RESULT 1 BX343071/c LOCUS DEFINITION ACCESSION VERSION KEYWODDS	BX343071 BX343071 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED Homo sapiens CDNA clone CSODL009YC19 3-PRIME, mRNA sequence. BX343071 BX343071.1 GI:30334165
SOURCE ORGANISM REFERENCE	Homo sapiens (human) Homo sapiens Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 1201)

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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CD365404/c
LOCUS
DEFINITION
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AUTHORS
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KEYWORDS
SOURCE
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                                                                                          Generation Control of Sequence de Generage

BP 191 91006 EVRY cedex - France

BP 191 91006 EVRY cedex - France

BRail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 4797.f For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CSODLO09ABIONPIEcluster=4797.f. Contact :

Feng Liang Email : fliang@lifetech.com URL :

Feng Liang Email : fliang@lifetech.com URL :

Fraday Avenue Genoscope sequence ID : CSODLO09ABIONPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerTrpAspSerThr11eSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             409 CCATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProGly1leAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .1201
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
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Query Match:
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TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_LIB-U1-H-FT2
TAG_SEQ-GGCCATGCCG"
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UI-H-FT2-bjj-h-03-0-UI.sl NCI CGAP_FT2 Homo sapiens cDNA clone
UI-H-FT2-bjj-h-03-0-UI 3', mRNA sequence.
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDA Library preparation: Dr. M. Bento Soares, University of Iowa
CDA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
Seg primer: Ml3 FORWARD
POLYA-Yes.
                                                                                                                                                  169 ACTACTGACATCCAAGGAGAAGTTTGCCAAAGTTATAGTACAAAATTGAAAGATAAC 110
                                                                                                                204
                                                                                                                                                                                                                                    224
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 744)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                              229 GACTATGAACTTGTTAGTACCAAGCCTACAAGGACBTCAAAAGTCAGACAATTACTAGAAC
                                                                                                                                                                                                                           205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu
165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp
                                                                                                                185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn
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     information
                    found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM2410 row: k column: 04
High quality sequence stop: 659.
Location/Qualifiers
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                                                                                                                                                                                                                                                    /clone="IMAGE:6257019"
                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 938)

                                                                                                        CTGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCAT
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: ATCC
                          CD365404
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC.clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAMSGE, row: g column: 24
High quality sequence stop: 739.
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                                                                                             LeuSerArglysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="MINIB MGC_48"
/clone_lib="MINIB MGC_48"
/clone_lib="MINIB MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E. (Bases I to 682)

NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (WGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Information can be found through the I.M.A.G.E. Consortium/Link at:

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:

High quality sequence stops 814.
                                                                                                                                                                                                                                     BG757422 852 bp mRNA linear EST 15-MAY-2001
602711061F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4851542 5',
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                              CAACCAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGGTTTCTAGATCCCCATCCT 795
nLysGlnMetGlyLeuGlnProTyrProGluIleLeuVal-ValSerArgSerProSerL 224
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4851542"
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Homo sapiens
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       /tissue type="large cell carcinoma, undifferentiated" /lab_host="DH10B (phage-resistant)" /clone lib="NIH MGC 69" /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insett size 1.1 kb. Library constructed by Life Technologies."
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 /clone="IMAGE:3888815'
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CB852764 683 bp mRNA linear EST 22-APR-2003 UI-CF-FNO-aex-p-08-0-UI.S1 UI-CF-FNO Homo sapiens cDNA clone UI-CF-FNO-aex-p-08-0-UI 3', mRNA sequence.

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Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems
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                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                           1 (bases 1 to 683)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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Homo sapiens (human)
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                                                                                                                                                                                                                 University of Iowa
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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I (Dases 1 to 812)

NIH-MGC http://mgc.nni.nh.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CODA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiML at:
http://image.llnl.gov
Plate: LLAM11259 row: j column: 15
High quality sequence stop: 806.

Location/Qualifiers

I. 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BI257472 812 bp mRNA linear EST 17-JUL-2001 602967861F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5107310 5', mRNA sequence.
BI257472 BI257472.1 GI:14812879
EST.
                                                                                                                                                                             GluAspileValAsnGlnMetThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeu 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="NIH MGC 12"
//note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies."
                                                                                                                 136
                                                                                                                                                                                                                                               176
                                                                                                                                                                                                                                                                                                                                                                              216
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                                                                                                                                   GCAGGAAACTCAGAACGTTTGCAGCCTGGTATAGCCCAGCAGCAGGAGGATCCAGAGCAAAAGG
                                                                                                                                                                                                                                               SerArgAspLeulleMetLysGluAspTyrGluLeuValSerThrLysProThrArgThr
                                                                                                                                                                                                                                                                TCAAAAGTCAGACAATTACTAGACACTACTGACATCCAAGGAGAAGAAGTTTGCCAAAGTT
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CTGCATCACTGTCCTGGAAATCACAGTTGGGATAGCACCATTTCTGGATCTCAAAGGGCT
                                                                                                                                                                                                                                                                                                                                                                                                            ATAGTACAAAATTGAAAGATAACAAATGGGTCTTCAGCCTTACCCGGAAATACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                           ValValSerArgSerProSerLeuAsnLeuLeuGlnAsnLysSerMet 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIGGITTTTAGAICACCAICTTTAAAITTACTICAAAATAAAAGCAIG 35
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/clone="IMAGE:5107310"
/lissue_type="cervical carcinoma cell line"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
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/d_one="UT-CE-TWO-DEM"
/clone="UT-CE-TWO-DEM"
/tissue_type="Human Lung Epithelial cells"
/tissue_type="Human Lung Epithelial cells"
/tissue_type="Human Lung Epithelial cells"
/lab hoff="MilloB (Life Technologies) (TI phage resistant)"
/clone_lib="UT-CF-FWO"
/clone_lib="UT-CF-FWO"
/note="Organ: Lung: Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: ECOR I; Site_2: Not I;
UT-CF-FWO is a subtracted cond libraries (ENI and normalized Human lung epithelial cell libraries (ENI and DUI) The library was subtracted according to according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact:
bentc-soares@ulowa.edu
TAG_SEQ=None found"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Iowa

2024 University of Iowa
2024 University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CLOne Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com) or from Open Biosystems
The following repetitive elements were found in this CDNA
sequence: 1-24, AT_rich#Low_complexity (matched compliment)
Seg primer: M13 FORWARD
POLYA=Yes:
                                                                                                                                                                                                                                                                                                                                                                CB851847 linear EST 22-APR-2003 UI-CF-FN0-aem-o-20-0-UI.S1 UI-CF-FN0 Homo sapiens cDNA clone UI-CF-FN0-aem-o-20-0-UI 3', mRNA sequence.
                                                 181 ACTACTICACATCCAAGGAGAAGAATTTGCCAAAGTTATAGTACAAAATTGAAAGATAAC 122
                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I (bases 1 to 715)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
ThrThrAspileGlnGlyGluPheAlaLysValileValGlnLysLeuLysAspAsn
                                                                                                       LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              541 TTATCTAGAAAGCTCAARACTGTTATTTTATGAAGCTGCATCACTGTCCTGGAAATCAC 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481 AGTTGGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCACT 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tione_lib="PLACENTA COT 25-NORMALIZED"
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/note="lst strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
                                           Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, whe : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4797.f For
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOD1037AA04NPl&cluster=4797.f. Contact :
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOD1037AA04NPl.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI037YA07"
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93.36%
92.92%
                        Contact: Genoscope
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/mol_type="mRNA"

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Plate: LLAMM10471 row: e column: 12
High quality sequence stop: 767.
Location/Qualifiers
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1. (bases 1 to 883)

NIH-MGC http://wgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                          CTGCCAGCTCCTCAAGACAATGATTTTTATCTAGAAAAGCTCAAGACTGTTATTTTATG
                                                                                                                                           CysAspLysLysLysMetGluLeuSerLeuAsnIleProValAsnHisGlyProGlnGlu
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CONTACT: Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                          GluSerCysGlySerSerGlnLeuHisGluAsnSerGlySerProGluThrSerArgSer
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// Cell Type="Epithelial"
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// Line="SNU-216"
// Line="Superior Stomach; Vector: pCNS; Site=1: EcoRI;
// Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacace acid pyrophosphatase (TRAP). The decapped with tabacco acid pyrophosphatase (TRAP) in the decapped inteact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coll DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The converted to a DNA strand by Okayama-Berg method. The competent cells E. coli Topolof' by electroporation method. The cDNA libraries constructed by this method are full-length enriched CDNA library."
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Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
                                    BM840808 660 bp mRNA linear EST 06-MAR-2002 K-EST0117952 S12SNU216 Homo sapiens cDNA clone S12SNU216-38-G08 5',
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                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                        Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
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Matches:
Conservative:
Mismatches:
Indels:
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21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
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/clone="S12SNU216-38-G08"
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Plate: 38 row: G column: 08
High quality sequence stop: 660.
Location/Qualifiers
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                                                                                                                                                  Homo sapiens (human)
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Namalia; Eutheria; Primates; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

El (Dasses 1 to 828)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DTP/Gazdar

CONA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLANGGS row: n column: 06

High quality sequence stop: 795.

Location/Qualifiers

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601486423F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888965 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364 CCATGCTCTTCAGCAATAATAAATACACTCTCAACTGCAGGAAACTCAGAACGTCTGCAG 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       424 CCTGGTATAGCCCAGCAGCAGTGGATCCAGAGAAAGGGAAGAATGTGTGAACCAAATGACA
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CTGAACATACCTGTAAATCATGGTCCACAAGAAATCATGTGGATCCTCTCAGCTCCAT 183
                                                                                                                                                                                                                                                             184 GAAAATAGTGGTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCCTGGAAATCAC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
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/organism="Homo sapiens"
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/clone lib="UJ-CF-FNO"
/clone lib= uJ-CF-FNO is a subtracted cDNA library derived from two normalized Human lung epithelial cell libraries (ENI and DUI) The library was subtracted according to according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact:
/clone library was pitchelial cells Tissue nos 359-368
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                                                                                                                                                                       2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
Seq primer: M13 FORWARD
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                                                                                                                                                          University of Iowa
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Best Local Similarity:
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
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Fukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 811)

S NIH-MGC http://mgc.nci.nih.gov/.

I National Institutes of Health, Mammalian Gene Collection (MGC)

L Onbublished (1999)

L Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://inage.llnl.gov

Plate: LLAM10172 row: g column: 09

High quality sequence stop: 721.
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|/mol_type="mRNA"|
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E. 1 (bases 1 to 654)

NIH-MCG http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Incyte Genomics, Inc.

CDNA Library Arrayed by: Incyte Genomics, Inc.

CDNA Library Preparation: MGC. Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM8425 row: o column: 08

High quality sequence stop: 650.
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Average insert size 1.3 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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Search completed: April 1, 2004, 12:07:12 Job time : 2717 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:

April 1, 2004, 02:20:16 ; Search time 6737 Seconds (without alignments) 10737.646 Million cell updates/sec

US-09-771-161A-2

1669 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

6940544 Total number of hits satisfying chosen parameters:

3470272 seqs, 21671516995 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:\*

gb\_htg:,
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

AY358814 2521 bp mRNA linear PRI 03-OCT-2003 Homo sapiens clone DNA43305 RIPK2 (UNQ277) mRNA, complete cds. AY358814 RESULT 1
AY358814
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
VERSION
CETWORDS
SOURCE
ORGANISM

AY358814.1 GI:37182745 FLI CDNA. Homo sapiens (human) Homo sapiens

Eukaryogia, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

I (bases 1 to 2521)

Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E.,

REFERENCE AUTHORS

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Submitted (01-AUG-2003) Department of Bioinformatics,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
Location/Qualifiers
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larity 99.9%; Pred. No. 2.2e-235;
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/organism="Homo sapiens"
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/clone="DNA43305"
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/locus_tag="UNQ277"
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Pred. No. 1e-230;
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| Ward,D.T. and Cowsert,L.M.
Antisense modulation of RIP2 expres
Patent: US 6426221-A 3 30-UUL-2002;
Location/Qualifiers

    2501
    /organism="unknown"
    /mol_type="genomic DNA"

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ilarity 99.0%;
Conservative
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Nunez, G., Inohara, N. and Koseki, T.
Compositions and methods for identifying apoptosis pathway inhibitors and activators
Patent: US 6348673-A 2 19-FEB-2002;
Location/Qualifiers
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/mol_type="unassigned DNA"
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                                             Length 2501;
                                          Score 1308; DB 9; Length 2
Pred. No. 1e-230;
0; Mismatches 5; Indels
                                          Query Match 78.4%;
Best Local Similarity 99.0%;
Matches 1329; Conservative
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Missouri 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 116650)
Ozersky, P., Holmes, A. and Broy, M.
The sequence of Homo sapiens BAC clone CTA-437L15
Unpublished
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Missouri 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington
Missouri 63108,
Homo sapiens BAC clone CTA-437L15 from 8q21, complete sequence. AC004003. GI:2772557
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This chromosome 8 clone was provided by Dr. Patrick Concannon
(patcon@vmmc.org) at the Virginia Mason Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Washington University Genome Sequencing Center
Center code: WUGSC
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The clone sequenced to the left is CTA-237G1. The
this clone is at base position 1 of CTA-437L15; ac
116650 of CTA-437L15.
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Submitted (21-DEC-1999) Department of Genetics,
University, 4444 Forest Park Avenue, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Genetics,
Park Avenue, St. Louis,
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Park Avenue, St. Louis,
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1. .116650
/organism="Homo sapiens/mol_type="genomic DNA"
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Submitted (15-JAN-1998)
University, 4444 Forest
3 (bases 1 to 116650)
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University, 4444 Forest
4 (bases 1 to 116650)
                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 116650)
Waterston, R.
                                                                                                                                                  sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                            Homo sapiens
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Matches 990; Conservative 0; Mismatches
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32339. 3246
3239. 3246
3215. 3248
/rpC_family="Ml"
/rpC_family="MIR"
33186. 33437
/rpC_family="MIR"
34433. 34514
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43357. .43658
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(6151. .26280
rpt_family="MER1_type"
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rpt_family="MER1_type"
6611. .27000
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4525. .34939
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בפבבי
/rpt_family≃"Alu"
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/rpt_family="Alu"
36686. .36985
/rpt_family="Alu"
37488. .37673
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'/rpt family="L1"
28128. .29109

29128. .29434

/rpt family="L1"
29128. .29434

/rpt family="Alu"
29135. .29752

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30205. .30341
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38297. .38599
/rpt_family="Alu"
41954. .42006
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/rpt_family="Alu"
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:5337. .25671
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|2596. .42777
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1552. 2:1611,22478. 22639,29890. 229975,33855. 33944,
6395. 36488,39123. 3984,39881. 40218)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             I PVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDFLSRKAQDCYFMKLHHCPGNH
SWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQPGIAQQWIQSKREDIVNQ
MTBACLNQSLDALLSRDLIMKEDYBLVSTKPTRTSKVRQLLDTTDIQGEEFAKVIVQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TWEVLSRKQPFEDVTNPLQIMYSVSQGHRPVINEESLPYDIPHRARMISLIESGWAQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDERPSFLKCLIELEPVLRTFEEITFLEAVIQLKKTKLQSVSSAIHLCDKKKMELSLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="serine/Ehreonine kinase RICK; match to protein AF027706 (NID:g3123887) and mRNA AF027706 (NID:g3123886); H_RG437L15.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LNELLHRKTEYPDVAMPLRFRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFH\
KIADFGLSKWRMMSLSQSRSSKSAPEGGTIIYMPPENYEPGQKSRASIKHDIYSYAVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110. 8040
note="Cpg island (%GC=69.1, o/e=0.80, #CpGs=93)"
872. 40218
gene="WUGSC:H_RG437L15.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM"
                                                                                                                                                                                                                                                                                                                                                                                                                                              rpt family="Retroviral"
133. .6433
rpt family="Alu"
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10435 .10540

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11790 .12009
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150. .530
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490 _ ...
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3845. .4563
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I. .23924
family="Alu"
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9. .16292
family="L1"
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                       platzer, M.
Direct Submission

Binect Submission

Submitted (04-NOV-2003) Genome Analysis, Institute of Molecular

Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany
On Nov 4, 2003 This sequence version replaced gi:4151947.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neighboring sequence information:
This entry is part of a larger genomic contig. The start of this sequence is directed towards the centronere. The end (31818. .320187) of this sequence overlaps with the start of Acc number AF049895. It covers RGP-64M4, SCb-282k6, SCb-273G1 entirely and is overlapped by SCb-296N11, SCb-316M22.
Platzer, M. and Varon, R.

Direct Submission
Submitted (30-DEC-1998) Genome Analysis, Institute of Molecular
Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
3 (bases 1 to 320187)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing vector: M13mp18; 100% of reads Chemistry: Dye-primer ET, Dye-terminator Big Consensus quality: 319496 bases at least Q40 Consensus quality: 320184 bases at least Q30 Consensus quality: 320187 bases at least Q20 Quality coverage: 7.63
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Corganism="Homo sapiens"

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/clone_lib="Research Genetics human PAC"
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                                                                                                                                                                                                                                                                                    Center: Institute of Molecular Biotechnology
Center code: IMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: NBSlocusA
Center clone name: RGP-64M4 to SCb-316M22
------ Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://genome.imb-jena.de/
Contact: gscj-submit@genome.imb-jena.de
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TITLE
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                                                                                                                                                                                                                   AGATCACCATCTTTAAATTTACTTCAAAATAAAAGCATGTAAGTGACTGTTTTTCAAGAA 1036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1157 CACTGCAGTATTTTTTTTAATTACAAGTAAAAAGTTTGAATTTTGCTACATAGTTCA 1216
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Platzer,M., Varon,R., Sperling,K., Reis,A. and Rosenthal,A. Chromosome 8 genomic sequence
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                                                                                                                                                                                                                                                                                                                                 1277 ATAACAGTGCCTTAAGGTATGATGTATTTCTGATGGAAGCCATTTTCACATTCATGTTCT
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DEFINITION

RESULT 7 AF117829

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL REFERENCE us-09-771-161a-2.rge

in clone: RGP .n clone: RGP .n clone: RGP		<pre>variation 67655  /note="G substituted in clone: RGP-64M4"  /replace="A"  variation 67777  /note="C substituted in clone: RGP-64M4"  /replace="T"  /note="A substituted in clone: SCD-228C20"  /replace="A substituted in clone: SCD-22BC20"</pre>	variation 6867 Variation / note="A substituted in clone: SCb-282k6" /replace="C" substituted in clone: RGP-64M4" /replace="A" / replace="A" / replace="T"	Query Match         59.3%;         Score 990;         DB 9;         Length 320187;           Best Local Similarity 100.0%;         Pred. No. 1.6e-172;         O;         Gaps 0;         O;           Matches 990;         Conservative 0;         Mismatches 0;         Indels 0;         Gaps 0;           Qy         677         TCAGAACGTCTGCAGCTGGTATAGCCCAGCAGTGGATCCAGAAAGGAAAAGATT 179476           Db         179417         TCAGAACGAAATGAAAAGAACCTGCCTTAACCAGTCGCTAGATGCCTACACCAGGGAC 796           Qy         737         GTGAAACCAAATGAAAGACCTGCCTTAACCAGTCGCTAACATGCCATCTCTGTCCAGGGAC 796           Db         179477         GTGAAACCAAATGAAAGACTGCCTTAACCAAGTCGCTAACAATGCCATTCTGTCCAGGGAC 796	199537 TIGATCATGAAAGAGACTATGAACTTGTTAGTACCAAGGCCTACAAGGACCTCCAAAAGTC 857 AGACAATTACTAGAACTGCTACAAGAACTCCAAGGACCTACAAGGACCTCAAAAGTC 857 AGACAATTACTAGACATACGACATCGTAGTACCAAGCCTACAAGGTACTACAAGTACAAAGTCTACAAGAACTTATAGTACAA 917 AAATTGAAAGATAACAAACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGCTTTCT 179657 AAATTGAAAGATAACAAACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCT 977 AGATCACCATCTTTAAATTACTTCAAATAAAAGCATGTAAGTGATTTTTCAAGAA 10977 AGATCACCATCTTTAAAATTACTTCAAAATAAAAGCATGTAGTGATTTTTCAAGAA 1097 GAAATGTGTTTAAAAAGATATTAATTAAAAAATAAAAATAAAAATAAAAATAAAAATAAAA
/mol_type="genomic DNA"  /db_xref="taxon:9606"  /clone="sCb-273G1"  /clone="lib="Research Genetics human BAC" 200838320187  /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /clone="sCb-296M1" /clone="sCb-296M1"	Clone lib="Research Genetics human BAC"   Source	misc_feature   single stranded/single chemistry region"   9549663	ature 2805128095 ature 7805128095 ature 7801228306 A1534 ature 44479 .44606 Anote="pcr product sequence or 41534 floate="pcr product sequ	Variation 63268  Variation /replace="C substituted in clone: SCb-282k6"  Variation 63794  Variation 63875  Variation 64018  Variation 7 oce="C substituted in clone: RGP-64M4"  Variation 64018  Variation 64018  Variation 64018  Variation 64018  Variation 64018  Variation 64018  Variation 64018  Variation 64018	clone:

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Location/Qualifiers
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Pred. No. 6.8e-152;
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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I (bases 1 to 2024)

I Hillman, J.L., Lal, P., Tang, T.Y., Corley, N.C., Guegler, K.J., Baughn, M.R., Patterson, C., Bandman, O., Young, J.A., Gorgone, G.A., Phosphorylation effectors

INCYTE PHARMACEUTICALS INC
OS Homo sapiens (human)

PN JP 200526035-A 6 20-AUG-2002;

INCYTE PHARMACEUTICALS INC
OS Homo sapiens (human)

PN JP 200526035-A/6

PF 28-JUL-1999 UP 2000562510

PR 28-JUL-1999 US 60/155213,14-SEP-1998 US 60/113796 PR

19-NOV-1998 US 60/155233, 22-DEC-1998 US 60/113796 PR
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M LU,
LEO L SHIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JENNIFER L HILLMAN, PREETI LAL, TOM Y TANG, NEIL C CORLEY, KARL
                                                                                                                        ATTTTTATGTCTCTTTTGTTAACAGAACCACTTTTAAAGGATAGTAATTATTCTTGTTT
                                                                         CACTGCAGTATTTTTTTAATTAATACAAGTAAAAAGTTTGAATTTTGCTACATAGTTCA
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                                             CACTGCAGTATTTTTTAATTAATACAAGTAAAAAGTTTGAATTT
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Homo sapiens (human)
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PC A61P21/04,
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PC A61P21/04,
PC A61P31/10, A61P31/12, A61P31/18, A61P33/00, A61P35/02,
PC A61P31/10,
PC A61P37/00,
PC A61P37/00,
PC A61P37/00,
PC A61P37/00, C07K16/40, C12N1/15, C12N1/19, C12N1/21, C12NS/10, C12N9/PC A61P37/08, G01N33/50, G01N33/56, C12N1/5/00, C12N5/00, A61K37/02 CC PC C12Q1/68, G01N33/50, G01N33/56, C12N15/00, C12NS/00, A61K37/02 CC PC C12Q1/68, G01N33/50, G01N31/56, C12N15/00, C12NS/00, A61K37/02 CC C12Q1/68, G01N33/50, G01N31/51, C12N15/00, C12NS/00, A61K37/02 CC C12Q1/68, G01N33/50, G01N31/51, C12N15/00, C12NS/00, A61K37/02 CC C12Q1/68, G01N31/51, C12N15/00, C12N15/00, A61K37/02 CC C12Q1/68, G01N33/50, G01N31/51, C12N15/00, C12N15/00, A61K37/02 CC C12Q1/68, G01N33/50, G01N31/51, C12N15/00, C12N15/00, A61K37/02 CC C12Q1/68, G01N33/50, G01N31/51, C12N15/00, C12N15/00, A61K37/02 CC C12Q1/68, G01N33/50, G01N31/51, C12N15/00, C12N15/00, A61K37/02 CC C12Q1/68, G01N33/50, G01N31/51, C12N15/00, C12N15/00, A61K37/02 CC C12Q1/68, G01N33/50, G01N31/51, C12N15/00, C12N15/00, A61K37/02 CC C12Q1/68, G01N33/50, G01N31/51, C12N15/00, C12N15/00, A61K37/02 CC C12Q1/68, G01N33/50, G01N31/51, C12N15/00, C12N15/00, A61K37/02 CC C12Q1/68, G01N33/50, G01N31/51, C12N15/00, C12N15/00, A61K37/02 CC C12Q1/68, G01N33/50, G01N31/51, C12N15/00, G01N31/51, C12N15/00, G01N31/51, C12N15/00, G01N31/51, C12N15/00, G01N31/51, C12N15/00, G01N31/51, C12N15/00, G01N31/51, C12N15/00, G01N31/51, C12N15/00, G01N31/51, C12N15/00, G01N31/51, C12N15/51, C12 1197 1257 1317 1437 1497 1557 1617 1677 ó 1318 TTTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCCTGGAAATCA 1377 810 AAATTTACTTCAAAATAAAAGCATGTAAGTGACTGTTTTTCAAGAAGAAATGTGTTTCAT 1050 ,A61P5/14,A61D5/38, PC A61P7/00,A61P9/10,A61P11/00,A61P17/00,A61P19/02,A61P19/06, PC 390 450 510 570 630 9 750 870 930 990 CAGTTGGGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCAC AGAAGCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGA ACAGITACAGAGIGITICAAGIGCCATICACCIATGIGACAAGAAGAAAATGGAATTAIC TCTGAACATACCTGTAAATCATGGTCCACAAGAGAATCATGTGGATCCTCTCAGCTCCA TCTGAACATACCTGTAAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCA TGAAAATAGTGGTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTT rgaaaatagregerrcrcrgaaacrrcaaggregergecagcregraagacaargarrr TITATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCCTGGAAATCA CAGTTGGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCAC TCCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCA TCCATGCTCTTCAGCAATAAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCA GCCTGGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAAATGAC GCCTGGTAIAGCCCAGCAGCAGATGGATCCAGAGAAAAGGGAAGAAATGTGTGAACCAAAATGAC AGAAGCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGA GGACTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGA .618 GGACTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGA CACTACTGACATCCAAGGAGAAGTTTGCCAAAGTTATAGTACAAAAATTGAAAGATAA CAAACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGGTTTCTAGATCACCATCTTT

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AAAGTTACAGAGTGTTTCAAGTGCCATTCACCTATGTGACAAGAAGAAAATGGAATTATC 1066
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                                                                                                                   TCTGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCTCAGCTCCA 1126
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JP 2002017375-A/3014.
Homo sapiens (human)
Homo sapiens (buman)
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1886)
1 (bases 1 to 1886)
2 Clark H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J.,
Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B.,
Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E.,
Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S.,
Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C.,
Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V.,
Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wieard, D., Woods, K.,
Kie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z.,
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
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KSAPEGGTIIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDYTNPLQIM
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EEITFLEAVIQLKKTKLQSVSSAIHLCDKKKWELSLNIPVNHGPQEESCGSSQLHENS
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CSSAIINPLSTAGNSERLQPGIAQQWIQSKREDIVNQWTEACLNQSLDALLSRDLIMK
EDYELVSTKPTRTSKVRQLLDTTDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRS
                                        AAAAGGATATTTATATCTCTGTTGCTTTGACTTTTTTTATATAAAATCCGTGAGTATTAA 1917
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Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
Location/Qualifiers
                                                                            AY358813 1886 bp mRNA linear PRI 03-OCT
Homo sapiens clone DNA43306 RIPK2 (UNQ277) mRNA, complete cds.
AY358813
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Pred. No. 1e-151;
0; Mismatches 1;
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.corganism="Homo sapiens"

/mol_type="mRNA"

/db xref="taxon:9606"

/clone="DNA43306"
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/locus tag="UNQ277"
483. .1694
/locus tag="UNQ277"
/note="PRO34092"
/codon_start=1
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Best Local Similarity 99.9%;
Matches 879; Conservative
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Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AK075213 2033 bp mRNA linear PRI 03-SEP-2002. Homo sapiens cDNA FLJ90732 fis, clone PLACE1010081, highly similar to Homo sapiens serine/threonine kinase RICK (RICK) mRNA.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens (human)
Homo sapiens
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/organism="Homo sapiens"
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Isogai, T. and Otsuki, T.
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07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
                         Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                              C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00
ner for synthesizing full-length cDNA and use thereof FH K
Location/Qualifiers
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                                                                                           Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 3014 22-JAN-2002;
HELIX RESEARCH INSTITUTE
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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JP 2002017375-A/3014
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Boldin, M. and Wallach, D.
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Patent: WO 9855507-A 2 10-DEC-1998;
BOLDIN MARK (IL); WALLACH DAVID (IL)
Location/Qualifiers

    .2098
/organism="unidentified"
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Discrete B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barran, N., Bastien, V., Bloom, T., Anderson, S., Arachchi, H.M., Barran, N., Bastien, V., Bloom, T., Anderson, S., Arachchi, H.M., Barran, N., Canger, J., Chorgel, Y., Collymore, A., Cooke, P., Corum, B., DeArellano, K., Disz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Farco, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Barchan, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Illev, T., Johnson, R., Johnson, R., Liudblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C., McCarthy, M., Macdonald, P., Manor, J., Manning, J., Matthews, C., McCarthy, M., Malor, J., Manor, T., Mlenga, V., Murphy, T., Naylor, J., Naylor, J., Nicol, K., Manor, T., Mlenga, V., Murphy, T., Naylor, J., Naylor, J., Naylor, J., Schauer, S., Schubback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stenge-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venketaraman, V.S., Viel, K., Zimmer, A. and Zody, M. Direct Submission

Submitted (03-FEB-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F. A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/Repeatmasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACL39421 61099 bp DNA linear HTG 03-FEB-2003
Homo sapiens chromosome 8 clone RP13-706H15 map 8, LOW-PASS
SEQUENCE SAMPLING.
1675 GGACTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGA 1734
                                                                              1735 CACTACTGACATCCAAGGAGAAGAATTTGCCAAAGTTATAGTACAAAAAATTGAAAGATAA 1794
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens chromosome 8, clone RP13-706H15
Unpublished
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C C12N15/12, C07K14/47, C07K16/18, C12Q1/68, A61K38/17, G01N33/68 CC
Strandedness: Single;
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synthetic construct
synthetic construct
artificial sequences.
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Wallach, D., Boldin, M. and Malinin, N.
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Patent. JP 2002502258-A 1 22-JAN-2002;
YEDA RESEARCH AND DEVELOPMENT CO LTD
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PI DAVID WATT
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* sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. * However, it should not be assumed that this clone * will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.
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 59457: gap of 100 bp
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                                                                                                                                                                                   Score 754.4; DB 2;
Pred. No. 4.2e-129;
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                                                                                                   organism="Homo sapiens"
                                                                                                                /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/chromosome="8"
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BC004553

BC004553 LOCUS DEFINITION

Homo sapiens receptor-interacting serine-threonine kinase 2, mRNA (cDNA clone MGC:10684 IMAGE:4026156), complete cds.

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MCGANISM Home Selver Canadata, Vertebrata; Bureleostomi; Bureleostomi; Burno Selvery Selvery Canadata, Vertebrata; Bureleostomi; Burno Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery Selvery
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AVKHLHIHTPLLDSERKDVLRRAEILHKARFSYILPILGICNEPEFLGIVTEYMPNGS
LNELLHKRTEYEPDVAWPLERRILHEILGUNYLHMOTPPLHHDLKTQNILLDNEFHV
KLADFGLSKWRRWAELGOSRSSRGAPEGGTIIYMPPENYEPGGKSRASIKHDIYSYAVI
TWEVLSRKQPFEDVTNPLQIMYSVSQGHRPVINEESLPYDIPHRARMISLIESGWAQN
PDERRSFLKCLIELEPVIRTEESITFLEAVIQUKKTKLQSVSSAIHLCDKKKWELSLN
PWNHQPGESGCSSQLHENSGSPFETSRSLFAPQDNDFLSRKAQDCYFMKLHCPGNH
SWDSTISGSQRAAFCCHHTPCSSAIINPLSTRSLFAPQDNDFLSRKAQDCYFMKLHCPGNH
SWDSTISGSQRAAFCCHHTPCSSAIINPLSTRAUFSTRANGSELQPGTAQQNYQSKREDIVNQ
MTEACLNQSLDALLSRDLIMKEDYELVSTKFFTRTSKVRQLLDTTDIGGEEFAKVIVQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1508. 1774 / Caspase recruitment domain. Motif / Note="CARD; Region: Caspase recruitment domain. Motif contained in proteins involved in apoptotic signaling. Predicted to possess a DEATH (pfam00531) domain-like fold" / db_xref="CDD:pfam00619"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1318 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCCTGGAAATCA 1377
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/db xref="CDD:pfam00069"
1508. .1774
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43.9%; Score 733.4; DB 9;
Best Local Similarity 99.9%; Pred. No. 4.8e-125;
Matches 734; Conservative 0; Mismatches 1;
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/protein_id="AAH04533.1"
/db_xref="G1:13528714"
/db_xref="LocusID:8767"
                                                             /note="synonyms: RICK, I
/db xref="LocusID:8767"
/db_xref="MIM:603455"
/note="Vector: pOTB7"
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Qy 931 CAAACAAATGGTCTTCAGCCTTACCGGAAATACTTGTGGTTTCTAGATCACCATCTTT 990

Db 1738 CAACAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTT 1797

Qy 991 AAATTACTTCAAAATAAAAGCATGTTTTTCAAGAAATGTGTTTCAT 1050

Db 1798 AAATTTACTTCAAAATAAAAGCATGTTTTTCAAGAAAAAGGTTTCAT 1857

Qy 1051 AAAAGGATATTTATA 1065

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	Description	Aac77779 Human can	Abk51169 cDNA enco	Aad45172 Human rec	Aaz48762 Human RIC	Aaz46143 cDNA segu	Aak94554 Human ful	Aax02558 Human B1	Adc99131 Human KPP	Aaz09246 Human CAR	Aaf30001 Human CAR	Abk89280 Human cDN	Aal40752 cDNA of h	Abx75869 Human cDN	Adb81363 Human cas	Abx75870 Human Cas	Aal40753 DNA of hu	Aak93010 Human cDN	Ach33353 Human end	Acd96414 Human col	Abk55074 Human col	Aat19776 Human gen	Abz10246 Haematopo	Abz10100 Haematopo
SUMMARIES	ID	AAC77779	ABK51169	AAD45172	AAZ48762	AAZ46143	AAK94554	AAX02558	ADC99131	AAZ09246	AAF30001	ABK89280	AAL40752	ABX75869	ADB81363	ABX75870	AAL40753	AAK93010	ACH33353	ACD96414	ABK55074	AAT19776	ABZ10246	ABZ10100
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	Query Match	79.8	78.4	78.4	78.4	52.7	52.5	51.6	47.1	43.8	43.8	43.8	43.8	43.8	43.8	40.9	40.1	26.8	21.8	17.0	16.2	6.1	4.1	4.1
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## ALIGNMENTS

Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiarthritic; antiarthritic; antiarthritic; antiarthritic; antiarthritic; antiarthrial; dermatological; neuroprotective; thrombolytic; captiant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; attoimmune disorder; allergic cell disorder; attoimmune disorder; haematopoietic cell disorder; attoimmune disorder; haemostetic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening; ss. Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer. Human cancer associated gene sequence SEQ ID NO:173. Claim 1; Page 751-752; 2352pp; English. BP. AAC77779 standard; cDNA; 2709 99US-0124270P. (HUMA-) HUMAN GENOME SCI INC. 08-MAR-2000; 2000WO-US005882. (first entry) WPI; 2000-587533/55. P-PSDB; AAB43570. Rosen CA, Ruben SM; WO200055350-A1. 12-MAR-1999; Homo sapiens. 08-FEB-2001 21-SEP-2000. AAC77779; RESULT 1 AAC77779 

AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB4239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities

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sapiens.
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include: cytostatic; proliferative; vulnerary; immunomodulator;
antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
antinflammatory; antithyroid; antialrayic; antibacterial; antiviral;
cermatological; neuroprotective; cardiant; thrombolytic; coagulant;
cootropic; vasotropic; antipsoriatic and antiangiogenic. The
cootropic; vasotropic; antipsoriatic and antiangiogenic. The
polynucleotides and polypeptides can be used for preventing, treating or
ameliorating medical conditions and diagnosing pathological conditions.
CP Polynucleotides, polypeptides, antibodies, agonists and antagonists from
the present invention may be used to treat immune disorders by activating
cc inhibiting the proliferation, differentiation or mobilisation of
immune cells, to treat disorders of haematopoietic cells, autoimmune
cdisorders, allergic reactions, graft versus host disease and organ
cejection, modulate haemostatic or thrombolytic activity, modulate
cc inflammation, cancers, cardiovascular disorders, neurological disease and
characterial or viral infections. The peptides, nucleotides, antibodies,
cc AACTBAST and AABA4240 represent sequences used in the exemplification of
the present invention
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Pred. No. 2.4e-259;
5; Mismatches 1; Indels 0:
                                                                                                                                                                                                                                                                     Sequence 2709 BP; 810 A; 580 C; 540 G; 769 T; 0 U; 10 Other;
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Matches 1330; Conservative
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                                                                                                                                                                                                                                                                TTTGTTAACAGAAACCACTTTTAAAGGATAGTAATTATTATTCTTGTTTATAACAGTGCCTTA
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                                                                                                                                                                                                                                 The present invention relates to a new method for identifying compounds for treating and/or preventing cytomegalovirus (CWV) infection and/or related diseases. The method of the invention comprises contacting a test compound with at least one of the cellular kinases RICK, RIP, Nck-Interacting kinase, MKK3 and SRRK-2 and detecting any change in kinase activity. The method of the invention can be used to treat and/or prevent CW infections and related diseases. Oligomucleotides that can detect the specified kinases can also be used for diagnosis of infection. The present uncleic acid sequence encodes the human cellular kinase RICK
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Best Local Similarity 99.0%;
Matches 1329; Conservative
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                                  Schubart D, Habenberger
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                                                                                                                                                                                                                                                                                                                                                                                                          ATTATTTGTTACTTGTCTAAGATGCAATTTGATTTTATGAAGTATATACCCTTTACCCAC
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                                                                                   ATGTCTCTTTTGTTAACAGAAACCACTTTTAAAGGATAGTAATTATTGTTTTATAACA
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                                                                                                                                                                                    New antisense oligonucleotide that targets regions of a nucleic acid encoding human receptor interacting protein (RIP)2, for treating diseases associated with RIP2 expression.
                                                                                                                                                                                                                                                                                The invention relates to antisense compounds targetted to a nucleic acid encoding human receptor interacting protein (RIP)2 to inhibit its expression. Antisense compounds are used for treating diseases associated with RIP2 expression. They are also useful in antisense gene therapy. The present sequence is human RIP2 DNA
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Pred. No. 2e-254;
0; Mismatches 5; Indels 8
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                                                                                                                                                                                                                                                       Claim 1; Col 49-54; 35pp; English
                                 2001US-00920663
 01-AUG-2001; 2001US-00920663
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 99.0%;
Matches 1329; Conservative
                                                                   (ISIS-) ISIS PHARM INC
                                                                                                   Ward DT, Cowsert LM,
                                                                                                                                    WPI; 2002-673017/72.
P-PSDB; AAE27882.
                               01-AUG-2001;
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                                                                                                                                                                                                                                                                                                                                      This sequence encodes the human RICK (RIP-like interacting CLARP kinase)

C f apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10

during CD95 signalling. The invention provides methods for identifying

apoptosis signalling pathway inhibitors and activators, and methods and

c compositions for screening compounds which will modulate the interactions

CC compositions for screening compositions identified: ARC, RICK, and the CIDB family of

activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening

CC assays for agents, useful in the diagnosis, prognosis or treatment of

cisease associated with excess cell growth and dysregulation of

cassays for agents, useful in the diagnosis, prognosis or treatment of

cisease associated with excess cell growth and dysregulation of

confloative complexes containing RICK and CLARP can be used in drug

creening assays to identify inhibitors molecules blocking CD95-mediated

confloatification of ARC-like inhibitory compounds may be useful for gene

confloatification of ARC-like inhibitory compositions of CIDEs can be used to

cherapy treatment of disease with increased cell death in muscle tissue

confloatification of ARC-like inhibitory compositions of CIDEs can be used to

create e.g. cancer, AIDS, neurodegenerative disease. AntiRICK antibodies

can be used as reagents for the preparation or affinity chromatography

cc media, and for diagnostically measuring RICK levels. A specific inhibitor

confloation with intracellular factors such as CLARP and FADD appears to

confloation with intracellular factors such as CLARP and FADD appears

confloation with intracellular decompositions of RICK binding to intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGTTGGGATAGCACCATTTCTGGTTCTCAAAGGGCTGCATTCTGTGATCACAAGACCAC 1460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 2e-254;
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                                                                                                                                                                                                                                                           useful for treating diseases.
                                                                                                                    Koseki
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Best Local Similarity 99.0%;
Matches 1329; Conservative
                          98US-00069023
                                                                   (UNMI ) UNIV MICHIGAN
                                                                                                                 Nunez G, Inohara N,
                                                                                                                                                             WPI; 2000-072163/06.
P-PSDB; AAY59404.
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Best Local Similarity
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1318 ITTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCCTGGAAATCA 1377
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                                     571 CAGTIGGGATAGCACCATITCIGGAICTCAAAGGGCTGCATICTGIGAICACAAGACCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAK94554 standard; cDNA; 2033
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGAAAATAGTGGTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTT 1317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baughn MR;
H, Azimzai
                                     cDNA sequence encoding a human phosphorylation effector PHSP-6.
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Pred. No. 6.2e-168;
0; Mismatches 1; Indels 0;
                                                                        phosphorylation effector; PHSP; proliferative disorder; disorder; neuronal disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2024 BP; 612 A; 445 C; 434 G; 533 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Guegler KJ,
                                                                                                                                                                                                                           /product= "phosphorylation effector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corley NC, Guegler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Au-Young J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Page 121-122; 142pp; English
                                                                                                                                                                  Location/Qualifiers
203. .1825
/*tag= a
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98US-0155136P.
98US-0155239P.
98US-0106889P.
98US-0103796P.
99US-0113796P.
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Best Local Similarity 99.9%;
Matches 880; Conservative (
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Patterson C, Bandman O, Av
Reddy R, Lu DAM, Shih LL;
(first entry)
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P-PSDB; AAY68774.
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03-NOV-1998;
19-NOV-1998;
22-DEC-1998;
16-MAY-2000
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971L-00121199.
971L-00121746.
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P-PSDB; AAW92795.
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                                                                                                                                               The invention relates to primers for synthesising full length cDNA clones 810 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5' and 3' ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly
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                                                                                   synthesizing full length cDNA clones and their use
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Ishii S, Kawai
3, Otsuki T, Ko
                                                                                                                          8; SEQ ID NO 3453; 1380pp + Sequence Listing; English.
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 Isogai T, Hayashi K, Isl
a T, Nagai K, Kojima S,
                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 99.8%;
Matches 878; Conservative
  Ota T, Nishikawa T, Isog
Wakamatsu A, Sugiyama T,
                                                                                 830 Primers useful for s
in genetic manipulation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes the isolation of a novel human B1 protein which can interact with, intracellular mediators or modulators of inflammation, cell death and/or cell survival pathways, directly or indirectly. Cells can be modulated or mediated in inflammation, cell death or cell survival pathways or another intracellular signalling activity using B1. Conditions such as AIDS and cancer can be treated using B1. Antibodies, oligonucleotides and ribozymes can also be used to regulate the above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B1 protein; intracellular mediator; modulator; inflammation; cell death; cell survival pathway; intracellular signalling; AIDS; cancer; human; ss.
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                                                                                                             1874 AAAAGGATATTTATATCTCTGTTGCTTTGACTTTTTTTATAAAATCCGTGAGTATTAA
      1814 AAATTTACTTCAAAATAAAAGCATGTAAGTGACTGTTTTTCAAGAAGAAATGTGTTTCAT
                                                                    AAAAGGATATTTATATCTCTGTTGCTTTTGACTTTTTTTATAAAATCCGTGAGTATTAA
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Pred. No. 3.2e-164;
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osteopathic; antiarthritic; antiparasitic; antihelminthic; antipsoriatic;

uropathic; ophthalmological; antirheumatic; haemostatic; antibacterial; virucide; protozoacide; fungicide; kinase; phosphatase; KPP; cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis; cancer; developmental; mental retardation; neurological; Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's; diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan; helminthic infection; transgenic; gene therapy; human; ss; gene.

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AAAAGGATATTTATATCTCTCTGTTGCTTTGACTTTTTTTATAAAATCCGTGAGTATTAA 1110
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AAAGTTACAGAGTGTTTCAAGTGCCATTCACCTATGTGACAAGAAGAAAATGGAATTATC 1254
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Jan BM;
Griffin JA;
Ta, Lee SY;
Tang YT;
Yao MG, Yue H;

Bandman O, Baughn MR, Becha SD, Borowsky ML, Duggan Emerling BM, Forsythe IJ, Gandhi AR, Gorvad AE, Grif Gururajan R, Hafalia AJA, Khan FA, Lal PG, Lee EA, Lindquist EA, Lu DAM, Lu Y, Marquis JP, Nguyen DB, Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J,

Guruzajan R, Hafalian Lindquist EA, Lu DAM, Ramkumar J, Recipon S! Thornton MB, Tran UK, Zebarjadian Y;

WPI; 2003-403214/38.

P-PSDB; ADC99079

2001US-0343910P. 2001US-0333098P. 2001US-0332424P. 2001US-0334288P. 2001US-0345474P

(INCY-) INCYTE GENOMICS INC.

17-OCT-2002; 2002WO-US033723

19-OCT-2001; 02-NOV-2001; 13-NOV-2001; 16-NOV-2001; 30-NOV-2001;

WO2003033680-A2. Homo sapiens.

24-APR-2003

H,

New human kinases and phosphatases and polynucleotides, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis, cancer or hepatitis.

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AAAGGAATCATGTGGATCCTCTCAGCTCCATGAAATAGTGGTTCTCCTGAAACTTCAAG 1215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel isolated polypeptide which is a human kinase and phosphatase (KPP). The KPP polypeptides, polymuclectides, agonists and antagonists are useful for diagnosing, treating or preventing cell proliferative disorders such as atherosclerosis, cirrhosis, hepatitis and cancer, developmental disorders e.g. mental retardation, neurological disorders including Alzheimer's disease and Parkinson's disease, autoimmune and inflammatory disorders such as Crohn's disease, autoimmune and inflammatory disorders such as fungal, parasitic, protozoan or helminthic infections. Furthermore, tholynucleotides encoding KPP may be useful for creating transgenic animals to model human disease, as well as during gene therapy of the mand inflammatory of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the co
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Pred. No. 4e-149;
0; Mismatches 3;
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ilarity 99.6%;
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Best Local Similarity
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1275

anti-HIV; antiallergic; antinflammatory; antianaemic; antiparkinsonian; nootropic; antiaonulsant, antiarteriosclerotic; antiasthmatic; immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological; antidabetic; nephrotropic; antigout; thyromimetic; neuroprotective;

BP

ADC99131 standard; cDNA; 1959

ADC9913

Human KPP cDNA - SEQ ID 84.

(first entry)

01-JAN-2004

ADC99131;

540

ö 480 /product= "CARD-3"

99WO-US002544.

98US-00099041. 98US-00207359. 98US-00019942

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(MILL-) MILLENNIUM PHARM INC.
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17-JUN-1998;
08-DEC-1998;
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systemic lupus erythematosis, immune-mediated glomerulonephritis; stroke, Parkinson's disease, amyotrophic lateral sclerosis; retinitis pigmentosa; spinal muscular dystrophy; cerebellar degeneration; anaemais drug; myelodysplastic syndrome; myocardial infarction; cell proliferation; cell differentiation; cell survival; CARD-41; CARD-45; CARD-47; CARD-47; caspase activation; detection; screening; therapy; diagnosis; disease; apoptoric cell death; Fas/APO-1 receptor complex; TW receptor complex; cancer; follicular lymphoma; carcinoma; p53 mutation; viral infection; hormone-dependent tumour; autoimmune disorder; Alzheimer's disease. CARD-3; caspase recruitment domain; CARD-4; regulation; detection; Human CARD-3 cDNA. human; RESULT 9
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AAZ09246 standard; cDNA; 1931 BP

25-OCT-1999 (first entry)

AAZ09246;

Homo sapiens.

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Location/Qualifiers
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This invention describes the isolation of novel human caspase recruitment domain, CARD-3 and CARD-4 polynucleotides and proteins and a partial carried commain, CARD-4 protein and genes. The genes and proteins of the invention are involved in the regulation of caspase activation. The caspase criminal carried in the regulation of caspase activation. The caspase activation and the regulation of caspase activation. The caspase activates and antibodies can be used in screening assays, detection assays, predictive methods may be used to diagnose and treat patients which are suffering from a disorder associated with abnormal level or rate of apoptotic cell death, abnormal activity of the TMF receptor complex, or abnormal activity of a caspase. Complex associated with abnormal activity of a caspase. Component activity of the TMF receptor complex, or abnormal activity of a caspase. Diseases that may be treated include cancer (particularly follicular lymphoma, carcinomas associated with mutations in p53 and hormone-cappendent tumours), autoimmune disorders (e.g. systemic lugus carpendent tumours), autoimmune disorders (e.g. systemic lateral sclerosis, arthematosis, immune-mediated glomerulonephritis), viral infections, also parkinson's disease, amyorcaphic lateral sclerosis, retinitis pigmentosa, spinal muscular dystrophy, cerebellar degeneration, anaemia, myelodysplastic syndrome, myocardial infarction, and stroke. CARD-3 protein interacts with other cellular proteins, and so can be used for survival. The CARD proteins may also be used to for screen drugs or compounds which modulate their activity. The CARD-4 gene can express a long transcript that encodes CARD-41, and GARD-42. This sequence compounds which modulate activity. The CARD-4 and CARD-42. This sequence compounds which madulate their activity. The CARD-4 and cARD-42. This sequence compounds which modulate their activity and card of the invention and condess the human CARD-3 protein described in the method of the invention
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Novel CARD-3 and CARD-4 genes and polypeptides used or treating regulation of cellular proliferation and differentiation and cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1931 BP; 613 A; 429 C; 416 G; 473 T; 0 U; 0 Other;
                                                                                                                                                                           Example 2; Fig 1; 181pp; English.
                                                                                          survival.
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The present sequence is that of cDNA encoding human caspase recruitment domain 3 (CARD-3, see AAB20079). The CDNA was isolated following a database search using known CARD sequences. Plasmid pxE17A containing CARD-3 cDNA is deposited as ATCC 203037. CARD-3 is an intracellular protein predicted to be involved in regulating caspase activation. It is useful as a modulating agent in regulating callular processes include cell growth and cell death. Methods of diagnosing and treating patients suffering from a disorder associated with an abnormal level or rate of apoptotic cell death, abnormal activity of the Fas/ADO-1 receptor complex, complex, abnormal activity of the tumour necrosis factor receptor complex or abnormal activity of the tumour necrosis factor receptor complex or abnormal activity of the tumour necrosis factor receptor complex or abnormal activity of the cumour administering a compound that modulates the expression or activity of CARD-3, CARD-4, CARD-5 or CARD-6 e.g. a small molecule, antisense nucleic acid, ribozyme or polypeptide. Such disorders include cancer, viral infection, autoimmune disorders, neurological diseases, haematological disorders, inflammatory disorders and immune disorders. CARD nucleic acids can be used to express CARD proteins in a host cell e.g. for gene therapy applications, to detect a genetic lesion and to modulate CARD activity
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Isolated intracellular proteins predicted to be involved in regul cappae activation are used for diagnosis and treatment of e.g. viral infections, autoimmune diseases, neurological diseases and hematological diseases and hematological diseases.
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Pred. No. 3.8e-138;
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                                                                                                                                                                                                        Claim 1(a); Fig 1; 208pp; English..
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Best Local Similarity 99.7
Matches 733; Conservative
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                                               990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; ss; gene; caspase recruitment domain; CARD-1; CARD-4; LRR; leucine rich repeat; LPS; lipopolysaccharide; NP-KB; nuclear factor-kappa B; cancer; viral infection; autoimmune disorder; systemic lupus erythematosus; immune-mediated glomerulonephritis; archritis; immune disorder; multiple sclerosis; Hashimoto's thyroiditis; atopic condition; asthma; allergy; psoriasis; contact dermatitis; gastrointestinal allergy; insulin-dependent diabetes; bacterial infection; tuberculosie.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARD-
                                                                    CAAACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying modulators of long form of caspase recruitment domain, (4L useful for treating cancer, infections, and immune disorders, by contacting test compound with CARD-4L and determining effect of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cDNA encoding caspase recruitment domain protein CARD-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          srial infection; tuberculosis; lepromatous leprosy; signalling disorder; tissue disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "CARD-3"
                                                                                                                                                                                                                                                                                                                                                                             BP.
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P-PSDB; ABG31075.
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harbouring LBS, exposing the cell to a test compound and measuring NF-kB cativation, where altered NF-kB activation polypeptide in the presence of activation, where altered NF-kB activation polypeptide in the presence of the test compound compared to the binding in the absence of the test compound indicates that the test compound is a candidate compound for modulating LPS-mediated activation of NF-kB. Modulators identified by (MJ) are useful for treating a disorder Naracterised by aberrant CARD-4. Protein or nucleic acid. Compounds that modulate the activity of CARD-4. The are useful to treat or diagnose disorders such as cancer, viral infections, autoimmune disorders e.g. systemic lupus erythematosus, immune-mediated glomerulonephritis and arthritis, immune disorders, such as multiple sclerosis, Hashimoto's thyroiditis, atopic conditions such as asthma, allergy, psoriasis, contact dermatitis gastrointestinal callergies, insulin-dependent diabetes, bacterial infections, including tuberculosis, and lepromatous leprosy, disorders of cell signalling and disorders of tissues. The present sequence is the human cDNA encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1931 BP; 613 A; 429 C; 416 G; 473 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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The invention relates to novel isolated Caspase Recruitment Domain (CARD) polypeptides, CARD-4L and CARD-4S. The CARD proteins of the invention may be used to treat disorders associated with decreased CARD expression by supplementing the patient's own production of CARD. Disorders associated with the expression and activity of CARD include cancers (particularly follicular lymphomas, carcinomas associated with mutations in p53, and covarian cancer), autoimmune disorders (such as systemic lupus erythematosus, immune-mediated glomerulonephritis), viral infections erythematosus, immune-mediated glomerulonephritis), viral infections (such as those caused by herpes viruses, poxylruses, and adenoviruses), neurological diseases (such as Alzeimer's disease, Parkinson's disease, amylotrophic lateral sclerosis (ALS) retinitis pigmentosa, spinal muscular atrophy, and various forms of cerebellar degeneration), anaemia and the myelodysplastic syndromes. This polynuclectide sequence and the myelodysplastic syndromes. This polynuclectide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated Caspase Recruitment Domain (CARD) polypeptides (CARD-4L and CARD-4S) useful for diagnosing and treating e.g. Parkinson's and Alzheimer's disease, cancers and viral infections.
                                                                                                                                                                                                                                                                                                                                                      Cytostatic; virucide, immunomodulatory; neuroprotective, antialzheimers; cerebroprotective, antiparkinsonian; antisclerotic; ophthalmological; nootropic; antianaemic; Caspase Recruitment Domain; CARD, GARD-4E, p33; cancer; CARD-4S; follicular lymphoma; carcrinoma; autoimmune disorder; hormone-dependent tumour; breast cancer; prostate cancer; ovarian cancer; systemic lupus; herpes virus; poxvirus; adenovirus; neurological disease; anaemia; neutropenia; myelodysplastic syndrome; human; gene; ss.
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Pred. No. 3.8e-138;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                          human CARD-3 SEQ ID No 1.
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Best Local Similarity 99.7
Matches 733; Conservative
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08-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; 88; gene; CARD-3; CARD-4; caspase recruitment domain; apoptosis; p75; tumour necrosis factor; TNF; neutrophin receptor; cancer; autoimnume disorder; systemic lupus; immune mediated glomerulonephritis; viral infection; neurological; retinitis pigmentosa, haematologic; chronic neutropenia; myocardial infarction; stroke; RIP; RICK; CARDIAK.
                                                                                                                             1569 AGAAGCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated polypeptide, comprising at least 25 contiguous amino acids of a human caspase recruitment domain (CARD)-4Y, human CARD-4Z or murine CARD-4L (all splice variants of CARD-4) comprising the polypeptide. Also included is an isolated fusion protein, comprising the colypeptide. Also included is an isolated fusion protein, comprising the CARD polypeptide. The CARD polypeptide is useful in screening assays, colypeptide. The CARD polypeptide is useful in screening assays, detection assays (e.g. chromosomal mapping, tissue typing and forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, detection diagnostic end pharmacogenomics), and in therapeutic and prophylactic treatments (in diseases associated with apoptotic call death crophylactic treatments (in disease associated with apoptotic call death crophylactic treatments disorders (e.g. systemic lupus erythemacosus and immunodeficiency syndrome), neurological disease (e.g. systemic lupus erythemacosus chisease, parkinson's disease, amyotrophic lateral sclerosis, retinitis pigmentosa, spinal muscular arrophy and cerebellar degeneration), haematological diseases (e.g. anaemia, neutropaenia and myelodysplastic syndromes), myocardial infaction and stroke). The CARD polypeptide is useful as bait protein in a two-hybrid assay or three hybrid assay to identify other proteins, which bind too interact with other CARD proteins. Also disclosed are CARD-3 proteins and cDAMA. The gene for human CARD-4 is located on chromosome 7. The present sequence is a human constant and stroke of the constant sequence is a human constant and stroke of the constant sequence is a human constant and stroke of the constant sequence is a human constant and stroke of the constant sequence is a human constant and stroke of the constant sequence is a human constant constant sequence is a human constant sequence is a human constant sequence is a part and constant sequence is a part of the constant sequence is a part of the constant sequence o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated human caspase recruitment domain (CARD)-4Y or CARD-4Z polypeptide, or murine CARD-4L polypeptide, useful in screening assays, detection assays, predictive medicine, and in therapeutic applications.
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       98US-00207359.
                                                                              98US-00019942.
98US-00099041.
                                                                                                                                                                                            (MILL-) MILLENNIUM PHARM INC.
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       08-DEC-1998;
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This invention relates to two novel genes CARD-3 and CARD-4 (caspase recruitment domains), which are mediators of apoptosis and are useful in the indentification of compounds that modulate apoptosis. Specifically, CARD-3 (also known as RIPZ, RICK and CARDIAK) is known to be a mediator.

CARD-3 (also known as RIPZ, RICK and CARDIAK) is known to be a mediator.

CARD-4 (also known as RIPZ, RICK and CARDIAK) is known to be a mediator.

CARD-5 (a member of the tumour necrosis factor (TNF) family), and is mediated by this p75 neutrophin receptor. Accordingly these genes, and the proteins encoded thereof, are linked to certain disorders especies apoptosis is inhibited. These include cancer, autoliferating when apoptosis is inhibited. These include cancer, autolimmune disorders especies as those caused by the herpesvirus, neurological disorders such as cretinitis pigmentosa, haematologic diseases including chronic retinitis pigmentosa, haematologic diseases including chronic neutropenia, as well as myocardial infarction and strokes. The present compound alters the binding of CARD-3 to p75, which comprises measuring the binding of a polypeptide containing the CARD domain of CARD-3 to a polypeptide comprising the death domain of p75 in the presence and absence of the test compound, and determining if binding is altered. This polymucleotide is the human CARD-3 CDNA sequence of the invention.
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43.8%; Score 731.8; DB 9; Length 1931;
Best Local Similarity 99.7%; Pred. No. 3.8e-138;
Matches 733; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1931 BP; 613 A; 430 C; 416 G; 472 T; 0 U; 0 Other;
                   Disclosure; Fig 2; 40pp; English
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The invention relates to an isolated polypeptide, comprising at least 25 contiguous amino acids of a human caspase recruitment domain (CARD)-4Y, human CARD-4Z or murine CARD-4L (all splice variants of CARD-4) collypeptide. Also included is an isolated fusion protein, comprising the CARD polypeptide covalently linked by a peptide bond to a heterologous polypeptide. The CARD polypeptide is useful in screening assays, ceed etection assays (e.g. chromosomal mapping, tissue typing and forensic biology), predictive medicine (e.g. diagnostic assays, prophylactic treatments (in diseases associated with apoptotic cell death company autoimmune disorders (e.g. systemic lupus erythematosus and immune related glomerulonephritis), viral infections, AIDS (acquired immune disorders (e.g. systemic lupus erythematosus and issuence, parkinson's disease, amyotrophic lateral sclerosis, retinitis disease, parkinson's disease, amyotrophic lateral sclerosis, retinitis pigmentoea, spinal muscular atrophy and cerebellar degeneration), susemital as bait protein in a two-hybrid assay or three hybrid assay to identify other proteins, which bind to or interact with other CARD
                amyotrophic lateral sclerosis; retinitis pigmentosa; spinal muscular atrophy; cerebellar degeneration; haematological disease; anaemia; neutropaenia; myelodysplastic syndrome; myocardial infarction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated human caspase recruitment domain (CARD)-4Y or CARD-4Z polypeptide, or murine CARD-4L polypeptide, useful in screening assays, detection assays, predictive medicine, and in therapeutic applications.
                                                                                                                                                                                                                                                                                                                                                                                          CARD-4L; CARD-4S; CARD-4Y; CARD-4Z; apoptosis; cancer; AIDS; autoimmune disorder; systemic lupus erythematosus; viral infection; immune related glomerulonephritis; acquired immunodeficiency syndrome; neurological disease; Alzheimer's disease; Parkinson's disease;
AAATTTACTTCAAAATAAAAGCATGTAAGTGACTGTTTTTCAAGAAGAAATGTGTTTCAT
                                                                                                                                                                                                                                                                                                                                                                          gene; caspase recruitment domain; CARD; CARD-3; CARD-4;
                                                                                                                                                                                                                                                                                                                                     Human Caspase recruitment domain protein 3, open reading frame.
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                                                                                                                                                                                                                    ABX75870 standard; cDNA; 1620 BP.
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                                                                                                                     1869 AAAAGGATATTTATA 1883
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                                                                                                                                                                                                                                                                                                (first entry)
                                                                                1051 AAAAGGATATTTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stroke; chromosome 7.
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proteins. Also disclosed are CARD-3 proteins and cDNAS. The gene for human CARD-4 is located on chromosome 7. The present sequence is a human CARD cDNA
                                                                                                                                                                                                                                                                                                                                                                  TGAAAATAGTGGTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTT
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40.9%; Score 681.8; DB 7; Length
Best Local Similarity 99.7%; Pred. No. 4.5e-128;
Matches 683; Conservative 0; Mismatches 2; Indels
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
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GenCore version 5.1.6
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US-09-65-364-3

US-09-641-628-13

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4 4	701 832 6669							ULT.1  109-920-663.3  409-920-663.3  4cent No. 642621  ENREAL INFORMATION:  ENREAL INFORMATION:  APPLICANT:  Lex M. Cowsert  TITLE OF INVENTION:  ANTISENSE MODULATI  TITLE OF INVENTION:  ANTISENSE MODULATI  TURE REFERENCE: RTS-0233  CURRENT FILING DATE: 2001-08-01  CURRENT FILING DATE: 2001-08-01  CURRENT FILING DATE: 2001-08-01  NUMBER OF SEQ ID NOS: 49  LENGTH: 2501  TYPE: DNA  CREANISM: Homo sapiens  FRATURE:  NAME/KEY: CDS  LOCATION: (225)(1847)  09-920-663-3  uery Match  atches 1329; Conservative O; Mism  331 ACAGTTACAGAGTGTTTCAAGTGCCAT  1160 AAAGTTACAGAGTGTTTCAAGTGCCAT  11220 TCTGAACATACCTGTAAATCATGGTCC  391 TCTGAACATACCTGTAAATCATGGTCC  1220 TCTGAACATACTACTGTAAATCATGGTCC  1220 TCTGAACATACTACTGTAAATCATGGTCC  1220 TCTGAACATACTACTGTAACTACTGTTCC  1220 TCTGAACATACTACTACTATACTGTTCC  1220 TCTGAACATACTACTACTATACTATACTGTCC  1221 TCTGAACATACTACTATACTATACTATACTATACTATAC	AGTGGTTC          AGTGGTTC	AGAAAAGC
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Sequence 1, Appli Sequence 1, Appli Sequence 18033, A Sequence 63, Appl	Sequence 701, Sequence 2813, Sequence 6, Ap	Sequence 1, Ap Sequence 1, Ap Sequence 35, A	Sequence 14, Appl Sequence 786, App	Sequence 11, Ap Sequence 1137,	ים ת			EXPRESSION  Length 2501;  indels 8; Gaps  ACAGAGAAAATGGAATTATC  ACAGGAGATCAGCTCA  CATGTGGATCATCTCAGCTCA  CATGTGGATCATCAGATTATC  CATGTGGATCATCAGATTATC  CATGTGGATCATCAGATTATC  CATGTGGATCATCAGATTATC  CATGTGGATCATCAGATTATC  CATGTGGATCATCAGATTATC  CATGTGGATCATCAGATTATC  CATGTGGATCATCAGATTATC  CATGTGGATCATCAGATTATC  CATGTGGATCATCAGATTATC  CATGTGGATCATCAGAGATCAGACACCAGACACCAGAGATCATC  CATGTGGATCATCATCATCAGAGATCAGACACCAGACACCAGACACCAGACACCACACACCACACCAC	TCCTCAAGACAATGATTT 	<b>TCACTGTCCTGGAAATCA</b>

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1821 AAATTTACTTCAAAATAAAAGCATGTAAGTGACTGTTTTTCAAGAAGAAATGTGTTTCAT 1880
## APPLICANT: Numez, Gabriel
### APPLICANT: Inohara, Nachiro
### APPLICANT: Inohara, Nachiro
### APPLICANT: Koseki, Takeyoshi
### TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
### TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
### CURRENT APPLICATION NUMBER: US/09/069,023A
### CURRENT FILING DATE: 1998-04-27
### NUMBER OF SEQ ID NOS: 38
### SOCTIVARE: Patentin Ver. 2.0
### SEQ ID NO 2
### IENTH: 2502
### TENTH: 2502
### TENTH: 2502
### TENTH: 2502
### TENTH: 2502
### CRAMISM: Homo sapiens
### US-09-069-023-2
### SCOIE 1308; DB 4; Length 2502;
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5-09-069-023-2 Sequence 2, Application US/09069023A Patent No: 6348573 GENERAL INFORMATION:

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                                                                                                                                                                                                             Length 1931;
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                                                                                                                                                                                                           43.8%; Score 731.8; DB 3; 99.7%; Pred. No. 4.1e-160; ive 0; Mismatches 2;
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TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1931 base pairs
TYPE: nucleic acid
STRANDENNESS: single
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Matches 733; Conservative
                                                                                                                                      linear
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US-09-019-942-2
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                       TTTTAATTAATACAAGTAAAAGTTGAATTTGGTTGAATTTGCTACATAGTTCAATTTTT
                                                                                                                                      ATGTCTCTTTTGTTAACAGAAACCACTTTTAAAGGATAGTAATTATTCTTGTTTATAACA
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 GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
TITLE OF INVENTION: DOMAIN POLYPEPTIDES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STREET: ADDRESSE: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 0110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IEM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,942
FILING APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/068001
TELECOMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
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Patent No. 6033855
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US-09-019-942-2
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                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: Bertin, John
TITLE OF INFORMATION:

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVER: US 09/245,281
CURRENT APPLICATION NUMBER: US 09/207,359
EARLIER APPLICATION NUMBER: US 09/207,359
EARLIER PILING DATE: 1998-12-08
EARLIER PILING DATE: 1998-06-17
EARLIER FILING DATE: 1998-06-17
EARLIER FILING DATE: 1998-06-17
EARLIER FILING DATE: 1998-06-17
EARLIER FILING DATE: 1998-06-17

SARLIER FILING DATE: 1998-06-17

SARLIER FILING DATE: 1998-06-17

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1
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Pred. No. 4.1e-160;
0; Mismatches 2;
                                                                                                                     Sequence 1, Application US/09245281
Patent No. 6369196
  1869 AAAAGGATATTTATA 1883
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Best Local Similarity 99.7%;
Matches 733; Conservative
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (214)...(1833)
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                                                                          RESULT 5
JS-09-245-281-1
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                 TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED FITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF FILE REFERENCE: 07334-076001.

CURRENT APPLICATION NUMBER: US/09/099,041A
CURRENT FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 09/019,942
PRIOR PILING DATE: 1998-02-06
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 731.8; DB 4;
Pred. No. 4.1e-160;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 99.7%;
Matches 733; Conservative
                                                                                                                                                                                                                                                                                                                                                                   , NAME/KEY: CDS
, LOCATION: (214)...(1833)
US-09-099-041A-1
                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                       LENGTH: 1931
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; Batent No. 6469140
; Patent INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-112010
; CURRENT APPLICATION NUMBER: US/09/207,359B
CURRENT FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO : 47
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Pred. No. 4.1e-160;
0; Mismatches 2;
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Best Local Similarity 99.7%;
Matches 733; Conservative 0
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; LOCATION: (214)...(1833)
US-09-207-359B-1
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ORGANISM: Homo sapiens
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US-09-207-359B-1
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                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09470271

Patent No. 6410689
GENERAL INFORMATION:
GENES ENCODING CASPASE RECRUITMENT
TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
TITLE OF INVENTION: DOMAIN POLYPEPTIDES
VORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
OPERAE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/470,271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
PRICR APPLICATION DATA:
APPLICATION NUMBER: 09/019,942
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/068001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 617/542-5070
TELERAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1931 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches 733; Conservative
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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; Patent No. 6613521
; GENERAL INFORMATION: John
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
                                                                                                                                                                       Score 731.8; DB 4;
Pred. No. 4.1e-160;
0; Mismatches 2;
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ilarity 99.7%;
Conservative
             LENGTH: 1931
TYPE: DNA
ORGANISM: Homo sapiens
FRATURE:
NAME/KEY: CDS
LOCATION: (214)...(1833)
US-09-340-620A-1
                                                                                                                                                                       Query Match
Best Local Similarity
Matches 733; Conserv
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TITLE OF INVENTION: NOVEL MOLECULES OF THE CAP
FILE REFERENCE: 0734-12401
CURRENT APPLICATION NUMBER: US/09/340,620A
CURRENT FILING DATE: 1999-06-28
PRIOR PELING DATE: 1999-06-28
PRIOR PELING DATE: 1999-06-28
PRIOR PILING DATE: 1999-06-08
PRIOR FILING DATE: 1998-06-08
PRIOR FILING DATE: 1998-12-08
PRIOR FILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 71
SOFTWARE: FASTESEQ for Windows Version 4.0
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Patent No. 6482933
GENERAL INFORMATION:
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APPLICANT: Bertin, John
APPLICANT: Chao, Moses V.
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILE AND USES THEREC
FILE REPERBACKE: 07334-316001
CURRENT APPLICATION NUMBER: US/09/748,537
CURRENT APPLICATION NUMBER: US 09/099,041
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FASTERQ for Windows Version 4.0
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Pred. No. 4.1e-160;
0; Mismatches 2;
                                                                                                                            ; Sequence 2, Application US/09748537; Patent No. 6680167; GENERAL INFORMATION:
                     43.8%;
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     1051 AAAAGGATATTATA
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CORGANISM: Homo sapiens
US-09-748-537-2
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US-09-748-537-2
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TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF FILE REFERENCE: 07334-112001
CURRENT APPLICATION NUMBER: US/09/865,364
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/207,359
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR APPLICATION NUMBER: US 09/019,942
SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                             ch 43.8%; Score 731.8; DB 4; al Similarity 99.7%; Pred. No. 4.1e-160; 733; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                     ... (1833)
                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: (214)
US-09-865-364-1
                                                                                                                                                                                                                                               LENGTH: 1931
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Best Local S:
Matches 733
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                                                                                                                                    TTTTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCCTGGAAATC
                                                                                                                                                                     532 TTTTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCCTGGAAATC
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APPLICANT: Bertin, John
TITLE OF INVENTION:
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-07601
CURRENT PELLING NUMBER: US/09/099,041A
CURRENT FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
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99.7%; Pred. No. 1.4e-148;
iive 0; Mismatches 2;
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; ORGANISM: Homo sapiens
US-09-091A-3
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CAAACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTT 1808
                                                                                                                                                               1809 AAATTTACTTCAAAATAAAAGCATGTAAGTGACTGTTTTTCAAGAAGAAATGTGTTTCAT 1868
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                                                                                                AAATTTACTTCAAAATAAAAGCATGTAAGTGACTGTTTTTCAAGAAGAAATGTGTTTTCAT
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41.7%; Score 695.4; DB 4; Length 1060;
Best Local Similarity 99.7%; Pred. No. 8.8e-152;
Matches 707; Conservative 0; Mismatches 1; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 684, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Deffrey J. Seilhamer
ITILE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
                                                                                                                                                                                                                                                               1051 AAAAGGATATTTATA 1065
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LIBRARY: MPHGNOT03
; CLONE: 445186
US-09-023-655-684
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-09-023-655-684
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FACELL NO. 0193140;
GENERAL INCRMATION: JOHN
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
CURRENT APPLICATION WUMBER: US/09/207,359B
CURRENT FILING DATE: 1998-12-08
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1620
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Patent No. 6469140
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CORGANISM: Homo sapiens
US-09-207-359B-3
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Best Local Similarity
Matches 683; Conserv
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US-09-207-359B-3
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APPLICANT: Bertin, John
TITLE OF INVENTION:
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL NO 18001
CURRENT APPLICATION NUMBER: US 09/245,281
CURRENT FILING DATE: 1999-02-06
EARLIER FILING DATE: 1999-02-06
BARLIER PLILING DATE: 1998-06-17
EARLIER PLILING DATE: 1998-06-17
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1620
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Pred. No. 1.4e-148;
0; Mismatches 2; Indels 0;
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Patent No. 6369196
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Best Local Similarity 99.7%;
Matches 683; Conservative
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; ORGANISM: Homo sapiens
US-09-245-281-3
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                                                Score 681.8; DB 4;
Pred. No. 1.4e-148;
0; Mismatches 2;
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                                                Query Match
Best Local Similarity 99.7%;
Matches 683; Conservative
; ORGANISM: Homo sapiens
US-09-340-620A-3
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TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE CURRENT APPLICATION NUMBER: US 09/245,281

PRIOR APPLICATION NUMBER: US 09/245,281

PRIOR FILING DATE: 1999-02-05

PRIOR FILING DATE: 1999-02-05

PRIOR FILING DATE: 1998-02-05

PRIOR FILING DATE: 1998-04-17

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 71

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LENGTH: 1620

TYPE: DNA
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| Cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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	Description	Sequence 2, Appli	Sequence 173, App	Sequence 13, Appl	Sequence 2, Appli	Sequence 1, Appli	Sequence 2, Appli	_	Sequence 1, Appli		~	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 20565, A	Sequence 544, App
	ID	US-09-771-161A-2			-				US-10-118-984-1	US-10-295-981-1	US-09-728-721-3	US-10-105-931-3	US-10-118-984-3	US-10-295-981-3	US-09-918-995-20565	US-09-919-580-544
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Db 2282 GTACAGAATCCCTGAAAATCCCAGGCTTAATTGCCTTAAAAGGTTATTAATTTA 2341  Cy 1471 AAACTCCATTATTAGGATTTAAAGTTTTATTATGAATTCCCTTAAAAATGAT 1530  Db 2342 AAACTCCATTATTAGGATTACATTTTAAAGTTTTATTATGAATTCCCTTTAAAAATGAT 2401  Cy 1531 ATTTCAAAGGTAAAACAATACAATATAAGAAAAAAAAAA	RESULT 3 US-09-981-397A-13 i Sequence 13, Application US/09981397A ; Publication No US20030082519A1 ; GENERAL INFORMATION:     APPLICANT: Axxima Pharmaceuticals AG     APPLICANT: Schubart, Daniel     APPLICANT: Stein-Gerlach, Matthias     APPLICANT: Bevoc. Dorian     APPLICANT: AXX-004.1 US     CURRENT APPLICATION NUMBER: 0S/09/981,397A     CURRENT FILING DATE: 2000-10-16     NUMBER OF SEQ ID NOS: 22     SEQ ID NO 13     LENGTH: 2501     TYPE: DATE: AXX-004.1 US     CURRENT: Patentin version 3.1     TYPE: DATE: AXX-004.1 US     CURRENT: AXX-013     TYPE: DATE: AXX-013	Query Match         78.44;         Score 1308;         DB 10;         Length 2501;           Best Local Similarity         99.04;         Pred. No. 2.6e-267;         14           Matches 1329;         Conservative         0;         Mismatches         5;         Indels         8;         Gaps         1;           My         331 ACAGTTACAGAGTGTTTCAAGTGCCATTCACCTAGAGAGAAAATGGAATTATC         390         1160 AAAGTTACAGAGGTGTTCAAGTCCATAGAGAAAAAAGGAATTATC         1219           My         391 TCTGAACATACCTGTAAATCATGGTCCACAAGAGAAAAAAGGAATTATC         1219           My         451 TGAAAATAGTGGTTCTCCTGAAACTCTCAAGGTCCTCTCAGGTCCTCTCAGGTCCTCAGGTCCTCTCAGGTCCTCTCAGGTCCTCTCAGGTCCTCTCAGGTCCTCTCAGGTCTCTCTC
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APPLICANT: Bertin, John
APPLICANT: Chao, Moses V.
TITLE OF INVENTION: NOVEL MOLECULES OF THE C.
FILE REPERENCE: 07334-316001
CURRENT APPLICATION NUMBER: US/09/748,537
CURRENT FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR FILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5.
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US-09-748-537-2
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RESULT 4 US-09-748-537-2 Sequence 2, Application US/09748537 ; Patent No. US20020061833A1

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Best Local Similarity 99.7%;
Matches 733; Conservative g ò

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CACTACTGACATCCAAGGAGAAGTTTGCCAAAGTTATAGTACAAAAATTGAAAGATAA 1748
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GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
DOMAIN POLYPEPTIDES
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43.8%; Score 731.8; DB 13
Best Local Similarity 99.7%; Pred. No. 4.5e-145;
Matches 733; Conservative 0; Mismatches 2;
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TELECOMMUNICATION INFORMATION:
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FILING DATE: 06-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
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APPLICATION NUMBER: US/10/133,780
FILING DATE: 26-Apr-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Richardson P.C.
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MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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CORRESPONDENCE ADDRESS: 4
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
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; Sequence 2, Application US/10133780
; Publication No. US20020123115A1
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TELEFAX: 617/542-8906
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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STRANDEDNESS: single
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                                                                                                        Sequence 1, Application US/09728721
Patent No. US20020061845A1
GENERAL INFORMATION:
THE CARD-RELATE BETLIN, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
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Pred. No. 4.5e-145;
0; Mismatches 2;
                                                                                                                                                                                                                 FILE REFERENCE: 07334-124001
CURRENT APPLICATION NUMBER: U5/09/728,721
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: 09/340,620
PRIOR PELING DATE: 1999-06-28
PRIOR PELING DATE: 1999-06-28
PRIOR FILING DATE: 1998-12-08
PRIOR FILING DATE: 1998-06-17
PRIOR PELING DATE: 1998-06-17
PRIOR PELING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 71
SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
    1869 AAAAGGATATTTATA 1883
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Best Local Similarity 99.73
Matches 733; Conservative
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; LOCATION: (214)...(1833)
US-09-728-721-1
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ORGANISM: Homo sapiens
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                                                                    RESULT 5
US-09-728-721-1
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| Sequence 1, Application US/10105931
| Publication No. US20020150987A1
| GENERAL INFORMATION:
| APPLICANT: Bertin, John
| TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF FILE REFERENCE: 07334-07601
| CURRENT FAPPLICATION NUMBER: US/10/105,931
| CURRENT FILING DATE: 2092-06-17
| PRIOR APPLICATION NUMBER: 09/099,041
| PRIOR APPLICATION NUMBER: 09/099,041
| PRIOR FILING DATE: 1998-02-06
| NUMBER OF SEQ ID NOS: 37
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO. | LENGTH 1931
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; LOCATION: (214)...(1833)
US-10-105-931-1
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-10-105-931-1
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Publication No. US20020197693A1

GENERAL INFORMATION:

APPLICANT: Bertin, John

ITTLE OF INVENTION: AND USES THEREOF

TITLE OF INVENTION: AND USES THEREOF

TITLE OF INVENTION NUMBER: US/10/118,984

CURRENT APPLICATION NUMBER: BALLIER APPLICATION NUMBER: US/09/245,281

PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05

PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-08

PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-08

PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-08

PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-08

PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-17

PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-17

PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-06-17
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; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISH: Homo sapiens
; FAATURE:
; NAME/KEY: CDS
; LOCATION: (1833)
US-10-118-984-1
                                                                                                                                       Score 731.8; DB 13;
Pred. No. 4.5e-145;
0; Mismatches 2;
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US-10-295-981-1
Sequence 1, Application US/10295981
; Publication No. US20030120055A1
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Best Local Similarity 99.7%;
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GENERAL INFORMATION:

APPLICANT: Bertin, John
TITLE OF INVENTION: NOWED MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREC
FILE REFERENCE: 07334-12401
CURRENT APPLICATION NUMBER: US/10/295,981
CURRENT APPLICATION NUMBER: US/09/340,620
PRIOR PILING DATE: 1999-06-28
PRIOR PLING DATE: 1999-06-28
PRIOR PLING DATE: 1999-02-05
PRIOR PLING DATE: 1999-02-05
PRIOR PLING DATE: 1998-02-05
PRIOR PLING DATE: 1998-02-05
PRIOR PLING DATE: 1998-02-05
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PRECED FOR Windows Version 4.0
SEC ID NO 1
LENGTH: 1931
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Pred. No. 4.5e-145;
0; Mismatches 2; Indels 0;
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Matches 733; Conservative
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; LOCATION: (214)...(1833)
US-10-295-981-1
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ORGANISM: Homo sapiens
FEATURE:
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0y         811 GGACTATGAACTTGTTAGTACCAAGGCCTACAAGGACCTCAAAGTCAGACAATTACTAGA 870           Db         1416 GGACTATGAACTTGTTAGTACCAAGGCCTACAAGGTCAAAGTCAGACACAATTACTAGA 1475           Qy         871 CACTACTGACATCCAAGGAGAAGTTATGCCAAAGTTATAGTACAAAAATTGAAAAATTGAAAAATTGAAAAATTGAAAAAATGAAAAAA	RESULT 11 US-10-105-931-3 ; Sequence 3, Application US/10105931 ; Publication No. US20020150987A1 ; GENERAL INFORMATION:     APPLICANT: Bertin, John ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED ; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF ; FILE REFERENCE: 07334-076001 ; CURRENT APPLICATION NUMBER: US/10/105,931 ; CURRENT FILING DATE: 1908-06-17 ; PRIOR FILING DATE: 1998-06-17 ; PRIOR FILING DATE: 1998-06-17 ; PRIOR FILING DATE: 1998-06-17 ; ROFFWARE: FSELSEQ for Windows Version 4.0 ; SEQ ID NOS: 37 LENGTH: 1620	TYPE: DNA ORGANISM: Homo sapiens -10-105-931-3 Query Match Best Local Similarity 99.7%; Pred. No. 1.7e-134; Matches 683; Conservative 0; Mismatches 2; Indels 0; Gaps	Oy 331 ACASTACAGGGTTTCACTGCCATTGGGGACAGAGAAGAATGGAATGGATTTTC 390  Db 936 AAAGTTACAGGGGTTTCAAGTGCCATTCACCTATGTGACAGAAGAATGGAATTTTC 390  Oy 391 TCTGAACATACAGGGTTTCAAGTGCCACAAGAGGAATCATGTGGAATTTTC 995  Oy 392 TCTGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCA 450	QY         451 TGAAAATAGTGGTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTT 510           Db         1056 TGAAAATAGTGGTTCTCCTGAAGTCCCTGCCAGCTCCTCAAGACATGATTT 1115           QY         511 TTATCTAAAAAGCTCCAAGACTGTTATTTTATAGAACTGCATCCTCGCAAATCA 570           Db         1116 TTATCTAGAAAAGCTCAAAAACTGTTATTTTATGAAAGCTGCATCCTGGAAATCA 1175	QY         571 CAGTIGGGATAGCACCATTICTGGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCAC 630           Db         1176 CAGTIGGGATAGCACCATTICTGGATCTCAAAGGGCTGCATTCTGTGATCACAGAACCAT 1235           Oy         631 TCCATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCA 690           Db         1236 TCCATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCA 1295           Oy         691 GCCTGGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGAAACATTCTGAACCAAATGAC 750           Db         1296 GCCTGGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGAAACATTGTGAACCAAATGAC 750           CD         671 [
Db 1749 CAAACAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACTTTT 1808  Qy 991 AAATTTACTTCAAAATAAAAGCATGTAAGTGACTTTTTCAAGAAGAAATGTTTTCAT 1050	APPLICANT: Bertin, John  TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE FILE REFERENCE: 07334-124001 CURRENT APPLICATION NUMBER: US/09/728,721 CURRENT FILING DATE: 2000-12-01 PRIOR FILING DATE: 1999-06-28 PRIOR FILING DATE: 1999-06-28 PRIOR FILING DATE: 1998-06-28 PRIOR FILING DATE: 1998-06-12-08 PRIOR FILING DATE: 1998-06-17 PRIOR FILING DATE: 1998-06-17 PRIOR FILING DATE: 1998-06-17 PRIOR FILING DATE: 1998-06-17 PRIOR FILING DATE: 1998-06-17 PRIOR FILING DATE: 1998-06-06 PRIOR APPLICATION NUMBER: US 09/019,942 PRIOR APPLICATION NUMBER: US 09/019,942 PRIOR FILING DATE: 1998-06-06 TRIANG PRIOR FILING DATE: 1998-06-06 TRIANG PRIOR FILING DATE: 1998-06-06 TRIANG PRIOR FILING DATE: 1998-06-06 TRIANG PRIOR FILING DATE: 1998-06-06 TRIANG PRIOR FILING DATE: 1998-06-06 TRIANG PRIOR FILING DATE: 1998-06-06 TRIANG PRIOR FILING DATE: 1998-06-06 TRIANG PRIOR FILING DATE: 1998-06-06 TRIANG PRIOR FILING DATE: 1998-06-06 TRIANG PRIOR FILING DATE: 1998-06-06 TRIANG PRIOR FILING DATE: 1998-06-06 TRIANG PRIOR FILING DATE: 1998-06-06 TRIANG PRIOR FILING DATE: 1998-06-06 TRIANG PRIOR FILING DATE: 1998-06-06 TRIANG PRIOR FILING DATE: 1998-06-06 TRIANG PRIOR FILING DATE: 1998-06-178-178-178-178-178-178-178-178-178-178	Query Match         40.9%;         Score 681.8;         DB 9;         Length 1620;           Best Local Similarity         99.7%;         Pred. No. 1.7e-134;         Pred. Soc. 1.7e-134;         Pred. No. 1.7e-134;           Matches 683;         Conservative         0;         Mismatches         2;         Indels         0;           Qy         331 ACAGTTACAGAGTGTTTCAAGTGCCATTCACCTATGTGACAAGAAGAAAATGGAATTATC         390           Db         936 AAAGTTACAGAGTGTTTCAAGTGCCATTCACCTATGTGACAAGAAGAAGAATTATC         995	QY         391         TCTGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCA         450           Db         996         TCTGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCA         1055           QY         451         TGAAAATAGTGCTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACATT         510           Db         1056         HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII		Db

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Sequence 3. Application US/10295981

Sequence 3. Application US/10295981

Publication No. US20030120055A1

GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREF

FILE REFERENCE: 07334-124001

CURRENT PILING DATE: 1090-06-28

PRIOR FILING DATE: 1999-06-28

PRIOR FILING DATE: 1999-06-06

PRIOR FILING DATE: 1999-06-06

PRIOR FILING DATE: 1998-02-06

PRIOR PRIOR PRIOR DATE: 1998-02-06

PRIOR PRIOR PRIOR DATE: 1998-02-06

PRIOR PRIOR DATE: 1998-02-06

PRIOR PRIOR DATE: 1998-02-06

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40.9%; Score 681.8; DB 14
Best Local Similarity 99.7%; Pred. No. 1.7e-134;
Matches 683; Conservative 0; Mismatches 2;
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; ORGANISM: Homo sapiens
US-10-295-981-3
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CACTACTGACATCCAAGGAGAAGAATTTGCCAAAGTTATAGTACAAAAATTGAAAGATAA
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                                                                                    GGACTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGA
                                                                                                                                                                                                                                                                                                       CAAACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTT
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TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
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Pred. No. 1.7e-134;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/118,984
CURRENT APPLICATION NUMBER: US/10/118,984
CURRENT PILING DATE: 2002-04-09
PRIOR PILING DATE: BARLIER APPLICATION NUMBER: US, PRIOR PILING DATE: BARLIER APPLICATION NUMBER: US, PRIOR PILING DATE: EARLIER FILING DATE: 1999-02-05
PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-08
PRIOR PILING DATE: EARLIER FILING DATE: 1998-12-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US PRIOR APPLICATION NUMBER: US PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-02-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3 LENGTH: 1620
                                                                                                                                                                                                                                                                                                                                                                                                               AAATTTACTTCAAAATAAAAGCATG 1015
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Publication No. US20020197693A1
GENERAL INFORMATION:
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Best Local Similarity 99.7%;
Matches 683; Conservative
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US-10-118-984-3
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                                                                            CAGTTGGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCAT 1235
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GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT FALLING DATE:
PRIOR PELICATION NUMBER: US/09/918,995
CURRENT FILIAG DATE:
PRIOR APPLICATION NUMBER: US/09/218,096
SPIOR PRILICATION NUMBER: US/09/215,076
PRIOR PILICATION NUMBER: US/09/235,076
SPIOR PRILICATION NUMBER: US/09/235,076
SPIOR APPLICATION NUMBER: US/09/235,076
SPIOR PILICATION NUMBER: US/09/235,076
SPIOR APPLICATION UMBER: US/09/2055
SPIOR UMBER: US/09/2055
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4; Conservative
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US-09-918-995-20565
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307 TITATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCCTGGAAATCA 366
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Facent No. US20020110832A1

GENERAL INFORMATION:

APPLICANT: Pyle, Ruth

APPLICANT: Serist, Heather

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF COLON CURRENT APPLICATION NUMBER US/09/919, 580

CURRENT FILING DATE: 2001-07-30

NUMBER OF SEQ ID NOS: 934

SEQ ID NO 544

IENGTH: 299
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Best Local Similarity 97.9%; Pred. No. 1.1e-47;
Matches 274; Conservative 0; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 243
CTHER INFORMATION: n = A,T,C or G
US-09-919-580-544
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GCCTG 491
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Scoring table:

Searched:

Database

Perfect score:

Sequence:

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E 1 (Dases 1 to 1201)

S Li,W B., Gruber, C., Jessee, J. and Polayes, D.

Full-length CDNA libraries and normalization
Unpublished (2001)

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen This sequence belongs to sequence cluster 4797.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODKOIlAEO9NPl&cluster=4797.f. Contact :
Feng Liang Email: fliangpallfetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                     1201 bp mRNA linear EST 13-MAY-2003 EX401255 Homo sapiens HELA CELLS COT 25-NORWALIZED Homo sapiens CDNA clone CS0DK011Y117 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CA314123
BM973770
BE551615
AW150819
CD368863
BQ000991
BM840808
                                                               BQ008463
CB851847
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BE875947
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BE877822
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Homo sapiens (human)
Homo sapiens
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BM014010 603639652
AI824070 wj35g07.x
AW978568 EST390677
                                                                                     April 1, 2004, 02:23:55 ; Search time 4639 Seconds (without alignments) 10743.690 Million cell updates/sec
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                                                                                                                                                                   1 acctagtttatacccagata........caacagcctgatgtgtaaaa 1669
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             version 5.1.6
- 2004 Compugen Ltd.
                                                                                                                                                                                                                                  27513289 seqs, 14931090276 residues
                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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BM014010
AI824070
                                                              nucleic search, using sw model
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            GenCore
Copyright (c) 1993
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em_gss_inv:*
em_gss_pln:*
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Maximum DB seq length: 2000000000
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em_gss_fun:*
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Match Length
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46.9
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Score

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1033.4 783 732.8 721

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1571 ATATATTAATACCGGCTTCCTGTCCCCATTTTTAACCTCAGCCTTCCCTACTGTCACCAA 1630
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                                                                                                                                          195 TACAAAGGGTTATTATTAAAACTCCATTATTAGGATTACATTTTAAAGTTTTATTAT 136
255 cccrtrracccaccagagacagracagaarcccrgcccraaaarcccaggcrraarrgccc 196
                                                                                                                                                                                                                                              135 GAATTCCCTTTAAAAATGATATTTCAAAGGTAAAACAATACAATATAAAGAAAAATAA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /notes-Torgan: Dreast; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally; oligo-dT primed. Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 834)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Outputzered ... 1999/
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMISGO row: h column: 13
High quality sequence stop: 829.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                         75 ATATATATAACGGCTTMCTGTCCAMATWATAAACNTNAGCNTCCNTAATTCACCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="mammary adenocarcinoma, cell line"
/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC 87"
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46.9%; Score 783; DB 12; Length 834;
Best Local Similarity 98.0%; Pred. No. 7.5e-122;
Matches 814; Conservative 0; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAAACTCAGAACGTCTGCAGCCTGGTATAGCCCAGCAGTGKATCCAGAGGCAAAAGGGAA 916
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/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACATTGTGAAACCAAATGACAGAAGCCTGCCTTAACCAGTGGCTGAGATGCCCTTCTGTCC
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                                                                                                                                                                                                                                                                                                                           61.9%; Score 1033.4; DB 13; Length 1201; larity 97.0%; Pred. No. 6.3e-164; Conservative 6; Mismatches 25; Indels 2; (
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Location/Qualifiers
1. .1201
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COMMENT Contact: Robert Strausberg, Ph.D.  Email: cgapbs-romail.nih.gov  Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  Emmert-Buck, M.D., Ph.D.  CDNA Library Arrayed by: Greg Lennon, Ph.D.  CDNA Library Arrayed by: Greg Lennon, Ph.D.  DNA Sequencing by: Washington University Genome Sequencing Center  Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:  Naww-bio.linl.gov/bbry.lange/image.html  Insert Length: 432 Std Error: 0.00  Seq primer: -400P from Gibco  High quality sequence stop: 460.  Location/Qualifiers  1. 738 = "Homo sapiens"  Anol_type="MRN" = "Homo sapiens"  Anol_type="MRN" = "Dooled tumors (clear cell type)"  Abste="Washe: Dooled tumors (clear cell type)"  (issue type="The High State = "Dooled tumors (clear cell type)"  (issue type="The High State = "Dooled tumors (clear cell type)"  (issue type="The High State = "Dooled tumors (clear cell type)"  (issue type="The High State = "Dooled tumors (clear cell type)"  (issue type="The High State = "Dooled tumors (clear cell type)"  (issue type="The High State = "Dooled tumors (clear cell type)"  (issue type="The High State = "Dooled tumors (clear cell type)"  (issue type="The High State = "Dooled tumors (clear cell type)"  (issue type="The High State = "Dooled tumors (clear cell type)"  (issue type="The High State = "Dooled tumors (clear cell type)"  (issue type="The High State = "Dooled tumors (clear cell type)"  (issue type="The High State = "Dooled tumors (clear cell type)"  (issue type="The High State = "Dooled tumors (clear cell type)"  (issue type="The High State = "Dooled tumors (clear cell type)"  (issue type="The High State = "Dooled tumors (clear cell type)"  (issue type="The High State = "Dooled tumors (clear cell type)"  (issue type="The High State = "Dooled tumors (clear cell type)"  (issue type="The High State = "Dooled tumors (clear cell type)"  (issue type="The High State = "Dooled tumors (clear cell type)"  (issue type="The High State = "Dooled tumors (cle	Ouery Match Best Local Similarity 99.3%; Pred. No. 2.1e-113; Length 738; Best Local Similarity 99.3%; Pred. No. 2.1e-113; Length 738; Best Local Similarity 99.3%; Pred. No. 2.1e-113; Local Similarity 99.3%; Pred. No. 2.1e-113; Local Similarity 99.3%; Pred. No. 2.1e-113; Local Similarity 99.3%; Pred. No. 2.1e-113; Local Similarity 99.3%; Pred. No. 2.1e-113; Local Similarity 99.3%; Pred. No. 2.1e-113; Local Similarity 99.3%; Pred. No. 2.1e-113; Local Similarity 99.3%; Pred. No. 2.1e-113; Local Similarity 99.3%; Pred. No. 2.1e-113; Pred. No. 2	
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883 bp mRNA linear EST 12-MAR-2001
mRNA sequence.
BG393551
EG393551.1 GI:13286999
1088 TATATAAAATCCGTGAGTATTAAAGCTTTATTGAAGGTTCTTTGGGTAAATATTAGTCTC 1147
                                                                                                                                                                                 CATAGITCAATITITATGICICITITGITAACAGAAACCACITITAAAGGATAGIAAITA 1267
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATC
CODM Library Preparation: Life Technologies, Inc.
CDMA Library Preparation: Life Technologies, Inc.
CDMA Library Preparation: Life Technologies, Inc.
COMA Library Preparation: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:
http://image.llnl.gov
Plate: LiAM10471 row: e column: 12
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 883)
                          TATATAAAATCCGTGAGTATTAAAGCTTTATTGAAGGTTCTTTGGGTAAATATTAGTCTC
                                                                                                                 CCTCCATGACACTGCAGTATTTTTTTAATTAATACAAGTAAAAAGTTTGAATTTTGCTA
                                                                                                                                                                                                         378 CATAGTTCAATTTTTATGTCTCTTTTGTTAACAGAAACCACTTTTAAAGGATAGTAATTA
                                                                                          CCTCCATGACACTGCAGTATTTTTTTAATTAATACAAGTAAAAAGTTTGAATTTTGCTA
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/organism="Homo sapiens"
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                       AACTCCATTATTAGGATTACATTTTAAAGTTTTATTTATGAATTCCCTTTAAAAATGATA 1531
                                               AACTCCATTATTAGGATTACATTTTAAAGTTTTATTTATGAATTCCCTTTAAAAAATGAT 139
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Contact: John Quackenbush
The Institute for Genomic Research
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 738)
                                                                                                                                                   738 TCAAAAGTCAGACATTTACTAGCCACTTCTGACATCCAAGGAGAAGTTTGCCAAAAGTT
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/db_xref="taxon:9606"
/clone_lib="MAGE resequences,
/note="Vector: pBluescriptSKm"
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/organism="Homo sapiens"
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Catarrhini, Hominidae, Homo.

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Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4797.f F
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODLO09ABIONPl&cluster=4797.f. Contac
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODL009ABIONPl.
Location/Qualifiers
            Eukaryota; Metazoa; Chordata; Craniata; Verte
Mammalia; Butheria; Primates; Catarrhini; Hor
1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                        Contact: Genoscope
Genoscope - Centre National de Se
BP 191 91006 EVRY cedex - France
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/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally; oligg-dT primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
                                                                                                                                                             TGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCATGAAAATAGTGG
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                                                                                                                                                                                                                                                                                121 AGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCCTGGAAATCACAGTTGGGATAG
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                                                                                          Score 702.6; DB 12; Length 883; Pred. No. 2.2e-108;
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larity 98.6%;
Conservative
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CELL LINE) COT 25-NORMALIZED"

/cell\_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZE. /cell\_line="RAMOS CELL LINE" /clone\_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"

'organism="Homo sapiens" /mol\_type="mRNA" /db\_xref="taxon:9606" /clone="CS0DL009YC19"

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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR v sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                                                               41.7%; Score 695.8; DB 13; Length 1201; 97.9%; Pred. No. 2.6e-107; ive 10; Mismatches 5; Indels 0;
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BX343071 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED HOmo sapiens cDNA clone CS0DL009YC19 3-PRIME, mRNA sequence.

BX343071

DEFINITION ACCESSION VERSION KEYWORDS SOURCE

GI:30334165

sapiens (human)

BX343071.1 EST. Homo sapiens

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TCTGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCA
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VERSION
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//clone_libe_NTGIC CGAP_FT2"
//note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR 1; Site_2: Not I; NCI_CGAP_FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_TISSUE=Human Lung Aveolar Macrophage
                                                                                                                                                                                                                                                                                                                     29-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
Seg primer: M13 FORWARD
POLYA-Yes.
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230 GGACTATGAACTTGTTAGTACCAAGCCTACAAGGACBTCAAAAGTCAGACAATTACTAGA 171
                                                                                                                                                51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 744)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                        170 CACTACTGACATCCAAGGAGAAGAATTTGCCAAAGTTATAGTACAAAAATTGAAAGATAA
                                                                                                           931 CAAACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTT
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                                                                                                                                                110 CADACAAAIGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTT
                                                                                                                                                                                                                                                                                                                   CD365404 1inear EST 29-MAY.
UI-H-FT2-bjj-h-03-0-UI.s1 NCI CGAP_FT2 Homo sapiens cDNA clone
UI-H-FT2-bjj-h-03-0-UI 3', mRNA sequence.
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                                                                                                                                                                                     991 AAATTTACTTCAAAATAAAAGCATGTAAGTGACTGTTTTTCAAGAAGA 1038
                                                                                                                                                                                                          AAATTTACTTCAAAATAAAAGCATGTAAGTGACTGTTTTCWGGWNGM
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/lab_host="DH10B (Life Technologies)"
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/organism="Homo sapiens"
/or____type="mRNA"
/db xref="taxon:9606"
/clone="UI-H-FT2-bjj-h-03-0-UI"
/tissue_type="Ayeolar Macrophage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"
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CD365404.1 GI:31149494
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99.3%;
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Best Local S
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Orthoapedics CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CA413941 1inear EST 07-NOV-2002
UI-H-EZ0-bau-f-07-0-UI.s1 NCI CGAP_Ch1 Homo sapiens cDNA clone
UI-H-EZ0-bau-f-07-0-UI 3', mRNA sequence.
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
                                                                                                                                                                                                                                       570
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 709)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 CACTACTGACATCCAAGGAGAAGAATTTGCCAAAGTTATAGTACAAAAATTGAAAGATAA
TITATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCCTGGAAATCA
                                                                                                                                                                                                                                                                                                         540 TINATCIAGAAAAGCICAAGACIGITATITIAIGAAGCIGCAICACIGICCIGGAAAICA
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                                                                                                                                           600 TGAAAATAGTGGTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTT
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                                                                                                   TGAAAATAGTGGTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTT
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The following repetitive elements were found in this cDNA
sequence: 1-64, >AT_rich#Low_complexity (matched compliment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  991 AAATTTACTTCAAAATAAAGCATGTAAGTGACTGTTTTTCAAGAAGAAA 1040
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Homo sapiens (human)
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EST 02-MAY-2003
   169 TTTATATATCTCTGTTGCTTTTGACTTTTTTTTAAAATCCGTGAGTATTAAAGCTTTTATT 110
                                                                                                                                                                                                                                                                                                                                                                                                                              1201 bp mRNA linear EST 02-MAY-200;
ACENTA COT 25-NORMALIZED Homo sapiens CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4797.f For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq=CSODIO37AA04NPl&cluster=4797.f. Contact
Feng Liang Email : filangalifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODIO37AA04NPl.
                                                                                               109 GAAGGTTCTTTGGGTAAATATTAGTCTCCCTCCATGACACTGCAGTATTTTTTTAATTA
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                                                                                                                                                                                                                                                                                                                                                                                                                              LAU1 DP MRNA LAU1 DP MRNA Clone CSODI037YA07 3-PRIME, MRNA BEGUENCE. BX337147
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/db_xref="taxon:9606"
/clone="CS0DI037YA07"
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BX337147/c
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/doctor libe "NOT CAPP CHI"
/doctor libe "NOT CAPP CHI"
/note "Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NOT CAPP CHI is a cDNA library containing the following
tissue(8): Chondrosarcoma Grade II. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonuclectide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property contains and the property c
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                                                                                                                                                                                                                         /clone="UI-H-E20-bau-f-07-0-UI"
Fitssue type="Chondrosarcoma Grade II"
/dev stage="Adult"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAG_TISSUE=grade-2-chondrosarcoma
TAG_LIB=UI-H-EZ0
TAG_SEQ=ATCTAATATG"
                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                Location/Qualifiers
Seq primer: M13 FORWARD POLYA=Yes.
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UI-H-EDI-ayk-k-19-0-UI.sl NCI_CGAP_ED1 Homo sapiens cDNA clone
IMAGE:5840010 3', mRNA sequence.
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CODA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov
POLYA=Yes.
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                       CAGTTGGGATAGCACCATTTCTGGATCTCAAAGGCTGCATTCTGTGATCACAAGACCAC
                                                                                         TCCATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCA
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                                                                                                                                                                                                                         CAGTTGGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCAC
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                                                                   TCCATGCTCTTCAGCAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCA
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/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:5840010"
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TITLE
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KEYWORDS
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/note="Organ: Left Public Bone; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: ECOR I; Site 2: Not I; NCI CGAP_ED1 is a normalized CDNA library containing the following tissue(s): Chondrosarcoma cell line CS5. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GCTCAAGGCT.
TAG_INB-U1-H-ED1
TAG_SEQ=CGTCAAAGGCT"
'clone lib="NCI CGAP ED1"
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5 473 372 833 312 672 533 612 593 552 653 492 713 432 773 611 GTTATTTTATGAAGCTGCATCACTGTCCTGGAAATCACAGTTGGGATAGCACCATTTCTG 431 recagadeaaaagggaagacarrergaaceaaargacagaageergeerraaceagrege 774 TAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGGACTATGAACTTGTTAGTACCA 729 GTCCACAAGAGGAATCATGTGGA-CCTCTCAGCTCCATGAAAATAGT-GTTCTCCTGAAA 551 GATCTCAAAGGGCTGCATTCTGTGATCACAAGACCACTCCATGCTCTTCAGCAATAATAA 491 ATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAGCCTGGTATAGCCCCAGCAGTGGA GTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCATGAAAATAGTGGTTCTCCTGAAA GITAITITAIGAAGCIGCATCACIGICCIGGAAATCACAGIIGGGAIAGCACCATITCIG GATCTCAAAGGGCTGCATTCTGTGATCACAAGACCACTCCATGCTCTTCAGCAATAATAA ATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAGCCTGGTATAGCCCAGCAGTGGA Gaps 2; Length 734; Indels .. ); DB 12; 4.7e-106; 0; Mismatches Score 689; Pred. No. 4 41.3%;

191 ACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAAATTTACTTCAAAATAAAAGCA 132 ACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAAATTTACTTCAAAATAAAGCA TGTAAGTGACTGTTTTTCAAGAAGAATGTGTTTTCATAAAAGGATATTTATATCTCTGTT

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131 TGTAAGTGACTGTTTTTCAAGAAGAATGTGTTTCATAAAAGGATATTTATATATCTCTGTT .074 GCTTTGACTTTTTTTTTATAAAATCCGTGAGTATTAAAAGCTTTATTGAAGGTT 1126 19 GCTTTGACTTTTTTTTATATAAATCCGTGAGTATTAAAAGCTTTATTGAAGGTT

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Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procuremnt: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@ulowa.edu
The following repetitive elements were found in this cDNA
sequence: 1.22, AAT_rich#Low_complexity (matched compliment)
Seq primer: M13 FORWARD
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BQ774940 11near EST 26-JUL-2002 UI-H-FH0-bcd-1-20-0UI.sl NCI CGAP_FH0 Homo sapiens cDNA clone UI-H-FH0-bcd-1-20-0-UI 3', mRNA sequence.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                   297 TCTGTCCAGGGACTTGATCATGAAAGAGGACTATGAACTTGTTAGTACCAAGCCTACAAG
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                                               537 GAAGCTGCATCACTGTCCTGGAAATCACAGTTGGGATAGCACCATTTCTGGATCTCAAAG
                                                                                            GGCTGCATTCTGTGATCACAAGACCACTCCATGCTCTTCAGCAATAATACAATCCTCTC
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="UI-H-FH0-bcd-1-20-0-UI"
/tissue_type="Human Chondrosarcoma Cell Line"
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/tasue_type="Human Lung Epithelial cells"
/lab_host="DHJUB (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-FN0"
/note="Grgan: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-CF-FN0 is a subtracted cDNA library derived from two normalized Human lung epithelial cell libraries (EN1 and DU1) The library was subtracted according to according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1966. For additional information, contact:
                                             CB851847 11near EST 22-APR-2003
UI-CF-FN0-aem-o-20-0-UI.sl UI-CF-FN0 Homo sapiens cDNA clone
UI-CF-FN0-aem-o-20-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: paul-mcray@wliowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Blosystems
(www.openblosystems.com)
The following repetitive elements were found in this cDNA
sequence: 1-24, AAT_rich#Low_complexity (matched compliment)
BOLYA=Yes.
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                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. [1 (bases 1 to 715)]
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Matches 699; Conservative
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BI257472 812 bp mRNA linear EST 17-JUL-2001
602967861F1 NIH_MGC_12 Homo sapiens CDNA clone IMAGE:5107310 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life Technologies."
                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 812)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Enall: cgapbs-r@mail.nih.gov
Tissue procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
DNA Asquencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can letus; //image_llnl.gov
http://image_llnl.gov
Plate: LiAMIL159 row, j column: 15
High quality sequence stop: 806.
Location/Qualifiers
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/lab host="DH10B"
/clone_lib="NIH_MGC_12"
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ilarity 97.6%; Pred. No. 3.2e-101;
Conservative 0; Mismatches 15;
53 GCTTTGACTTTTTTTTATATAAAATCCGTGAGTATTAAA
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/db_xref="taxon:9606"
/clone="IMAGE:5107310"
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EST.
                                                                                                                                                                                                                                                             Homo sapiens (human)
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             /lab_host="DATOR (Life Technologies)"
/lab_host="NATOR GAP FH0"
/clone lib="NOI CGAP FH0"
/note="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: BcoR 1; Site 2: Not 1;
NOI CGAP FH0 is a cDNA library containing the following tissue(s): Human Grade according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer scheduling a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, disested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGAARCGGC. The cell line was provided by Dr James Martin from University of Iow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1073
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Pred. No. 2.3e-103;
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TAG_SEQ=AGAATCCGGC"
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BE875947
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                                                                                                          645
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTP/DTP/Gazdar
Tissue Procurement: DCTP/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9669 row: n column: 06
High quality sequence stop: 795.
                   526
                                          810
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                                                                                                                              CACTACTGACATCCAAGGAGAAGAATTTGCCAAAGTTATAGTACAAAAATTGAAAGATAA 930
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to, 828)
          467 GCCTGGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAAATGAC
                                                      AGAAGCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCA-GGACTTGATCATGAAAGA
                                                                                   GGACTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGA
                                                                                               105 CAAACAAATGGGTCTTCAGGCCTTACCCGGAAATACTTGTGGTTCTAGATCACCATCTTT
                                          AGAAGCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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39.4%; Score 657.2; DB 10;
Best Local Similarity 96.8%; Pred. No. 9.5e-101;
Matches 726; Conservative 0; Mismatches 13;
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403 TGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCATGAAAATAGTGG 462

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CB852764 683 bp mRNA linear EST 22-APR-2003 UI-CF-FNO-aex-p-08-0-UI.51 UI-CF-FNO Homo sapiens cDNA clone UI-CF-FNO-aex-p-08-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                 762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 663 TATATCTCTGGTG--TTGACTTTTTTTTATAAA----TCCGGAGTATAAGCTTATTGA 715
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 683)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                        63
                                                                                           523 AGCTCAAGACTGTTATTATGAAGCTGCATCACTGTCCTGGAAATCACAGTTGGGATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACACTACTGACAT
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CACCATTTCTGGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCACTCCATGCTCTTC
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McCray Lab
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MEDLINE
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COMMENT
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/clone="UI-CETSNICTOR"
/(issue_type="Human Lung Epithelial cells"
/lab_host="MulloB (Life Technologies) (TI phage resistant)"
/(lone lib="UI-CE-FNO"
/(lone lib="UI-CE-FNO"
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                                                                                                                                                                Tissue Procurement: Dr. M. J. Welsh, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research (www.openbiosystems.com) or from Open Biosystems from Research POLYA-Yes.
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Email: paul-mccray@uiowa.edu
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RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC; caspase-10; CD95 signalling; apoptosis signalling pathway; CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation; gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS; aplastic anaemia; ischaemic injury; toxin-induced liver disease.
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-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USFTO_spool_p/US09771161/runat_29032004_124824_13654/app_query.fasta_1.1863
-Q=/cgn2_1/USFTO_spool_p/US09771161/runat_29032004_124824_13654/app_query.fasta_1.1863
-Q=/cgn2_1/USFTO_spool_p/USFGERIAN_FIRENTENDELSON_1-LOOPECL=0
-LOOPETTO_0-UNITS=bits -START=1 -END--1 -MATRIX-blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -TRR*SGORE=pct -TRR*NI=NX=100 -TRR*NIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -WORM=ext -HPAPSIZE=500 -MINIEN=0 -MAXIEN=200000000
-USFR-USO9771161 - GCGN - GWAT - PSPBLOCK=100 -LONGLOG
-NO MMAP - LARGEQUERY -NEG-SCORES=0 -WAIT - DSPBLOCK=100 -LONGLOG
-TRR*NIN=0 -LARGEQUERY -NEG-SCORES=0 -WAIT - NET SPBLOCK=100 -LONGLOG
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11572.314 Million cell updates/sec
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Aay59404 B
Aaw92795 B
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Aae27882 B
Aab43570 B
Aay31140 B
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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This sequence is a fragment of the human RICK (RIP-like interacting CLARP kinase) protein of the invention. RICK acts as a positive regulator of apoptosis, protein of the invention. RICK acts as a positive regulator of apoptosis, protein and activators, and methods and compositions signalling pathway inhibitors and activators, and methods and compositions for screening compounds which will modulate the interactions of the various compositions identified. ARC, RICK, and the CIDE family of activators (CIDE-A, USE-I). RICK is useful in screening assays for agents, useful in the diagnosis, prognosis or treatment of disease associated with excess cell growth and dysregulation of apoptosis. Overexpression of ARC and CLARP can be used in drug screening assays to identify inhibitor molecules blocking CD95-mediated apoptosis. Overexpression of ARC in an in vitro cell system can be used to identify inhibitors of the enzymatic activity of caspase-8 concanion of ARC-like inhibitory compounds may be useful for gene therapy treatment of disease with increased cell death in muscle tissue and cardiac disorders. Therapeutic compositions of CIDEs can be used to treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia, ischaemic injury, and toxin-induced liver disease. AntiRICK antibobies can be used as reagents for the preparation or affinity chromatography media, and for diagnostically measuring RICK levels. A specific inhibitor of an essential step in the biochemistry of apoptosis is needed. RICK interaction with intracellular factors such as CLARP and ADD appears to che essential for apoptosis, inhibitors of RICK binding to intracellular apoptosis factors are potential drug candidates. Note: This sequence was considered using information given in the specification. Claim 6; Page; 93pp; English. 

Sequence 284 AA;

Conservative: Mismatches: Length: Matches: Indels: Gaps: US-09-771-161A-2 (1-1669) x AAY59406 (1-284) 2.52e-119 1182.00 .99.56% 41.048 Percent Similarity: Best Local Similarity: Alignment Scores: 392 Query Match: DB: .. No.: ò a à

CAGTTACAGAGTGTTTTCAAGTGCCATTCACCTATGTGACAAGAAAAATGGAATTATCT 391 CTGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCAT 17 유

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117 LeuSerArginysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 136 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCCTGGAAATCAC 512

AGTIGGGATAGCACCATITCTGGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCACT CCATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAG 137 572

631 156 691 176 751

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GAAGCCTGCCTTAACCAGTCCCTAGAGCCCTTCTGTCCAGGGCTTGATCATGAAAGAG GlualaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu

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236 871 932 AAACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTA 812 GACTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGAC 872 ACTACTGACATCCAAGGAGAAGTTTGCCAAAGTTATAGTACAAAAATTGAAAGATAAAC 992 AATTTACTTCAAAATAAAAGCATG 1015 277 AsnLeuLeuGlnAsnLysSerMet 284 g ò 셤 셤 8 ò

AAY59405 standard; protein; 478 AA. AAY59405

AAY59405;

21-MAR-2000 (first entry)

Human RICK protein sequence residues 54-531.

RICK, human, RIP-like interacting CLARP kinase, apoptosis regulator; ARC, caspase-8; caspase-10; CD95 signalling, apoptosis signalling pathway; CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation; gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS; aplastic anaemia; ischaemic injury; toxin-induced liver disease. 

Homo sapiens

W09955134-A2.

04-NOV-1999.

99WO-US009183. 27-APR-1999;

98US-00069023 27-APR-1998;

(UNMI ) UNIV MICHIGAN

Nunez G, Inohara N, Koseki

VPI; 2000-072163/06.

Compositions for identifying apoptosis signaling pathway inhibitors useful for treating diseases.

Claim 6; Page; 93pp; English.

kinase) protein of the invention. RICK acts as a positive regulator of apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10 apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10 during CD95 signalling. The invention provides methods for identifying apoptosis signalling pathway inhibitors and activators, and methods and compositions for screening compounds which will modulate the interactions of the various compositions identified: ARC, RICK, and the CIDE family of activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening assays for agents, useful in the diagnosis, prognosis or treatment of disease associated with excess cell growth and dysregulation of apoptosis. Complexes containing RICK and CLARP can be used in drug screening assays to identify inhibitor molecules blocking CD95-mediated apoptosis. Overexpression of ARC in an in vitro cell system can be used to the continuous inhibitors of the enzymatic activity of caspase-8.

The continuous compositions of the enzymatic activity of caspase-8.

The charty treatment of disease with increased cell death in muscle tissue therapy treatment of disease with increased cell death in muscle tissue. sequence is a fragment of the human RICK (RIP-like interacting CLARP) or protein of the invention RICK acts as a positive regulator of Therapeutic compositions of CIDEs can be used to , neurodegenerative disorders; aplastic anaemia, rreat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia ischaemic injury, and toxin-induced liver disease. AntiRICK antibodies cardiac disorders.

use-8; caspase-10; CD95 signalling; apoptosis signalling pathway; A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation; therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;

CLARP kinase;

human; RIP-like interacting

Human RICK protein sequence.

aplastic anaemia; ischaemic injury; toxin-induced liver disease.

Homo sapiens

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 350
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used as reagents for the preparation or affinity chromatography
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AAY59404 standard; protein; 531 AA

RESULT 3
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AAY59404

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protein of the invention. The RICK protein acts as a positive regulator of apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10 during CD95 signalling. The invention provides methods for identifying apoptosis signalling apoptosis inventions and activators, and methods and compositions for screening compositions dentified. RICK, and the CIDE family of activators (CIDE-A, CIDE-B and DREP-1). RICK, and the CIDE family of assays for agents, useful in the diagnosis, prognosis or treatment of assays for agents, useful in the diagnosis, prognosis or treatment of assays for agents, useful in the diagnosis, prognosis or treatment of assays complexes containing RICK and CLARP can be used in drug screening assays to identify inhibitor molecules blocking CD95-mediated of apoptosis. Overexpression of RRC in an in vitro cell system can be used to identify inhibitors compounds may be useful for gene Identify inhibitors compounds may be useful for gene Identify inhibitors with increased cell death in muscle tissue therapy treatment of disease with increased cell death in muscle tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and cardiac disorders. Therapeutic compositions of CIDEs can be used to treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia, ischaemic injury, and toxin-induced liver disease. AntiRICK antibodies can be used as reagents for the preparation or affinity chromatography media, and for diagnostically measuring RICK levels. A specific inhibitor of an essential step in the biochemistry of apoptosis is needed. RICK interaction with intracellular factors such as CLARP and FADD appears to be essential for apoptosis, inhibitors of RICK binding to intracellular apoptosis are potential drug candidates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Compositions for identifying apoptosis signaling pathway inhibitors
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Boldin M,
                  WPI; 1999-070258/06.
N-PSDB; AAX02558.
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Best Local Similarity:
Query Match:
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                                                                                               TTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCCTGGAAATCAC
                                                                                                                                      AGTTGGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCACT
                             LeuAsnIleProValAsnHisGlvProGlnGluGluSerCvsGlvSerSerGlnLeuHis
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                                                         GAAAATAGTGGTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTT
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cell survival pathway; intracellular signalling; AIDS; cancer; human
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11-SEP-1997;
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New B1 protein regulates cell death and cell survival pathways -derivatives, DNA and antibodies, also regulate intracellular inflammation; for treating AIDS, cancer.
                                                                                                                                                                            This invention describes the isolation of a novel human B1 protein which can interact with, intracellular mediators or modulators of inflammation, cell death and/or cell survival pathways, directly or indirectly. Cells can be modulated or mediated in inflammation, cell death or cell survival pathways or another intracellular signalling activity using B1. Conditions such as A1DS and cancer can be treated using B1. Antibodies, oligonucleotides and ribozymes can also be used to regulate the above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             493 ThrThrAspIleGlnGlyGluGluPheAlaLysVallleValGlnLysLeuLysAspAsn
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98US-0155196P. 98US-0155239P. 98US-0106889P. 98US-0109031P. 98US-0113796P.

99WO-US017132. 98US-0155213P.

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14-SEP-1998;
14-OCT-1998;
03-NOV-1998;
19-NOV-1998;
22-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                  AAY68769-95 and AAY68797-99 represent human phosphorylation effectors (PHSP), designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not gluon in the specification). The sequences were isolated from cDNA libraries prepared from various human tissues. The PHSP proteins are useful for the diagnosis, treatment and prevention of proliferative disorders, immune disorders and neuronal disorders. The PHSP proteins form pharmaceutical compositions which useful for treating or preventing disorders associated with decreased PHSP expression/activity. PHSP antagonists are useful for treating or preventing disorders associated with increased PHSP expression/activity.
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H, Azimzai Y;
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prevention of proliferative, immune and neuronal disorders.
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n O, Au-Young J, Gorgone GA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primers useful for synthesizing full length cDNA clones and their use
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                                                                                                  GACTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGAC 871
                                                                                                                                                                ACTACTGACATCCAAGGAGAAGATTTGCCAAAGTTATÄGTACAAAAATTGAAAGATAAC 931
                                                                                                                                                                                                                                                                              AAACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTA 991
               GAAGCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAG
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K, Kojima S, Otsuki T, Koga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; full length cDNA; cDNA synthesis; oligo-capping
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Wakamatsu A, Sugiyama T, Nagai
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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The invention relates to antisense compounds targetted to a nucleic acid encoding human receptor interacting protein (RIP)2 to inhibit its expression. Antisense compounds are used for treating diseases associated with RIP2 expression. They are also useful in antisense gene therapy. The present sequence is human RIP2 protein
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                                                                                                                                                                                                GACTATGAACTTGTTAGTACCAAGGCTACAAGGACCTCAAAAGTCAGACAATTACTAGAC 871
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; receptor interacting protein; RIP2; antisense; gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                         for treating and/or preventing cytomegalovirus (CMV) infection and/or related diseases. The method of the invention comprises contacting a test compound with at least one of the cellular kinases Ruck, RIP, NGK-Interacting kinase, MKK3 and SRRY-2 and detecting any change in kinase activity. The method of the invention can be used to treat and/or prevent CMV infections and related diseases. Oligonucleotides that can detect the specified kinases can also be used for diagnosis of infection. The present amino acid sequence represents the human cellular kinase RICK protein of the invention, as described above
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                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a new method for identifying compounds
                                                                                                                                                                                                                                                                                                  infection, comprises contacting test compound with cellular kinase and detecting change in cellular kinase activity.
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   RIP; Nck-Interacting kinase; MKK3; SRPK-2.
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                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 23-24; 49pp; English.
                                                                                                                                15-OCT-2001; 2001EP-00124604.
                                                                                                                                                                16-OCT-2000; 2000US-0240750P
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                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuasnIleProValasnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis
                                                                                                                               GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe
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                                                                         CTGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCAT
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                                                                                                                     GAAAATAGTGGTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTT
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Homo sapiens

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AAC77607 to AAC7848 encode the human cancer associated proteins given in AAG43398 to AAB4239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antialergic; antiacthritic; antinflammatory; antithyroid; antialergic; antibacterial; antiviral; certainfolgical; neuroprotective; cardiant; thrombolytic; coagulant; coorropic; vasotropic; antipsoriatic and antianglogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides and diagnosing pathological conditions. Co inhibiting the proliferation, differentiation or mobilisation of cimmune cells, to treat disorders immune disorders by activating cor inhibiting the proliferation, differentiation or mobilisation of ciscular disorders, allergic reactions, graft versus host disease and organ calection, modulate haemostatic or thrombolytic activity, modulate conference inflammation, cancers, cardiovascular disorders, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to the versus invarient sequences used in the exemplification of the present invarient sequences used in the exemplification of
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                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer.
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08-MAR-2000; 2000WO-US005882.
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                                                                                                                         (HUMA-) HUMAN GENOME
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N-PSDB; AAC77779.
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Query Match:
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caspase recruitment domain, CARD-4; regulation; detection; caspase activation; detection; screening; therapy; diagnosis; disease; apoptotic cell death; Fas/APO-1 receptor complex; TWF receptor complex; cancer; follicular lymphoma; carcinoma; p53 mutation; viral infection; hormone-dependent tumour; autoimmune disorder; Alzheimer's disease; systemic lupus erythematosis; immune-mediated glomerulonephritis; stroke; parkinson; s disease; amyotrophic lateral sclerosis; retinitis pigmentosa; spinal muscular dystrophy; cerebellar degeneration; anaemia; drug; myelodysplastic syndrome; myocardial infarction; cell proliferation; cell differentiation; cell survival; CARD-41; CARD-45; CARD-42;
SerTrpAspSerThr11eSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 416
                          CCATGCTCTTCAGCAATAATAAATCCCCTCTCAACTGCAGGAAACTCAGAACGTCTGCAG 691
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                                                                                                                        GAAGCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAG
                                                                                                                                                                        GACTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGAC
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432. .540
/note= "predicted CARD domain"

    .300
    /note= "predicted kinase domain"
    .431

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17-JUN-1998;
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This invention describes the isolation of novel human caspase recruitment domain, CARD-1 and CARD-4 polynucleotides and proteins and a partial article domain, CARD-4 protein and genes and proteins of the invention are involved in the regulation of caspase activation. The caspase activation are involved in the regulation of caspase activation. The caspase activation are bused in screening assays, detection assays, predictive methodies can be used in screening assays, detection assays, predictive methodies may be used to diagnose and treat patients which are suffering methodis may be used to diagnose and treat patients which are suffering death, abnormal activity of the TMF receptor complex, abnormal activity of the TMF receptor complex, abnormal activity of the TMF receptor complex, or abnormal activity of a caspase. Complexes that may be treated include cancer (particularly follicular lymphoma, carcinomas associated with muttations in p53 and hormone-capped the caspase that may be treated include cancer (particularly follicular lymphoma, carcinomas associated with muttations in p53 and hormone-capped particularly associated with mutuations in p53 and hormone-capped particularly follicular lymphoma, carcinomas associated with mutuations in p53 and hormone-capped particularly follicular lymphoma, spinal muscular dystrophy, cerebellar degeneration, ansemia, myelodysplastic syndrome, myocardial infarction, and stroke. CARD-3 protein interacts with other cellular proteins, and so can be used for regulation of cellular proliferation and differentiation and cell correctly and capped compounds which modulate their activity. The CARD-4 gene can express a compounds which modulate that a activity. The CARD-4 and CARD-4 sor two CARD-4 splice variants, CARD-4 and CARD-4. and secured correctly represents the human CARD-3 protein described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGGATCCTCTCAGCTCCAT 451
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                                                                                                                              Novel CARD-3 and CARD-4 genes and polypeptides used or treating regulation of cellular proliferation and differentiation and cell
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Matches:
Conservative:
Mismatches:
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1176.00
99.56%
99.12%
40.83%
                                                                                                                            CARD-4
                                                            WPI; 1999-494269/41.
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Best Local Similarity:
                                                                                     N-PSDB; AAZ09246.
                                                                                                                            Novel CARD-3 and
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                                                                                                                                                                      survival.
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ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated intracellular proteins predicted to be involved in regulating caspase activation are used for diagnosis and treatment of e.g. cancer, viral infections, autoimmune diseases, neurological diseases and hematological disorders.
                                                                                                                                                                                                                                                                                                                                                                  CARD-3; caspase recruitment domain; human; cancer; infection; autoimmune disease; neurological disease; haematological disease; immune disease; inflammation; antitumour; antiseptic; immunomodulator; antiinflammatory; apoptosis; diagnosis; gene therapy.
                              ACTACTGACATCCAAGGAGAAGAATTTGCCAAAGTTATAGTACAAAAATTGAAAGATAAC
                                                                                                                                                     ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn
                                                                                                                                                                                             CCTGGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAAATGACA
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/note= "kinase domain"
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/note= "linker
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/note= "CARD"
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                                                                                                                                                                                                                                                                                                                                                 Human CARD-3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        401.
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N-PSDB; AAF30001.
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The present sequence is that of human caspase recruitment domain 3 (CARD-3), an intracellular protein predicted to be involved in regulating caspase activation. The sequence is predicted from an isolated CDNA clone (see AAF30001). Methods of diagnosing and treating patients suffering from a disorder associated with an abnormal level or rate of apoptotic cell death, abnormal activity of the Fas/APO-1 receptor complex, abnormal activity of a caspase involve administering a compound that modulates the activity of a caspase involve administering a compound that modulates the expression or activity of ASRD-3, CARD-5 or CARD-6 e.g. using capter therapy methods. Such disorders include cancer, viral infection, cautoimmune disorders, neurological disorders, viral infection, contominated disorders. CARD-3, -4, -5 and -6 or proteins can be used to regulate cell proliferation, cell survival and cell growth. They can also be used to screen drugs or compounds that. Cell growth. They can also be used to screen drugs or compounds that. Cell modulate their activity or expression and to treat disorders associated with insufficient or excessive production of CARD-3, -4, -5 or -6 or -6 protein, or production of an aberrant protein
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Best Local Similarity:
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Co bypeptide with a by contacting the polypeptide with a test compound and determining the effect of the test compound on the activity of the collypeptide to identify a compound which binds to the IRR (lough may be adapted for identifying a compound which binds to the IRR (loucine rich repeat) domain of CARD-4. Also included is a method of identifying a candidate compound for modulating LPS, (loopolysaccharide).

Comediated activation of nuclear factor-kappa B (NF-kB), by providing a cell expressing a polypeptide comprising the LPR domain of CARD-4 and harbouring LPS, exposing the cell to a test compound and measuring NF-kB activation polypeptide in the presence of the test compound indicates that the test compound is a candidate compound for modulating LPS-mediated activation of NF-kB. Modulators identified by (MI) are useful for treating a disorder such as cancer, viral compound infections, autoimmune disorders such as cancer, viral infections, autoimmune disorders e.g. systemic lupus erythematosus, immune-mediated glomerulosephatis and arthritis, immune disorders is munitalle sclerosis, Hashimoto's thyroiditis, atopic conditions such as asthma, allergies, insulin-dependent diabetes, bacterial infections, including tuberculosis, and lepromatous leprosy, disorders of cell signalling and tuberculosis, and lepromatous leprosy, disorders of cell signalling and
                                                                                                                                                                                                                                   Human; caspase recruitment domain; CARD-3; CARD-4; LRR; leucine rich repeat; LPS; lipopolysaccharide; NP·kB; muclear factor-kappa B; cancer; viral infection; autoimmune disorder; systemic lupus erythematosus; immune-mediated glomerulonephritis; arthritis; immune disorder; multiple sclerosis; Hashimoto's thyroiditis; atopic condition; asthma; allergy; psoriasis; contact dermatitis; gastrointestinal allergy; insulin-dependent diabetes; bacterial infection; tuberculosis; lepromatous leprosy; cell signalling disorder; tissue disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying modulators of long form of caspase recruitment domain, (4b useful for treating cancer, infections, and immune disorders, by contacting test compound with CARD-4L and determining effect of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sansonetti P, Girardin S;
                                                                                                                                                                                                       Human caspase recruitment domain protein CARD-3.
           Example 2; Fig 2; 139pp; English
                                                                                                        ABG31075 standard; protein; 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39-DEC-2000; 2000US-0258724P.
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                                                                                                                                                                      21-OCT-2002 (first entry)
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N-PSDB; ABK89280.
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disorders of tissues. The present sequence represents human CARD-3
                                                                                                           Conservative:
Mismatches:
Indels:
                                                                                  Length:
Matches:
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Best Local Similarity:
                                         Sequence 540 AA
                                                                   Alignment Scores:
Pred. No.:
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The invention relates to novel isolated Caspase Recruitment Domain (CARD) polypeptides, CARD-41 and CARD-45. The CARD proteins of the invention may polypeptides, CARD-41 and CARD-45. The CARD proteins of the invention may be used to treat disorders associated with decreased CARD expression by supplementing the patient's own production of CARD. Disorders associated with the expression and activity of CARD include cancers (particularly follicular lymphomas, carcinomas associated with mutations in p53, and covarian cancer, autoimmune disorders (such as systemic lupus erythematosus, immune-mediated glomerulonephritis), viral infections, eurological diseases by herpes viruses, parkinson's disease, amylotrophic lateral sclerosis (ALS) retinitis pigmentosa, spinal muscular atrophy, and various forms of careballar degeneration), anaemia associated with chronic disease, aplastic anaemia, chronic neutropenia, and the myelodysplastic syndromes. This sequence represents a human CARD protein relating to the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cerebroprotective; antiparkinsonian; antisolerotic; ophthalmological; nootropic; antianaemic; Caspase Recruitment Domain; CARD; CARD-4L; p53; cancer; CARD-4S; follicular lymphoma; carctinoma; autoimmune disorder; hormone-dependent tumour; breast cancer; prostate cancer; systemic lupus; herpes virus; poxvirus; adenovirus; neurological disease; anaemia; neutropenia; myelodysplastic syndrome; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated Caspase Recruitment Domain (CARD) polypeptides (CARD-4L and CARD-4S) useful for diagnosing and treating e.g. Parkinson's and Alzheimer's disease, cancers and viral infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCAT
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98US-00099041.
98US-00207359.
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                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PHARM INC
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N-PSDB; AAL40752, AAL40753.
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Best Local Similarity:
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Pred. No.:
                                                                                                                                 Homo sapiens
                                                                                                                                                                US6369196-B1
                                                                                                                                                                                                                               05-FEB-1999;
                                                                                                                                                                                                                                                                                 17-JUN-1998;
08-DEC-1998;
                                                                                                                                                                                                                                                                06-FEB-1998;
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and CARD

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      AGTIGGGAIAGCACCAITICIGGAICTCAAAGGGCTGCAITCIGIGAICACAAGACCACT 631
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                                                                                                                                         The invention relates to an isolated polypeptide, comprising at least 25 contiguous amino acids of a human caspase recruitment domain (CARD)-47, human CARD-42 or murine CARD-4L (all splice variants of CARD-4) comprising the collaboration of the comprising the polypeptide. Also included is an isolated fusion protein, comprising the collaboration polypeptide is useful in screening assays, collaboration polypeptide. The CARD polypeptide is useful in screening assays, detection assays (e.g. chromosomal mapping, tissue typing and forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, controling clinical trials and pharmacogenomics), and in therapeutic and prophylactic treatments (in diseases associated with apoptotic call death comprophylactic treatments (in diseases associated with apoptotic and prophylactic treatments (in diseases associated with apoptotic and communodeficiency syndrome), neurological disease (e.g. systemic lupus erythematosus and immunodeficiency syndrome), neurological disease (e.g. Alzheimer's disease, parkinson's disease, amyotrophic lateral sclerosis, retinitis configuration and stroke). The CARD polypeptide is susful as bait protein in a two-hybrid assay or three hybrid assay to identify other proteins, which bind to or interact with other CARD proteins. Also disclosed are CARD-3 proteins and cDNAS. The gene for human CARD-4 is located on chromosome 7. The present sequence is a human human CARD-4 is located on chromosome 7. The present sequence is a human human CARD-4 is located on chromosome 7. The present sequence is a human human CARD-4 is located on chromosome 7. The present sequence is a human care and continue of the care and continue to the care and care and care and care and care and care and care and care and care and care and care and care and care and care and care and care and care and care and care and care and care and care and care and care and care and care and care and care and care and care and care and care and care and care and care and care an
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                                   Novel isolated human caspase recruitment domain (CARD)-4Y or CARD-4Z polypeptide, or murine CARD-4L polypeptide, useful in screening assays, detection assays, predictive medicine, and in therapeutic applications.
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Best Local Similarity:
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Detecting compounds which alter binding of the caspase recruitment domain (CARD) of CARD-3 polypeptide to the neurotrophin receptor p75 is useful to provide compounds for treating CARD-3 mediated disorders.
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GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472
                               871
                                              This invention relates to two novel genes CARD-3 and CARD-4 (caspase recruitment domains), which are mediators of apoptosis and are useful in the identification of compounds that modulate apoptosis. Specifically, CARD-3 (also known as RIP2, RICK and CARDIAK) is known to be a mediator of p75 (a member of the tumour necrosis factor (TNF) family), and is
                                                                                                                                                                                                                                                                                                                                                                                                                                        human, CARD-3; CARD-4; caspase recruitment domain; apoptosis; p75; tumour necrosis factor; TNF; neutrophin receptor; cancer; autoimmune disorder; systemic lupus; immune mediated glomerulonephritis; viral infection; neurological; retinitis pigmentosa; haematologic; chronic neutropenia; myocardial infarction; stroke; RIP; RICK; CARDIAK.
                                                                                                            ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLsBAspAsn
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                                                                                            872 ACTACTGACATCCAAGGAGAAATTTGCCAAAGTTATAGTACAAAAATTGAAAGATAAC
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mediated by this p75 neutrophin receptor. Accordingly these genes, and the provide the switch for cell survival and cell death decisions mediated by this p75 neutrophin receptor. Accordingly these genes, and the process of the proteins encoded thereof, are linked to certain disorders associated with an increased number of cells surviving and proliferating when apoptosis is inhibited. These include cancer, autoimmune disorders e.g. systemic lupus and immune mediated glomerulomephitis, viral infections such as those caused by the herpesvirus, neurological disorders such as retinitis pigmentosa, haematologic diseases including chronic retinitis pigmentosa, haematologic diseases including chronic invention further describes a novel method for determining whether a test compound alters the binding of CARD-3 to p75, which comprises measuring the binding of a polypeptide containing the CARD domain of CARD-3 to a polypeptide comprising the death domain of p75 in the presence and passence of the test compound, and determining if binding is altered. This polypeptide is the human CARD-3 protein sequence of the invention. \$

Sequence 540 AA

Length:
Matches:
Conservative:
Mismatches:
Indels: 1.49e-118 1176.00 99.56% 99.12% 40.83% Best Local Similarity: Query Match: DB: Percent Similarity: Alignment Scores: Pred. No.:

US-09-771-161A-2 (1-1669) x ADB81362 (1-540)

751 GAAGCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAG 811 GACTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGAC 871 872 ACTACTGACATCCAAGGAGAAGAATTTGCCAAAGTTATAGTACAAAAATTGAAAGATAAC 931 932 AAACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTA 991 CTGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCAT 451 GAAAATAGTGGTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTT 511 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCCTGGAAATCAC 571 AGTIGGGATAGCACCATITCIGGATCICAAAGGGCTGCATICIGIGATCACAAGACCACT 631 691 332 CAGTTACAGAGTGTTTCAAGTGCCATTCACCTATGTGACAAGAAAAAAAGAAATTATCT 391 CCATGCTCTTCAGCAATAATAAATCCACTCTCAAACTGCAGGAAACTCAGAACGTCTGCAG CCTGGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAAATGACA 392 433 453 473 493 333 353 512 373 572 393 632 413 692 752 812 452 셤 g g ò g ò ò 엄 ò 셤 ò ద ð g δ δ

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Search completed: March 29, 2004, 14:19:30 Job time : 93.5 secs

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APPLICANT: Inchara, Nachiro
APPLICANT: Inchara, Nachiro
APPLICANT: Koseki, Takeyoshi
TITLE CANTING APPLICANTIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
CURRENT APPLICATION NUNBER: US/09/069,023A
CURRENT FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.0
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US-09-865-364-5

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; LENGTH: 284
; TYPE: PRT
; ORGANISM: Homo &
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-G=/cgn2 1/05FO° spool | b/US09711161/runat 29032004 124825 13720/app_guery.fasta_1.1863
-DB=Issued patents AA -OFMT=fastan -SUFFTX=n2p.rai--MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=Dits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pot -THR MAX=100 -THR MIN=0 -AALIGN=15
-MODE=LOCAL -OUTFWT=pto -NORM=ext -HBAPSIZE=500 -MINLEN=0 -MAXIEN=200000000
-USER=US09771161 @CGN 1 1 27 @runat 29032004 124825 13720 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DBT TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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1: /cgn2 6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2 6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2 6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2 6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2 6/ptodata/2/iaa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PcTuS_COMB.pep:*
                     version 5.1.6
- 2004 Compugen Ltd.
                                                                                                   protein search, using frame_plus_n2p model
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US-09-099-042-1
US-09-099-041-2
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US-09-340-620A-2
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Copyright (c) 1993
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Sequence 4, Application US/09069023A
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Sequence 4, Application US/09069023A
GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM 03333
CURRENT APPLICATION NUMBER: US/09/069,023A
CURRENT FILING DATE: 1938-04-27
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
LENGTH: 478
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                 AGTTGGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCACT
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US-09-069-023-3
Sequence 3, Application US/09069023A
Sequence 3, Application US/09069023A
Patent No. 6348573
GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Nachiro
APPLICANT: Inohara, Nachiro
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDE
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND
FILE REFERENCE: UM-0333
CURRENT APPLICATION NUMBER: US/09/069,023A
CURRENT FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
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; ORGANISM: Homo sapiens
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Sequence 1, Application US/09069023A

Sequence 1, Application US/09069023A

GENERAL INFORMATION

APPLICANT: Nunez, Gabriel

APPLICANT: Nonez, Gabriel

APPLICANT: Nonex, Danis

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APPROPRIATION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS

TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS

FILE REFERENCE: UM-03333

CURRENT APPLICATION NUMBER: US/09/069,023A

CURRENT FILING DATE: 1998-04-27

NUMBER OF SEQ ID NOS: 38

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 531

TYPE: PRT
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Percent Similarity:
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Query Match:
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US-09-069-023-1
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APPLICANT: Inohara, Naohiro
APPLICANT: Inohara, Naohiro
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
CURRENT APPLICATION NUMBER: US/09/069,023A
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Length:
Matches:
Conservative:
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US-09-345-473E-28
Sequence 28, Application US/09345473E
Patent No. 6558903
GENERAL INFORMATION:
APPLICANT: Hodge, Martin
CURRENT FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27
LENGTH: 540
TYPE: PRT
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                                            , ORGANISM: Homo sapiens
US-09-069-023-27
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TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof FILE REFERENCE: 35800/183781
CURRENT PELLING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 62
SOFTWARE: RestSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 540
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US-09-019-942-1
; Sequence 1, Application US/09019942
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CORGANISM: Homo sapiens
US-09-345-473E-28
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GENERAL INFORMATION:
APPLICANT: BERTIN, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILER REFERENCE: 07334-076001;
CURRENT APPLICATION NUMBER: US/09/099,041A
CURRENT FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 540
TYPE: PRT
CORGANISM: Homo sapiens
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Bertin, John
TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
TITLE OF INVENTION: DOMAIN POLYPEPTIDES
NUMBER OF SEQUENCES:
ADDRESSOE: ALSO FEASTS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
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1126
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                                                                                                                                                                             COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDLUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Fast SEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,942
FILING APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/068001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPHAX: 617/542-8906
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Percent Similarity:
Best Local Similarity:
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COUNTRY: U
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                                                             TTATCTAGAAAAGCTCAAGACTGTTATTATGAAGCTGCATCACTGTCCTGGAAATCAC
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; Sequence 1, Application US/09470271
; Patent No. 6410689
; GENERAL INFORMATION:
    APPLICANT: Bertin, John
    TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
    TITLE OF INVENTION: DOMAIN POLYPEPTIDES
    NUMBER OF SEQUENCES: 4
    NUMBER OF SEQUENCES: 4
    STREET: 225 Franklin Street
    CITY: Boston
    STATE: MA
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ZIP: 02110-2804

ZIP: 02110-2804

COMPUTER READABLE FORM:

WEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

FILLING DATE: WINDER: US/09/470,271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Meiklejohn, Ph.D., Anita L. REGISTRATION WINGBER: 35,283 REFERENCE/DOCKET NUMBER: 07334/068001 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: · 09/019,942
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APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
TILE REPERENCE: 07334/18001
CURRENT APPLICATION NUMBER: US 09/245,281
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: US 09/207,359
EARLIER APPLICATION NUMBER: US 09/207,359
EARLIER APPLICATION NUMBER: US 09/019,941
EARLIER PILING DATE: 1998-06-17
EARLIER PILING DATE: 1998-06-17
EARLIER FILING DATE: 1998-06-17
EARLIER FILING DATE: 1998-06-17
SEALIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 2
LENGTH: 540
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Patent No. 6369196
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ORGANISM: Homo sapiens
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Best Local Similarity:
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GENERAL INFORMATION:
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Matches:
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                                                                                        4.85e-131
1176.00
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Sequence 2, Application US/09207359B Patent No. 6469140

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Matches:
Conservative:
Mismatches:
Indels: US-09-771-161A-2 (1-1669) x US-09-207-359B-2 (1-540) Gaps: 4.85e-131 1176.00 99.56% 99.12% 40.83% Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB: TYPE: PRT ORGANISM: Homo 513 ò 유

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Matches:
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Best Local Similarity:
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US-09-340-62/A-2.
US-09-340-62/A-2.
Patent No. 6482933
GENERAL INPORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARI
FILE REPERENCE: 0733-124001
CURRENT APPLICATION NUMBER: US 09/245,281
PRIOR APPLICATION NUMBER: US 09/245,281
PRIOR APPLICATION NUMBER: US 09/245,281
PRIOR APPLICATION NUMBER: US 09/207,359
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR FILING DATE: 1998-12-06
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-06
NUMBER OF SEQ ID NOS: 71
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO S
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        AATTTACTTCAAAATAAAAGCATG 1015
                  533 AsnLeuLeuGlnAsnLysSerMet 540
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1176.00
99.56%
99.12%
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Best Local Similarity:
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Oy 692 CCTGGTATAGCCCAGCAGTGGATCCAGAGCAAAGGGAAGACTTGTGAACCAAATGACA 751		GENERAL INFORMATION:  APPLICANT: Bertin, John APPLICANT: Chao, Moses V. TITLE COP INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILE AND USES THERE FILE REPERENCE: 07334-316001 CURRENT APPLICATION NUMBER: US/09/748,537 CURRENT FILING DATE: 1908-06-12-26 FRIOR FILING DATE: 1998-06-17 FRIOR FILING DATE: 1998-06-17 FRIOR FILING DATE: 1998-06-106 NUMBER OF SEQ ID NOS: 14 SOFTWARE: FASELSEQ for Windows Version 4.0 SEQ ID NO 1 LENGTH: 540 TENGRAPH: 540 TENGRAPH: SAC TYPE: PRT ORGANISM: Homo sapiens US-09-748-537-1	Alignment Scores:	Qy         392 CTGAACATACCTGTAAATCATGGTCCACAAGAGAATCATGTGGATCCTCTCAGCTCCAT         451           Db         333 LeuAsnileProValAsnHisGlyProGlndluGluSerCysGlySerSerGlnLeuHis         352           Qy         452 GAAAATAGTGGTTCTCCTGAACTTCAAGGTCCTGCCAGCTCCTCAAGACATGATTT         511           Db         353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe         372           Qy         512 TTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCAGAAATCAC         571           Db         373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis         392

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TATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTACACACT 874
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Search completed: March 29, 2004, 14:25:48 Job time : 36.5 secs

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Sequence 41, Appl
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Sequence 2, Appli
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Sequence 10, A
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TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 8026202005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001.01.26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR APPLICATION NUMBER: 136776
PRIOR APPLICATION NUMBER: 136776
PRIOR PILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PALCHIN VERSION 3.0
SEQ ID NO 93
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US-10-133-780-1

US-10-105-931-2

US-10-225-981-2

US-10-105-931-5

US-10-118-984-5

US-10-118-984-5

US-10-105-931-6

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US-10-105-931-11-11

US-10-105-931-01-11

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US-09-748-537-1
US-09-728-721-2
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US-10-118-984-8
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   Command line parameters:
-MODELE frame+ .ndp. model - DEV=xlp
-MODELE frame+ .ndp. model - DEV=xlp
-MODELE frame+ .ndp. model - DEV=xlp
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1. /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2. /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3. /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
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- 2004 Compugen Ltd.
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Fgapop 6.0 , Fgapext
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Query Match Length DB

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Scoring table:

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; Sequence 184, Application US/09771161A
; Patent No. US20020110811A1
; Patent No. US20020110811A1
; APPLICANT: LEVINE, et al.
; TILE OF INVENTION: VARIANTS OF PROTEIN KINAS;
TILE REPERBNCE: 802620-2005.1
; CURRENT FILING DATE: 2001-01-26
; PRIOR PILING DATE: 2000-11-28
; PRIOR PILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR APPLICATION NUMBER: 136776
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PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PatentIn version 3.0
SEQ ID NO 184
LENGTH: 540
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Patent No. US20020142428A1
GENERAL INFORMATION:
APPLICANT: Hodge, Martin E
                                                         sapiens
                                                                                                     Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                              TYPE: PRT
ORGANISM: Homo
                                                           ; ORGANISM: Homo
US-09-771-161A-184
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US-09-862-027-28
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Pred. No.:
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Sequence 14, Application US/09981397A

Publication No. US20030082519A1

Publication No. US20030082519A1

GENERAL INFORMATION:
APPLICANT: Axxima Pharmaceuticals AG

APPLICANT: Schubart, Daniel

APPLICANT: Stein-Gerlach, Matthias

APPLICANT: Stein-Gerlach, Matthias

APPLICANT: Bevec, Dorian

TITLE OF INVENTION: Inhibition

TITLE OF INVENTION: Inhibition

FILE REFERENCE: AXM-004.1 US

CURRENT APPLICATION NUMBER: US/09/981,397A

CURRENT APPLICATION NUMBER: 60/240,750

PRIOR APPLICATION NUMBER: 60/240,750

PRIOR FILING DATE: 2000-10-16

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn version 3.1

SEQ ID NO 14

LENGTH: $40

MANDER OF SEQ ID NOS: 20

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; TITLE OF INVENTION: NO. US20020142428Alel Kinases and Uses Thereof; FILE REFERENCE: 35800/234862
; CURRENT APPLICATION NUMBER: US/09/862,027
; PRIOR PEPLICATION NUMBER: US 09/345,473
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 540
; TYPE: PRI
; TYPE: PRI
; ORGANISM: Homo sapiens
US-09-862-027-28
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Matches:
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Mismatches:
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US-09-748-53/-1
; Sequence 1, Application US/09748537
; Patent No. US20020061833A1
; Patent No. US20020061833A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Chao, Moses V.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILE AND USES THEREC,
; TITLE OF INVENTION: NOVEL WOLECULES OF THE CARD-RELATED PROTEIN FAMILE AND USES THEREC,
; TILLE REFERENCE: 07344-316001
; CURRENT PAPLICATION NUMBER: US 09/099,041
; CURRENT FILING DATE: 1998-06-17
; PRIOR FILING DATE: 1998-06-17
; PRIOR FILING DATE: 1998-06-17
; SEQ ID NOS: 14
; SEQ ID NO 1
; SEQ ID NO 1
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-748-537-1
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; Sequence 1015, Application US/09925301
; Patent No. US2002052308A1
; GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Ant:
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
; SEQ ID NO 1015
LEASTHREE PATENTIN VET. 2.0
; SEQ ID NO 1015
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; ORGANISM: Homo sapiens
US-09-925-301-1015
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937 LeuserArglysAlaGlnAspCyGTyrPheMetLysLeuHisHisCysProGlyAshHis 392  94 S72 AGTTGGGATAGACCATTTCTGGATCTCAAGGCCCCCTTTTTGTATCCGAAGCCTC 531  95 SerTtpApSerThtileSIII	COUNTRY: USA ZIP: 0210-2804  ZIP: 02110-2804  COMPUTER READABLE FORM:  MEDIUM TYPE: Diskette  COMPUTER: IBM Compatible  OPERATING SYSTEM: Windows 95  SOFTWARE: FastSEQ for Windows Version 2.0b  CURRENT APPLICATION DATA:  APPLICATION NUMBER: US/10/133,780  FILING DATE: 26-Apr-2002  PRIOR APPLICATION NUMBER: US/09/019,942  FILING DATE: 86-Apr-2002  PRIOR APPLICATION NUMBER: US/09/019,942  ATTORINEY/AGENT INFORMATION:  NAME: Weiklejohn, Ph. D., Anita L.  REFERENCE/DOCKET NUMBER: 35,283  REFERENCE/DOCKET NUMBER: 35,283  TELECOMMUNICATION INFORMATION:  TELEPHANE: 617/542-5070  TELEPAX: 617/542-5070  TELEPAX: 200154  INFORMATION FOR SEQ ID NO: 1:  SEQUENCE CHARACTERISTICS:
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Qy         692 CCTGGTATAGCCCAGCAGTGGATCCAGAGCAAAACGCAAAACGAAAATGAA           Db         433 PCGJJJIIAAJGGIATTTJIGGIASETLYSATGGIAAGDIAGATTH           A33 PCGJJJIIAAJGGIATTTJIGGIASETLYSATGGAAATGAAGAAGAG           Bb         432 ACGTGCCTACAACTCCCTACAAGAGCTCCAAAATACAAAAAAAA	

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APPLICATION NUMBER: US/10/105,931
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US-10-105-931-2
Sequence 2, Application US/10105931
Sequence 10. Myplication US/20150987A1
GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-076001
                                                      540
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Matches:
Conservative:
Mismatches:
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TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID i
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Mismatches:
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Matches:
CURRENT APPLICATION NUMBER: US/10/105,931
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: 09/099,041
PRIOR FILING DATE: 1998-06-17
PRIOR PELLING DATE: 1998-06-17
PRIOR PELLING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SSEQ ID NO 2
LENGTH: 540
TYPE: PRI
TYPE: PRI
CORGANISM: Homo sapiens
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CCATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAG 691
                                                                                                        ; Sequence 2, Application US/10295981; Publication No. US20030120055A1; GENERAL INFORMATION:
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GENERAL INFORMATION
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APPLICANT: BERTIN. JOHN
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
CURRENT APPLICATION NUMBER: US/10/118,984
CURRENT FILING DATE: 2002-04-09
FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/207,359
FRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
FRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-06-17
FRIOR PLING DATE: EARLIER FILING DATE: 1998-06-17
FRIOR PLING DATE: EARLIER FILING DATE: 1998-02-06
FRIOR FILING DATE: PARLIER FILING DATE: 1998-02-06
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                                       AGTIGGGAIAGCACCAITICIGGAICICAAAGGGCIGCAIICIGIGAICACAAGACCACI 631
                                                     93 SerTrpAspSerThrIIeSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 112
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13 LysLeuGlnSerValSerSerAlalleHisLeuCysAspLysLysMetGluLeuSer
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                                                                                                             RESULT 13
US-10-105-931-5
Sequence 5, Application US/10105931
Sequence 5, Application US/10105931
Sequence 5, Application US/10105931
Sequence 5, Application Wo. US20020150987A1
SEQUENCE TO WO. US20020150987A1
SEQUENCE TO WORNETION: PAPER OF THE CARD-RELATED TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF TILE REFERENCE: 07334-076001
CURRENT APPLICATION NUMBER: US/10/105,931
CURRENT FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR PLILING DATE: 1998-02-06
SECONDARY OF SEQ ID NOS: 37
SOFTWARE FASTSEQ for Windows Version 4.0
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; Publication No. US20020197693A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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US-10-118-984-5
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LENGTH: 131
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TITLE OF INVENTION: 0320202012013
TITLE OF INVENTION: 03734-124001
CURRENT APPLICATION WINBER: US/09/728,721
CURRENT APPLICATION WINBER: US/09/728,721
CURRENT APPLICATION WINBER: US/09/340,620
PRIOR FILING DATE: 1999-06-28
PRIOR APPLICATION WINBER: US/09/09,041
PRIOR FILING DATE: 1998-12-08
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 71
SEQ ID NOS: 71
SEQ ID NOS: 71
SEQ ID NOS: 71
SEQ ID NO 5
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Patent No. US20020061845A1
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ORGANISM: Homo sapiens
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 71
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 131
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632.00
99.16%
98.32%
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                                                                                                                                        TYPE: PRT; ORGANISM: Homo sapiens
US-10-295-981-5
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Best Local Similarity:
Query Match:
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Publication No. US20030120055A1
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
FILE REFERENCE: 07334-124001
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: US/09/340,620
PRIOR FILING DATE: 1999-06-28
PRIOR FILING DATE: 1999-06-20
PRIOR FILING DATE: 1999-06-30
PRIOR FILING DATE: 1999-07-359
PRIOR PLICATION NUMBER: US 09/245,281
PRIOR PAPLICATION NUMBER: US 09/207,359
PRIOR FILING DATE: 1998-12-08
PRIOR PLILING DATE: 1998-12-08
PRIOR PLILING DATE: US 09/207,359
PRIOR PLILING DATE: US 09/099,041
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                      OF THE CARD-RELATED PROTEIN FAMILY
                                                                      CURRENT APPLICATION NUMBER: US/10/118,984

CURRENT FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281

PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05

PRIOR PILING DATE: EARLIER PELLIR APPLICATION NUMBER: US 09/207,359

PRIOR PILING DATE: EARLIER PELLIR APPLICATION NUMBER: US 09/099,041

PRIOR PILING DATE: EARLIER FILING DATE: 1998-02-17

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17

PRIOR PILING DATE: EARLIER FILING DATE: 1998-06-06

NUMBER OF SEQ ID NOS: 44

SOFTWARE: FRAUES FILING DATE: 1998-02-06

SEQ ID NO 5
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Mismatches:
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APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 07334/118001
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632.00
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GRGANISM: Homo sapiens
US-10-118-984-5
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Best Local Similarity:
Query Match:
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391

Length:
Matches:
Conservative:
Mismatches:
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM nucleic - protein search, using frame plus n2p model	04, 14:	Title: US-09-771-161A-2 Perfect score: 2880 Sequence: 1 acctagtttatacccagatacaacagcctgatgtgtaaaa 1669	Scoring table: BLOSUM62	Searched: 283366 segs, 96191526 residues Total number of hits satisfying chosen parameters: 566732	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	DEV=xlp /US09771161/runat_29032004_124825_1 -USPETX=xn2p.rpr -IMNAMATH=6.1_10\tilde{D} 01 FMATRIX=blosum62 -TRANS=bumand -pct -THR_MAX=100 -THR_MIN=0 -ALIGN 01 FMSIZE=200 -MININ=0 -TAXEN=20000 14.4 @runat_29032004_124825_13694 - 12.8C\tilde{D} FMININ=0 -MAXEN=20000 14.4 @runat_29032004_124825_13694 - 12.8C\tilde{D} FMININ=0 -MAYENEN=0 14.4 @runat_29032004_124825_13694 - 12.8C\tilde{D} FMININ=0 -MAYENEN=0 12.8C\tilde{D} FMININ=0 -MAYENEN=0 13.8 & THREADS=1 -XGAPOP=10 -XGAPOP=1	3 89 3.1 283 2 B81996 RNA polymerase 8 4 89 3.1 1360 2 T33922 hypothetical pro

413 GGTCCACAGAGGAATCATGTGGATCCTCTCAGGTCCATGAAAATAGTGGTTCTCCTGAA 472   13 GGTCCACAGAGGGAATCATGTGGATCCTCTCAGGTCCTCTGAAAATAGTGGTTCTCCTGAA 472   19   10   10   10   10   10   10   10	233 253 253 263 277 278 278 278 291 291 291 291 291 291 291 291 291 291
S12   TTATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGCTCCTGGAAATCAC 571   S11   S11   S12   S12   S12   S12   S13   S13   S13   S14   S14   S15	RESULT 2  MAINTENDED 551 TyrPheGliLeuAlalLySiPSTYHHISPYOASPVal 562  RESULT 2  T00029  Miranda protein - fruit fly (Drosophila melanogaster) C,Species: Drosophila melanogaster C,Becies: Drosophila melanogaster A,Reblima-Kataoka, H.; Skeath, J.B.; Nabeshima, Y.; Doe, C.Q.; Matsuzaki, F. A,Reference number: Z14067; MUID:9806592; PMID:9403694 A,Reference number: Z14067; MUID:9806592; PMID:9403694 A,Reference number: Z14067; MUID:9806592; PMID:9403694 A,Residues: 1-830 elike A,Residues: 1-830

A; Description: apoptotic suppressor	US-09-771-161A-2 (;	(1-1669) x A99106 (1-731)
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octe: core: 5imilarity: 44.78\$ Conservative: est Incal Similarity: 33.13\$ Mismatches	Db 136 LysS	.:: :::       ::       :::
uery Match: 3.40% Indels: 1 B: 2 Gaps: 3	Qy 317 TTTA'	TITATGIATICATIACAGITACAGAGIGITICAAGIGCCATICACCIAIGIGACAAGAAG 376
US-09-771-161A-2 (1-1669) x S68450 (1-618)	156	
SAGCAAAAGGGAAGACATTGTGAACCA	377	AAAATGGAATTATCTCTGGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGA 436
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479 LeuAspAsnLeuLeuLysAlaAsnValIleAsnLysGlnGluHisAspIleIleLysGln	Qy 497 CAAG	ACAATGATTTTTTATCTAGAAAAGCTCAAGACTG
OY 833 AAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACATTACTACTGACATCCAAGGAGAA 892    -  -  -  -  -  -  -  -  -  -  -  -  -	196	:::      ::: PheValPheTyrIle-PheSerSerValLeulleLeullePhePheAsnTyrT 213
3 GAATTTGCCAAAGTTATAGTACAAAAATTGAAAGAT	535	TTATTTTATGAAGCTGCATCACTGTCCTGGAAATCACAGTTGGGATAGCACCATTTCT 592
::   Db 519 AlaAlaAsnIlePheLysAsnCysLeuLySGluIleAspSerThrLeuTyrLysAsn 538	213	
929AACAAACAAATGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGA	Db 233 hell	General Commission
UD 539 LeuknevalasplysAsnmetLySlyrilekroinrGluAspvalserGlyLeuserLeu 558 Ov 980 TCACCATCTTTABABTTTACTTCBABABTBABAGGATGTBAGTGBATGTATTTTGBABAGBA 1039	Qy 646AA'	AATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAGCCTGGTATAGCC 703
559 GluGluGlnLeuArgArqLeuGlnGluArqThrCyslysValCysMetAspLysGlu 578	Db 253 leAs	leAsnAsnileIleTyrIleLeuIleLeuAsnPheThrAsnSerIleLeuPhe-SerLeu 272
ATGTGTTTCATAAAAGGATATTTATATATCTCTGT 1072	Qy 704 CAGC :::: Db 273 LysLy	CAGCAGTGGATCCAGAGCAAAAGGAAGACATTGTGAACCÁAATGACAGAAGCC 757 ::::::       LysLysTrpilePheLeuLeuLysLysThrGluTyrMetArgAsnAsnIleIleLeuIle 292
8/C	Qy 758 TGCC	TGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAAGAGGACTAT 817
Q.	Db 293 LeuT	LeuThrPheSerLysLeuSerAsnLysLeuAsnLysAsnValValTyr 308
ardia theta vestigial nu	818	GAACTIGITAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACACTACT 877
#text_change 24-May-2001	309	
K;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rel Nature 410, 1091-1096, 2001 A;Title: The highly reduced genome of an enslaved algal nucleus.	Oy 878 GACA Db 323 PheI	GACATCCAAGGAGAAGATTTTGCCAAAGTTATAGTACAAAAATTGAAAGATAACAAACA
A;keterence numoer: Asyukz; Mull:113436/1; FMID:113436/1 A;Accession: A99106 A;Status: Dreliminary	Qy 938 ATGG	AIGGGICTICAGCCTIACCCGGAAAIACTIGIGGTTICTAGAICCACCAICTITAAAITIA 997
A; Molecule type: DNA A: Regidings: 1-731 chom?	338	
	Qy 998 CTTC Db 351 nGln	CITCAAAATAAAAGCATGTAAGTGACTGTTTTTCAAGAAATGTGTTTCATAAAAGGA 1057        nGlnLysileSerthr-IleAsnileCysPheArgLeuPhePheIlePheHisGluLys- 370
A;Map position: 2 A;Genome: nucleomorph C:Kevwords: nucleomorph	Qy 1058 TATT	TATTTATATCTCTGTTGCTTTGACTTTTTTATATAAAATCCGGGGT 1105
Distribute Coves	371	
1.22 Length: 95.00 Matches: ty: 37.47% Conservative:	Oy 1106 ATTA 	ATTAAAGCTTTATTGAAGGTTCTTTGGGTAAATATTAGTCTCCCTCCATGACAC 1159
	-	160 IGCAGTATTTTTTAATTAATACAAGTAAAAAGTTTGAATTTTGCTACÁTAGTTCAAT- 1218
	Db 401 leTy:	rPhelleLeuArgLeulleLysPheLysLysTyrIleLysAspAsnLysPheSerL 421

•	1 H—> O + H = B + +	RESULT 6 T40525 T40515 T40515 T40515 T40515 T40515 T40515 T40515 T40515 T40515 T40515 T40515 T5050cies: Schizosaccharomyces pombe C;Species: Obec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000 C;Accession: Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000 C;Accession: T40953 R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G. Submitted to the RMEL Data Library, February 1999 A;Reference number: Z21940 A;Accession: T40953 A;Reference number: Z21940 A;Residues: 1-956 cWOO> A;Cross-references: EMBL:AL035592; PIDN:CAB38161.1; GSPDB:GN00068; SPDB:SPCC1393.05 A;Experimental source: strain 972h-; cosmid c1393 C;Genetics: A;Gene: SPDB:SPCC1393.05 A;Map position: 11/1; 36/2; 52/3; 69/2; 207/3; 634/2; 650/2; 687/2; 781/2; 810/2 C;Superfamily: Schizosaccharomyces hypothetical protein SPCC1393.05	Alignment Scores:
	Qy 1412 TACAGAATCCCTGCCCTAAAATCCCAGGCTTAATTGCCCTACAAAGGGTTATTAATTTAA 1471    1	A,Accession: T32960 A,Status: preliminary; translated from GB/EMBL/DDBJ A,Ancession: T32960 A,Status: preliminary; translated from GB/EMBL/DDBJ A,Molecule type: DMA A,Residues: 1-692 < buzza A,Cross-references: EMBL:AF045645; PIDN:AAC02606.1; GSPDB:GN00022; CESP:T21D12.7 A,Experimental source: strain Bristol N2; clone K02D7 A,Genetics: Brillarity: B,00 Matches: Conservative: Best Local Similarity: B,00 Matches: Best Local Similarity: B,00 Matches: Conservative: Best Local Similarity: B,00 Conservative: Best Local Similarity: B,00 Conservative: B,00 Cons	Qy       341 AGTGTTTCAAGTGCATTCACCTATGT

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ОР	297 LysHisAspGlyAspSerTyrGluLeuValProValPheAlaLysAsnPro 313	
ò	223TCTTTCCATGTATTTTGTACAAAAAATGTG 258	Oy 1117 ATTGA
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Š i		DNA polymerase III
qq	359 sThrSerSerAsnLeuSerIleProValLeuGlnLysProSerAsnPheHisSerSerSe 379	C;Species: Ureaplas C;Date: 18-Aug-2000
ò	TCCAT	C, Accession: F82935
셤	:::::    :::    379 rThrGluLeuSerAspAsnSerIleHisGlnGlyArgArgAlaValAspProVa 397	K;Glass, J.1.; berk submitted to GenBan
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DP	397 lValAsnGlnAsnAsnProSerAsnPheGluGluMetIleMetAsnLysLeuAsnLysLe 417	A;Status: prelimina
ò	559 TCCTGGAAATCACAGTTGGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATTCTGTGA 618	A;Residues: 1-597 <
Db	:::            ::: 417 uProThrIleAspLysGlnIleLeuGlyThrSerSerLeuThrHisPheGl 434	A; Cross-relerences: A; Experimental sour
ě		C; Genetics:
Š i		A,Genetic code: SGC
OP OP	434 nAspLysThrThrAlaIleGluHisSerIleAsnLysSerAsnSerLysGlnProProAr 454	Alignment Scores.
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Ę	454 aPhelivaPheGlnfenDroBroArdProThrSerAsnThrTenDrofenGlnGl 474	Score: Percent Similarity:
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ò	659 676 +	Query Match:
ф	474 uGluLeuValThrArgTyrSerValSerSerAspGlyAsnThrValAspGluAlalleTh 494	
ò	677TCAGAACGTCTGCAGCCTGGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGA 729	US-09-771-161A-2 (1
- 4		Qy 187 TTCAG
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Ωp	514 nAspValHisLysSerLeuArgGlnAsnCysAlaLysLeuAspPheAspAspSerLysSe 534	Š
ò	790 CAGGGACTIGAICAIGAAAGAGGACTAIGAACTIGITAGIACCAAGCCTACAAGGACCIC 849	
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g	554 OLYBSerGlySerLeuThrProSerlleAspMetLys 566	:   : Db 323 rLeuL
ò	910 AGTACAAAATTGAAAGATAACAAACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGT 969	Ov 319 TATGT
d G	567 -PheLeuArgLeuGlnAspGluLysMetAspAspLeuGlyAspAsnTyrTyrThrIleLe 586	646

ò	970	GGTTTCTAGATCACCA
рр	586	
٥٨	1009	AAGCATGTAAGTGACTGTTTTTCAAGAAGAAATGTGTTTCATAAAAGGATATTTATATCT 1068
qq	909	B11 607
ò	1069	CTGTTGCTTTGACTTTTTTATATAAAATCCGTGAGTATTAAAGCTTT 1116
qa .	607	eValCysSerGluLysTyrIleAsnHisGluGluIleAspAsnMetAsnLeuLysSerLe 627
ογ	1117	ATTGAAG1123
qa	627	ulisargirpLeuSerargSerLeuHisValLeuGlnSerPheSerGlyGluIleGluLe 647
ογ	1124	
Д	647	uAsnLeuGluPheGlyVallleLeuTyrProAsnIleSerSerAspValSerAlaCysSe 667
٥٨	1165	TATTTTTTTTAATTAATACAAG 1186
qa	667	
RESULT 7 F82935 DNA polymerase C;Species: Urea	erase : Ure	87 [imported] - Ureapla
C;Date: 1 C;Accessi R;Glass,	8-Auc on: F J.I.	-2000 #sequence_revision 20-Aug-2000 #text_cnange 20-Aug-2000 82935 - Lefkowitz, B.J.; Glass, J.S.; Heiner, C.R.; Chen, B.Y.; Cassell, G.H.
submitted A; Descrip	to (	reaplasma urealyticum: Alternate views
A; Accessi A; Status:	on: F	DEET: A020/U  82935   iminary 
A; Residue A; Cross-r A; Experim C; Genetic	s: 1. efere ental	A; Residues: 1-597 cGLA> A; Cross.references: GB:AE002108; GB:AF222894; NID:g6899034; PIDN:AAF30492.1; GSPDB:GN001; A;Experimental source: serovar 3; biovar 1 C;Genetics:
A,Gene: d A,Genetic	naX; code	UU087 : SGC3
Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity Query Match:	Scores: imilari l Simil	es: 3.59 Length: 597 90.00 Matches: 67 conservative: 53 ilarity: 19.31\$ Mismatches: 98 3.12\$ Indels: 15 2.2 Gaps: 15
US-09-771	-771-161A-2	(1-1669) x F82935 (1-5
ò	187	CTCTT
Dp	266	PhelletyrGluLeutyrAsnGlnGlyValAsnLeuGluAlaPheCysValGln 283
<i>λ</i> ο	247	AIATAAAATGTGTTAGATTGTATTTTACTTCTAT
qq	284	ileileäsnValLeu-ileAspTyrLeuIleTyrLeuLysThrAsnAspIleAsnAsnLe 303
<i>λ</i> ο	281	285 TIT 285
Dρ	303	uLysLysValSerValAspGluLeuLysLysMetLeuLeuleulleAsnPheAsnGlyAsnTy 323
ò à	286	CCTAATCATCTCCAGTTAAAGTGTATAT
au .	323	
<u>\$</u>	319	TATGTATTCATTACAGTTACAGAGTGTTTCAAGTGCCATTCACCTATGTGACAAGAA 375
αn	243	

GTTGTA, AAAGCT AAAAGCT AAAAGCT SILA SILA SILA SILA SILA SILA SILA SILA	er gene of Saccharomyces cerevis 2.1; PID:9243611	<pre>#text_change 19-Apr-2002 ara, S. S killer gene of Saccharomyces cerevis 68726</pre>	Coy cerevisiae)  #text change 19-Apr-2002 RESULT	Db 610 SerSerAsnAsnArgPheCysCysLeuLysSerIle	Qy 719 AGCAAA	ACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTT 990  ACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTT 990  ACCCGGAAATACTTGTGGTTTCTAGAATCACCATCTTT 990  ACCCGGAAATACTTGTGGTTTCTAGAATCACTATTAGAATCACTAGAATCACAGAATCACAGAATCACAACACTAGAATCACAACACTAGAATCACAACACAACACAACACAACACAACACAACACAACA	537 Db 570		A 870 QY	A	  Db 534 ArgAlaGlyAlaLeuLeuAspGlyArgValArgThr	AAATGACAGAAGCCTGCCTTAACCAGTCGCTAGATGC 780 Qy 458AGTGGTTCTCCTGAAACT	CGTCTGCAGCTGGTATAGCCCCAGCAGTGGATCCAGAG 720  OY 40/ AAICAICACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	456 Db 494	670 Qy 347	ThrGluLeuValAs 436 Db 474	78C W 213	570 QY	 	Query Match: 3.12% DB: DB: 2	GTGGTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCC 495 Score: 90.00 Matches: Percent Similarity: 37.86% Conservativ Conservativ Mismatches: Best Local Similarity: 20.87% Mismatches:	roduct: KHS Killer toxin #st Scores:	435   F:37-708/Product: KHS Killer t
000 316 36 3 6 3 6 3 6 3 6 3 6 3 6 3 6 3 6		31-N canc e of	1 8 3 r toxin KHS precursor - yeast (Saccharomyces cies: Saccharomyces cerevisiae cies: 31-Mar-1992 #secuence revision 31-Mar-1995	:::::: 49 uAsnIleIleAsnIleLys 55	91 AAATTTACTTCAAAATAAA 100	1 CAAACAAATGGGTCTTCAGCCTTACCCGGAA     7 eLysLeu		   uPheLeuGlyLeuIleAsn	GGACTATGAACTTGTTAGTACC	1 CCTTCTGTCCAGGGACTTGATCA	::: ::: 476 eLysAsnGluGluThrIleGlu	721 CAAAAGGGAAGACATTGTGAACCAAATGACAGAAG	GGAAACTCAGAAO	 		: . nGlnAsnAspLysGluSerGlyI				496 TCAAGACAATGATTTTTATCTAGAAAAGCTCAAG	CCATGAAAATA : e	376 GAAAATGGAATTATCTCTGAACATACCTGTAAATC             : :                 : :	ADAPATCH BATTATCH CAPACA

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, December 1995 nalysis of the complete nucleotide sequence of human h\epsilon
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|TyrSerSerGlnAsnAsnIleIleTyrIleTyrAsnSer 473
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gAsnCysLysProLeuLysAsnSerTrpCysGluThrThr 513
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aGluSerLeuGluGlnGlnTyrThrArgProLeuSer 609
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pGlyArgValArgThrIleArgPheLeu-------
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A;Map position: X
A;Introns: 43/2; 80/3; 110/3; 153/2; 274/3; 738/2; 1249/1; 1392/3; 1454/1; 1602/1; 1686/1
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                                                                                                hypothetical protein ZCB.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T2999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T29999
R;Latreille, P.; Bradshaw, H.
submitted to the EMBL Data Library, July 1996
A;Description: The sequence of C. elegans cosmid ZCB.
A;Reference number: Z20719
A;Accession: T29999;
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                             A;Residues: 1-2288 <LAT>
A;Cross-references: EMBL:U64862; PIDN:AAB52624.1; GSPDB:GN00028; CESP:ZC8.4
A;Experimental source: strain Bristol N2; clone ZC8
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732 IleGlnArgAspAspTyrGlnLysGlnLysAspGluHisAlaArgHisLeuPheAspIle
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A, Experimental source: strain JI C, Genetics:
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90.00
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575 LysCysPheMetAsnSerAsnArgTyrLeuArgLeuLèuSerThrArglleIleProLeu 594
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635 ThrLeuThrThrSerAsnAspValPheAspThrLeuLeuLeuLeuLysLeuIleAspIlePhe
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                                                                                                                                                                                                                                                                                                                                                                          -ATGGAATTATCTCTGAACATACCT
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64
44
126
13
               F.1918-1934/Domain: transmembrane #status predicted <TM8>
F,2126-2142/Domain: transmembrane #status predicted <TM9>
F,1688/Binding site: ATP/GTP (Lys) #status predicted
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nucleotide-binding motif A (P-loop)
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A;Residues: 1-2368 <BEC>
A;Cross-references: EMBL:Z36005; NID:g536429; PIDN:CAA85094.1; PID:g536430; MIPS:YBR136W
A;Experimental source: strain S288C
R;Becam, A.M.; Cullin. C · Creater.
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A Molecule type: DNA
A Molecule type: LNA
A Molecule type: 1-196,70', 198-2368 «KAT>
A Molecule type: LNBL:DI1088; NID:g506874; PIDN:BAA01860.1; PID:d1002337; PID:g506876
B Molecule A A Molecule Type See . 22, 3104-3112, 1994
A Molecule An essential gene, ESR1, is required for mitotic cell growth, DNA repair and me A Meference number: 847953; MUID:94344772; PMID:8065923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: strain S288C
R; Becam, A.M.; Cullin, C.; Grzybowska, E.; Lacroute, F.; Nasr, F.; Ozier-Kalogeropoulos, Vestet 10(Suppl.A), S1-S11, 1994
A; Title: The sequence of 29.7kb from the right arm of chromosome II reveals 13 complete A; Reference number: S46569; MUID: 94378717; PMID: 8091856
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R; Kato, R.; Ogawa, H.
Submitted to the EMBL Data Library, May 1992
A; Description: An essential gene, ESR1, is required for mitotic cell growth, DNA
A; Reference number: S46662
                                                                            866 CTAGACACTACTGACATCCAAGGAGAAGAATTT-----GCCAAAGTTATAGTACAAAAA 919
                                                                                                                           882 AlaArgAlaArgAspAlaAlaAsnGlnGlnLeuSerArgAlaAsnLeuLeuAsnLysGlu 901
       ESRI protein - yeast (Saccharomyces cerevisiae)
NiAlternate names: MEC1 protein; protein YBR1012; protein YBR136w
CiSpecies: Saccharomyces cerevisiae
CiSpecies: Saccharomyces cerevisiae
CiSpecies: 26-Aug-1994 #sequence revision 09-Sep-1994 #text_change 29-Oct-1999
CiAccession: S46063; S46578; S46663; S47954, S64663
Ribecam, A.M.; Herbert, C.J.; Nasr, F.; Slonimski, P.P.; Zagulski, M. gubmitted to the Protein Sequence Database, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-715,'P',717-1254,'Q',1256-1275,'G',1277-2368 <WEI>
A;Cross-references: EMBL:U31109; NID:g950172; PIDN:AAA74482.1; PID:g950173
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A;Molecule type: DNA
A;Residues: 195-196, D', 198-322;671-744;848-1796;1803-2003;2004-2368 <KAZ>
A;Cross-references: BMBL:D11088
R;Weinert, T.A.; Harlow, D.
submitted to the EMBL Data Library, July 1995
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F;74-90/Domain: transmembrane #status predicted <TM2>
F;718-234/Domain: transmembrane #status predicted <TM3>
F;718-738/Domain: transmembrane #status predicted <TM3>
F;712-1169/Domain: transmembrane #status predicted <TM5>
F;1152-1169/Domain: transmembrane #status predicted <TM5>
F;1188-1304/Domain: transmembrane #status predicted <TM5>
F;11815-1331/Domain: transmembrane #status predicted <TM6>
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A;Cross-references: EMBL:X75891; NID:g496856; PIDN:CAA53494.1; PID:g496866
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154 AspProAlaGlyValAlaAlaAlaAspLeuAsnGluSerLeuIleLeuGlnIleGluArg 173
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||| TyrThralaProalaArgGlnIleGlyGlyAspGluGlyGluAspMetLeuSerAsnIle
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A,Residues: 1-242. cDAV>
A,Cross-references: EMBL:X95469; NID:g1239958; PIDN:CAA64743.1; PID:g1239959
C,Superfamily: transcription factor squa; serum response factor DNA-binding d
C;Keywords: DNA binding; transcription regulation
C;Keywords: DNA binding; transcription regulation
F;2-57/Domain: serum response factor DNA-binding domain homology <SRF>
F;94-159/Domain: domain K <KDO>
                                                                               MADS box protein DEFH200 - garden snapdragon
C;Species: Antirrhinum majus (garden snapdragon)
C;Datte: 11-0ct-1997 #sequence_revision 24-0ct-1997 #text_change 20-Jun-2000
C;Accession: S7757
R;Davies, B.; Egaa-Cortines, M.; de Andrade Silva, E.; Saedler, H.; Sommer, EMBO J. 15, 4330-4343, 1996
A;Fitle: Multiple interactions amongst floral homeotic MADS box proteins.
A;Reference number: S71756; MUID:97015133; PMID:8861961
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Db 1098 ValSerCysCysProSerAlaGly11eTrpGlyGluTrpValSerValSerGlyCysAsn 1117  Qy 719	NiAlternate names: bimE protein homolog C;Species: Mus musculus (house mouse) C;Date: 28-Jul-1995 #text_change 17-Mar-2000 C;Date: 28-Jul-1995 #sequence_rely, k.; Hoeoeg, C. C;Accession: A55117 B;Starborg, M.; Brundell, E.; Gell, K.; Hoeoeg, C. J. Biol. CCHem. 269, 24133-24137, 1994 A;Fitle: A novel murine gene encoding a 216-kDa protein is related to a mitotic checkpoir A;Reference number: A55117; MUID:95014147; PMID:7929068 A;Accession: A55117 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-1944 <sta> A;Cross-references: GB:X80169; NID:9562764; PIDN:CAA56450.1; PID:9642252 C;Genetics: A;Gene: tsg24 C;Superfamily: bimE protein</sta>	ignment Scor ed. No.: rcent Simila st Local Sir ery Match: : -09-771-161P	TCATTACAGTTACAGAGTGTTTCAAGTGCCATTCACCTATGTGACAGAAGAAA 37 :::
Oy 214 SerGlyThrLeuGluAlaAlaLeuAspLeuIleAlaSerLeuAsnProCCGGAAATA 964  Db 214 SerGlyThrLeuGluAlaAlaLeuAspLeuIleAlaSerLeuAsnProBheProAlaVal 233  Qy 965 CTTGTGGTTTCTAGATCACCATCTTTAAATTTACTTCAA 1003  Db 234 GlyPheAlaSerSerThrProThrProTyrSerAspGluAlaLeuAlaAshLeuLeuAla 253  Qy 1004 AATAAAAGCATGTAAGTGACT 1024  Db 254 PheArgGlyMetGluValSer 260	TABSOLIT 14 TABSOLIT 14 TABSOLIT 14 TABSOLIT 14 TABSOLIT 14 TABSOLIT 14 TABSOLIT 14 TABSOLIT 14 TABSOLIT 14 TABSOLIT 14 TABSOLIT 14 TABSOLIT 14 TABSOLIT 14 TABSOLIT 14 TABSOLIT 15 TABSOLIT 13 TABSOLIT 13302 TABSOLIT 13302 TABSOLIT 13302 TABSOLIT 14 TABSOLIT 15 TABSOLIT 15 TABSOLIT 16 TABSOLIT	A; Cabrilla A; 134/3; 174/1; 604/2; 643/3; 718/3; 848/2; 944/2; 1044/2; 1. A; Introns: 43/3; 69/3; 134/3; 174/1; 604/2; 643/3; 718/3; 848/2; 944/2; 1044/2; 1. A; Introns: 43/3; 69/3; 134/3; 174/1; 604/2; 643/3; 718/3; 848/2; 944/2; 1044/2; 1. A; Introns: 43/8; 1360 Matches: 58 Mismatches: 68 Conservative: 25 Best Local Similarity: 20.53\$ Mismatches: 68 Conservative: 25 DBs: 1048/8; 1048/	Gaps:

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MEDLINE=98241596; PubMed=9575181;
Inohara N., del Peso L., Koseki T., Chen S., Nunez G.;
"RICK, a novel protein kinase containing a caspase recruitment domain, interacts with CLARP and regulates CD95-mediated apoptosis.";
J. Biol. Chem. 273:12296-12300(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37)
(RIP-1)ke interacting CLARP kinase) (Receptor-interacting protein 2)
RIP-2) (CARD-containing interleukin-1 beta converting enzyme associated kinase) (CARD-containing IL-1 beta ICE-kinase).
RIPR2 OR RIP2 OR CARDIAK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98381580; PubMed=9705938;
Johne M., Hofmann K., Burns K., Martinon F., Bodmer J.-L.,
Mattmann C., Tschopp J.,
"Identification of CARDIAK, a RIP-like kinase that associates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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P39970
O14310
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MEDINE=98307936; Pubmed=9642260;
MCGarthy JV., M. J., Dixit V.M.;
"RIP2 is a novel NF-kappaB-activating and cell death-inducing
                                         Q9ulh7
Q8wiv4
P19712
                                                                                   Q08641
P10335
                                                                                                             P33238
Q942464
Q998w3
Q8nyc2
Q60652
Q13489
Q918a9
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Q91095
Q810g5
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LIK1_RAT
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N106_SCHPO
SYAP MOUSE
MYC ASTVU
YBS4 YEAST
MRTB HUMAN
MATK CYRRA
POLG HCVA
                                                                                 ABPX_YEAST
LIP_STAAU
MX_ANAPL
AGI9_LYCES
ACE1_TRIRE
LIP_STAAW
KLRE_MOUSE
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BIR3_HUMAN
HIFA_XENLA
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VWF_CANFA
AHR_RAT
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PGF1 1
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Ozersky P., Holmes A., Broy M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Curr. Biol. 8:885-888(1998)
                             Homo sapiens (Human)
  NCBI_TaxID=9606;
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ID RIKZ HUMAN
AC 043353;
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(without alignments)
8478.545 Million cell updates/sec
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- 2004 Compugen Ltd.
                                                                  protein search, using frame_plus_n2p model
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RIKZ MOUSE
CAR4 HUMAN
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122.5
100.5
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Score

Result No.

Database :

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XX TESUSE-SKIND;

XX STEAUSHORY;

XX STEAUSHORY;

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XX STEAUSHORY;

XX STEAUSHORY;

XX STEAUSHORY;

XX ALAUSHORY;

XX Explecton M., Soarse M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

XX Brahs S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

XX Richards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,

XX Ilalon D.K., Muxry D.W., Sodergren E.J., Lu X., Gibbs R.A.,

XX Ilalon D.K., Muxry D.W., Sodergren E.J., Lu X., Gibbs R.A.,

XX Ilalon D.K., Muxry D.W., Sodergren E.J., Lu X., Gibbs R.A.,

XX Hating M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

XX Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

XX Butterfield X.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

XX Generation and initial analysis of more than 15,000 full-length

XX Generation and initial analysis of more than 15,000 full-length

XX Generation and initial analysis of more than 15,000 full-length

XX Graps-8-mediated apoptosis. Activates NP-kappaB.

XX FUNCTION: Activates pro-caspase-1 and pro-caspase-8. Potentiates

CASP-8-mediated apoptosis. Activates NP-kappaB.

XX FUNCTION: Activates pro-caspase-1 and pro-caspase-8. Functial Sunds to BIRC3/C-1AP2, TRAF!, TRAFS and

C. -- CATALVATY: ATP + a protein = ADP + a protein = ADP + a protein = ADP + a protein = ADP + a protein = ADP + a protein = ADP + a protein = ADP + a protein = ADP + a protein = ADP + a protein = ADP + a protein = ADP + a protein = ADP + a protein = ADP + a protein = ADP + a protein = ADP + a protein = ADP + a protein = ADP + a protein = ADP + a protein = ADP + a protein = ADP + a protein = ADP + a protein = ADP + a protein = ADP + a protein = ADP + a protein = ADP + a protein = ADP + a protein = ADP + a protein = ADP + a protein = ADP + a protein = ADP + a protein = ADP + a protein = ADP + a protein = A
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SUBCELLULAR LOCATION: Cytoplasmic (Probable).
TISSUE SPECIFICITY: Detected in heart, brain, placenta, lung, peripheral blood leukscytes, spleen, kidney, testis, prostate, pancreas and lymph node.
FTM: Autophosphorylated.
SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
SIMILARITY: Contains 1 CARD domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0004674; F:protein serine/threonine kinase activity; TAS. GO:0004871; F:signal transducer activity; TAS. GO:0006915; P:apoptosis; TAS. GO; GO:0006915; P:apoptosis; TAS. GO; GO:0006915; P:signal transduction; TAS.
                                                                                  the EMBL/GenBank/DDBJ databases
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001315; CARD.
InterPro; IPR000319; Prot kinase.
InterPro; IPR008271; Ser thr pkin AS.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF00619; CARD; 1.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
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EMBL, AF078530, AAC27722.1; --
EMBL, AF064824, AAC2568.1; --
EMBL, AC04003, AAC4561.1; --
EMBL, AF117829, AAD04553.1; --
EMBL, BC004553; AAH04553.1; --
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                                         SECUENCE FROM N.A.
Platzer M., Varon R.;
Submitted (DEC-1998) to
                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                      K->A: ABOLISHES KINASE ACTIVITY.
K->M: REDUCES FAS-MEDIATED APOPTOSIS.
D->N: ABOLISHES KINASE ACTIVITY.
; 575A692239505792 CRC64;
PROSITE; PS50209; CARD; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding; Phosphorylation; Apoptosis.
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227
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ATP (BY SIMILARITY).
ATP.
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Matches:
Conservative:
Mismatches:
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                                                                                                        DOMAIN
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371 571 631

691 431 751 451 811

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332 LeuAsnIleProAlaAsnHisProProGlnGluGluSerCysGlySerSerLeuLeuSer 351
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                                                                                                                 TISSUE=Endothelial cells;
MEDLINE=99240667; PubMed=10224040;
Bertin J., Nir W.-J., Fischer C.M., Tayber O.V., Errada P.R.,
Grant JR., Kellty J.J., Gosselin M.L., Robison K.E., Wong G.H.W.,
Glucksmann M.A., Distefano P.S.;
"Human CARD4 protein is a novel CED-4/Apaf-1 cell death family member
                                                                                                                                                                                                                                                                                             ||||||||||
|SerTrpAspGlyIleValSerValProProGlyAlaAlaPheCysAspArgArgAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        532 CCATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  432 IleGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAlaIleValSerGlnMetThr
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                                                                                            CAGTTACAGAGTGTTTTCAAGTGCCATTCACCTATGTGACAAGAAAATGGAATTATCT
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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09Y239; QBIMPE;
10.0033 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10.0077-2003 (Rel. 42, Last annotation update)
Caspase recruitment domain protein 4 (Nod1 protein)
                                              US-09-771-161A-2 (1-1669) x RIK2 MOUSE (1-539)
      Gaps:
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                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6;
MEDLINE=21891093; PubMed=11894097;
Chin A.I., Dempsey P.W., Bruhn K., Miller J.F., Xu Y., Cheng G.;
"Involvement of receptor-interacting protein 2 in innate and adaptive
                                                                                                                                                         28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Activates pro-caspase-1 and pro-caspase-8. Potentiates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CASP-8-mediated apoptosis. Activates NP-kappaB (By similarity).
CASP-8-mediated apoptosis. Activates NP-kappaB (By similarity).
CANTATTC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
SUBMINI: Binds to CHAR/CLARP and CASPI via their CARD domains
Binds to BIRC3/c-IAPI and BIRC2/c-IAP2, TRAF1, TRAF2, TRAF5 and
TRAF6. May be a component of both the TNFRSF1A and TNFFSF5/CD40
receptor complex (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
FTM: Autophosphorylated (By similarity).
SIMILARITY: Belongs to the Sar/Thr family of protein kinases.
SIMILARITY: Contains 1 CARD domain.
                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE: PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
42951BF97CA15DFA CRC64;
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InterPro; IPR001315; CARD.
InterPro; IPR001315; Prot kinase.
InterPro; IPR008271; Ser thr pkin AS.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PP00619; CARD; I.
Pfam; PP00669; pkinase; I.
PRINTS; PR00109; TYRKINASE.
AsnLeuLeuGlnAsnLysSerMet 540
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SMART; SM00114; CARD; 1.
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                                                                                                                                    (Rel. 41, Created)
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DOMAIN 18 294
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                                                                                        STANDARD;
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28-FEB-2003
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P58801;
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                                                                                                                                                                                                                                             MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; PubMed=12477932;
Attausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Attausherg R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A plachenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Branstein M.J., Uddin T.B., Fonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uddin T.B., Poshiyuki S., Carninci P., Prange C.,
A Brownstein M.J., Uddin T.B., Poters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., NcKernan K.J., Malek J.A., Gunaratne P.H.,
Brownstein M.S., McKernan R.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Pilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Brownstein M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Brownstein A.G., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Brownstein M.A., Sochein J.E., Jones S.J.M., Marra M.A.;
F. "Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21264704; PubMed=11058605;
Inohara N., Ogura Y., Chen F.F., Muto A., Nunez G.;
"Human Nod1 confers responsiveness to bacterial lipopolysaccharides.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 276:2551-2554 (2001).
- FUNCTION: Enhances caspase-9-mediated apoptosis. Induces NF-kappa-B activity via RICK (CARDIAK, RIP2) and IKK-gamma. Confers responsiveness to intracellular bacterial lipopolysaccharides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: Self-associates. Binds to caspase-9 and RICK by CARD-CARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interaction.
SUBCELULAR LOCATION: Cytoplasmic.
TISSUB SPECIFICITY: Highly expressed in adult heart, skeletal TISSUB SPECIFICITY: Highly expressed in adult heart, skeletal muscle, panoreas, spleen and ovary. Also detected in placenta, lung, liver, kidney, thymus, testis, small intestine and colon. SIMILARITY: Contains I CARD domain.
SIMILARITY: Contains 1 NACHT domain.
SIMILARITY: Contains 9 leucine-rich (LRR) repeats.
                                                                                      MEDLINE=99262599; PubMed=10329646; Inohara N., Koseki T., del Peso L., Hu Y., Yee C., Chen S., Carrio l Merino J., Liu D., Ni J., Nunez G.; Modl, an Apaf-1-like activator of caspase-9 and nuclear factor-kappas."; J. Biol. Chem. 274:14560-14567(1999).
                                                   SEQUENCE FROM N.A., AND MUTAGENESIS OF VAL-41 AND LYS-208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0006656; F:caspase activator activity; TAS. GO; GO:0006915; P:apoptosis; TAS. GO; GO:0007165; P:signal transduction; TAS. InterPro; IPR001315; CARD.
                 Biol. Chem. 274:12955-12958(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF126484; AAD29125.1; -.
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 that activates NF-kappaB.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:16390; CARD4.
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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|----LeuLeuGluIleGlyPheSerProSerLeu--- 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                707 CAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAAATGACAGAAGCC---TGCCTT 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              764 AACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGGACTATGAACTT 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 GlnLeuLeuLysSerAsnArgGluLeuLeuValThrHisIleArgAsnThrGlnCysLeu 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 ------ValAspAsnLeuLeuLysAsnAspTyrPheSerAlaGluAspAlaGluIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             884 CAAGGAGAA------GAATTTGCCAAAGTTATAGTACAAAAATTGAAAGATAACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 LysglyGluGluValSerGluPhePheLeuTyrLeuLeuGlnGlnLeuAlaAsp---Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            935 CAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAAAT
                                                                                                                                                                                                                                                                                                V->Q: ABOLISHES CASPASE-9 ACTIVATION AND INTERACTION WITH RICK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                       K->R: REDUCES CASPASE-9 ACTIVATION
                                                                                                                                                                                                                                                                                                                                                        -> H (IN REF. 3).
0A9DF5FC6487E21A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       953
39
119
6 111
                                                                                             , Leucine-rich repeat
                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical protein F22B7.5 in chromosome III.
                                                                                                                                              ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           943 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-771-161A-2 (1-1669) x CAR4_HUMAN (1-953)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                          LRR 3.
LRR 4.
LRR 5.
LRR 6.
LRR 7.
LRR 9.
                                                                                                              CARD.
                interPro; IPR007111; NACHT_NTPase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ::: |||:::|||:::
TyrValAspLeuArgProTrp-
                                                                                                                                                                                                                                                                                                                                                                         ₩,
                                                             PROSITE; PS50209; CARD; 1.
PROSITE; PS50837; NACHT; 1.
Apoptosis; ATP-binding; Repeat
DOMAIN 15
interPro; IPR007091; LRR_RNinh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTACTTCAAAATAAA 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 LeuThrGinSerLys 118
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55.24%
37.14%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F22B7.5.
Caenorhabditis elegans.
                                                                                                                               531
209
656
725
775
778
806
862
                              Pfam; PF00619; CARD; 1
Pfam; PF05729; NACHT;
                                                                                                                                                                                                                                                                                                                                                                         953 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
                                                                                                                                                                                                               755
                                                                                                                                                                                                                                                                                                                                            208
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           Aliqnment Scores:
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                                                                                                                             DOMAIN
NP BIND
REPEAT
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REPEAT
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MUTAGEN
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REPEAT
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No.:
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477
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494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-96149249; PubMed-8552191;
Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,
Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
"Suppression of apoptosis in mammalian cells by NAIP and a related
                                                                                                                                                                        ---TCTCAAAGGGCTGCA
                                                                                                      :::|||
458 SerAlaSerLysLysThrThrLysSerHisArgIleLeuProGlyLeuArgAlaAsnTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ::: ::: |||||||:::|||
478 ThrLysValGlnSerMetLysValLeuGlyMetPheVal------LeuAsnArgSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||||||||||||||||||||--SerGlyLeulleHisArgSerValProLeuLeuAlaGln------ValSerThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||| ||| |||:::||||::: ||||||
511 ProThrThrSerThrThrLysLeuAlaGlnLeuHisThrThrHisAlaLeuSerLysGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96128127; PubMed=8548810; Roche M., Goeddel D.V.; Roche M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.; "The Fignaling complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins."; Coharas 1252(1995).
                                                                                                                                                                                                                      418 LysLysGluAsnGluGluProValAspMetMetAspLeuIlePheSerMetSerArg
                                                                                                                                                                                                                                                                                                                       438 MetAspAspGlnArgThrGluLeuProAlaAlaArgPheIleProProArgProValSer
                                                                                                                                                                                                                                                                                                                                                                        ----AACTCAGAACGTCTGCAGCCTGGTATAGCCCCAGCAGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     773 CTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGACGACTATGAACTTGTTAGTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    833 AAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACACTACTGACATCCAAGGAGAA
                                                                                                                                                                                                                                                                         611 TTCTGTGATCACAAGACCACTCCATGCTCTTCAGCAATAATA.----AATCCACTCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      893 GAATTTGCCAAAGTTATA---GTACAAAATTGAAAGATAACAAA-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BIRZ HUMAN STANDARD; PRT; 618 AA.
013490; Q16516;
01-NOV-1997 (Rel. 35, Created)
10-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Baculoviral IAP repeat-containing protein 2 (Inhibitor of apoptosis protein 2) (HIAP2) (G-IAP1) (TNFR2-TRAF signaling complex BRC2 OR APII OR IAP2 OR MIHB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||||::: :::||||:::: 551 TyrPheGlnLeuAlaLysLysTyrHisProAspVal 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   935 -----CAAATGGGTCTTCAGCCTTACCCGGAAATA 964
                                                                          572 AGTIGGGATAGCACCATTICTGGA----
                                                                                                                                                                                                                                                                                                                                                                        665 ACTGCAGGA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      family of IAP genes.";
Nature 379:349-353(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
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TISSUE=Fetal liver;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      349 IleAspValAlaMetAsnGlnGluArgSerGluThrAlaThrAspGlnAspValCysLeu 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AlaIleAspSerSerProAspProThrSerSer------AsnAspMet 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCCTGGAAATCAC 571
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                                                                     Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Collson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Farser A.,
Fruiton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latraille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.
Sims M., Smaldon N., Smith A., Sonnammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                              ij
                                                                                                                                                                                                                                                                                                                                              Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J-DOMAIN.
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Contains 1 GoLoco domain. SIMILARITY: Contains 1 J domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L12018; AAA65459.1; -. PIR; S44656; S44636. HSSP; P08622; 1XBL. WOYMDED; F22B7.5; CE00158. InterPro; IPR001305; DnaJ.CXCXCXGX. InterPro; IPR001305; DnaJ.CXCXCXGX. InterPro; IPR001305; DnaJ.N. InterPro; IPR001305; HSP40. DnaJ. DnaJ. N. InterPro; IPR001309; HSP40. DnaJ. DnaJ. InterPro; IPR003091; HSP40. DnaJ. InterPro; IPR003091; HSP40. DnaJ. InterPro; IPR003091; HSP40. DnaJ. InterPro; IPR008941; TPR-11ke. Pfam; PF00265; DnaJ.; 1. Pfam; PF00265; DnaJ. C. 1. Pfam; PF00188; GoLoco; 1. Pfam; PF00188; GoLoco; 1. PR0011E; PS00636; DNaJ. 1. PR0SITE; PS00636; DNAJ.; 1. PROSITE; PS00636; DNAJ.; 1. PROSITE; PS00636; DNAJ.; 1. PROSITE; PS00637; GOLOCO; 1.
                         STRAIN=Bristol N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          943 AA; 105926 MW;
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100.50
38.36%
19.40%
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                                                                                                                                                                                                                                                                                                                                                                                               Nature 368:32-38(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity:
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Best Local Similari
                                                                                                                                                                                                                                                                                                                       Wohldman P.;
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DB:
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SOURCE STANTANT STANT

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                                                                                                                                                     TISSUETERON N.A.

TISSUETERIS, and Uterus;

TISSUETERIS, and Uterus;

TISSUETERIS, bubmed=1247932;

MEDINE-2238825; bubmed=12.A., Grouse L.H., Derge J.G.,

Rausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Rausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Buetow K.H., Scaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Mang J., Haich F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M.J., Usdin T.B., Ponaldo M.F., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevochenko Y., Bouffard G.G.,

A hilalon D.K., Muzny D.W., Schen E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Nexpwinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                мим; 601/12; -. F.apoptosis inhibitor activity; TAS.
GO; GO:0009189; F.apoptosis inhibitor activity; TAS.
GO; GO:0007166; P.cell surface receptor linked signal transdu. . .; TAS.
InterPro; IPR001370; BIR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: APPPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS WITH THE RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAFI AND TRAF2) TO FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TWFR2) TO SUBUNIT: Interacts with SMAC and with PRSS25; these interactions inhibit apoptotic suppressor activity.

SUBCELLUAR LOCATION: Cytoplasmic (Potential).

TISSUE SPECIFICITY: PRESENT IN MANY FETAL AND ADULT TISSUES.

MAINLY EXPRESSED IN ADULT SKELETAL MUSCLE, THYMUS, TESTIS, OVARY, THYMUSKASS, LOW OR ABSENT IN BRAIN AND PERIPHERAL BLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRUCTURE BY NMR OF 266-363.
MEDILES99332054; PubMed=10404221;
Hinds M.G., Norton R.S., Vanx D.L., Day C.L.;
Hinds M.G., Rorton C.S., Vanx D.L., Day C.L.;
"Solution structure of a baculoviral inhibitor of apoptosis (IAP)
         Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L., "Cloning and expression of apoptosis inhibitory protein homologs function to inhibit apoptosis and/or bind tumor necrosis factor receptor-associated factors";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEUKOCYTES.
--- SIMILARITY: Belongs to the IAP family.
--- SIMILARITY: Contains 3 BIR repeats.
--- SIMILARITY: Contains 1 CARD domain.
--- SIMILARITY: Contains 1 RING-type zinc finger.
                                                                                         receptor-associated factors.";
Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nat. Struct. Biol. 6:648-651(1999).
PubMed=8643514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U37547; AACKOSO811; --
EMBL; BC016174; AAH16174.1; --
EMBL; BC028578; AAH28578.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L49431; AAC41942.1; -.
EMBL; U45879; AAC50372.1; -.
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PDB, 1QBH, 20-OCT-99.
Genew, HGNC:590, BIRC2.
    MEDLINE=96209843;
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MIM; 60
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980 TCACCATCTTTAAATTTACTTCAAAATAAAAGCATGTAAGTGACTGTTTTTCAAGAAGAA 1039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            833 AAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACACTACTGACATCCAAGGAGAA
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31
29
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16
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Matches:
Conservative:
 R InterPro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro', Interpro'
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S -> P (IN R
C -> G (IN R
Q -> L (IN R
L -> W (IN R
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BIR 3.
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Best Local Similarity:
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Score:
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RA MEDININE-2134683; PubMedel 1. Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Baldarelli R., Bratel D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
Balke J.A., Bratel D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
Anai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
Anagaya A., Kurochkin I.V., Lee Y., Lenhard B. L., Jarvis E.D.,
Anagashina T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
Werardo R., Wagner L., Wahlestett C., Wang Y., Watanabe Y., Walls C.,
Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang I.,
Anai K., Kawai J., Alzawa K., Arakawa T., Fukuda S.,
Altara R., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
A Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
A Hara A., Hashizaki Z., Saski D., Shibata K., Shinagwa A.,
A Hara A., Hashizaki Z.,
A Hara A., Hashizaki Z.,
A Hara A., Hashizaki Z.,
A Hara A., Hashizaki Z.,
A Hara A., Hashizaki Z.,
A Hara A., Hashizaki Z.,
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A Hara A., Hashizaki Z.,
A Hara A., Hashizaki Z.,
A Hara A., Hashizaki Z.,
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A Harana A., Shinagasa A.,
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SEQUENCE FROM N.A., AND VARIANT ALA-884.

STRAIN-CZech II, and FVB/N; TISSUE-Breast cancer;

MEDINE-238825; PubMed-12477932.

Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Haich F.,

Appleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheeter T.E.,

Brownstein M.J., Usdin T.B., Toobhyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shewchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rutterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Bromeration and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
::: ::: ||| :::||| 579 ValSerValValPheIleProCysGlyHisLeuValValCys 592
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                            CARA MOUSE STANDARD; PRT; 953 AA. 08BHBG; 08BUTC; 100-CT-2003 (Rel. 42, Created) 10-CCT-2003 (Rel. 42, Last sequence update) 110-CCT-2003 (Rel. 42, Last annotation update) CARD4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=NOD; TISSUE-Cerebellum, and Spleen;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                CAR4 MOUSE

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   713 ATCCAGAGCAAAAGGGAAGACATTGTG---AACCAAATGACAGAAGCCTGCCTTAACCAG 769
  829
  40
   :::||| ||||||| |||||| 41 ---ValAspAsnLeuLeuGluAsnGlyTyrPheSerAlaGluAspAlaGluIleValCys 59
  -!- SUBUNIT: Salf-associates. Binds to caspase-9 and RICK by CARD-CARD interaction (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Contains 1 CARD domain.
-!- SIMILARITY: Contains 9 leucine-rich (LRR) repeats.
FUNCTION: Enhances caspase-9-mediated apoptosis. Induces NF-kappa-
  770 TCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGGACTATGAACTTGTTAGT
   23 LeuLyslleAsnArgGluHisLeuValThrAsnIleArgAsnThrGlnCysLeu----
  830 ACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACACTACTAGACATCCAAGGA
   EMBL, BC043670; AAH43670.1; -.
MGD, MGI:1341839; Card4.
MGD, MGI:1341839; Card4.
InterPro; IPR007091; LRR RNinh.
InterPro; IPR007101; NACHT_NTP88e.
Pfam; PF00619; CARD; 1.
Pfam; PF005729; NACHT; 1.
PROSITE; PS50209; CARD; 1.
PROSITE; PS50209; CART; 1.
Apoptosis; ATP-binding; Repeat; Leucine-rich repeat; Polymorphism.
                    B activity via RICK (CARDIAK, RIP2) and IKK-gamma. Confers responsiveness to intracellular bacterial lipopolysaccharides
   390 GAA-----GAATTTGCCAAAGTTATAGTACAAAATTGAAAGAT 928
  95
  -> A (in strain Czech II). 39C639621CEBIA58 CRC64;
   953
27
13
29
7
  Conservative:
Mismatches:
   ATP (POTENTIAL).
LRR 1.
LRR 3.
LRR 4.
LRR 5.
LRR 5.
LRR 6.
LRR 7.
   Length:
Matches:
   Indels:
  US-09-771-161A-2 (1-1669) x CAR4_MOUSE (1-953)
  CARD.
  ^
  EMBL; AK082663; BAC38566.1; -. EMBL; AK089662; BAC40940.1; -.
  107739 MW;
   EMBL; BC042670; AAH42670.1; -. EMBL; BC043670; AAH43670.1; -.
  (LPS) (By similarity).
  96.50
52.63%
35.53%
3.35%
  783
839
867
895
923
884
953 AA;
  Percent Similarity:
Best Local Similarity:
   Alignment Scores:
Pred. No.:
  VARIANT
SEQUENCE
   DOMAIN
DOMAIN
NP_BIND
REPEAT
   Query Match:
  REPEAT
REPEAT
   REPEAT
  REPEAT
  REPEAT
  REPEAT
   REPEAT
  REPEAT
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995 ITACTICAAAATAAAAGCATGTAAGTGACTGTTTTTCAAGAAAAAGAAATGTGTTTCATAAAA 1054
   |||||| :::||| :::||| :::
303 LeuLeuGlyHisLySLySIJeLeuGlnThr-PheThrLySGlnLySASpThrAlaArgAl 322
  683 CGTCTGCAG-----CCTGGTATAGCCCCAGCAGTGGATCCAGAGCAAAAGGGAAGAC 733
   ATTGTGAACCAAATGACAGAAGCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGG 793
------GlyGlyHisThrGln 197
  Genomics 46:495-503(1997).

-i- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
-i- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
WITH THE RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
NECROSIS FACTOR RECEPOR 2 (TNFR2).

-i- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions
   TISSUE-Skeletal muscle;
MEDIINE-98110590; PubMed-9441758;
Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
"Genomic characterization of the mouse inhibitor of apoptosis protein
  GluGluSerGluAlaLeuAspThrThrSerAsnGlyLeuAspAlaLeuAsnThrGlnIle
   881 -----ATCCAAGGAGAAGTTTGCCAAAGTTATAGTACAAAAATTGAAAAGATAACAAA
   935 CAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAAAT
   286 ------LeuArgThrSerProThrGlnLeuGluGluCysArgLysAlaAlaValPhe
  623 AAGACCACTCCATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAA
   GACTTGATCATGAAAGAGGACTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAA
   062210; 008864;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Baculoviral IAP repeat-containing protein 2 (Inhibitor of apoptosis
protein 2) (MIAP-2)
  Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
  [1] — SEQUENCE. SEQUENCE. SEQUENCE. SEQUENCE. SEQUENCE. SEQUENCE. SEQUENCE. SEQUENCE. SEQUENCE. SECUENTE 96128127; PubMed=8548810; Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.; Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.; Trother TURRZ-TRAF signaling complex contains two novel proteins to baculoviral inhibitor of apoptosis proteins."; cell 83:1243-1252(1995).
   GluLeuGlnPheMetAlaThrAsnValArgLysValTrpile------
   612 AA
  LysthrLeuIleSerCysLysAlaLeuPhe-
  PRT;
   1055 GGATATTTATATCTCTGTT 1073
  322 aLeuPheTyrileAsnLeu 328
  STANDARD;
   SEQUENCE FROM N.A.
  NCBI_TaxID=10090;
   and 2 genes.
  BIR2 MOUSE
  183
   198
   794
  229
  734
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
   GGAAATCACAGTTGGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATTCTGTGATCAC 622
  --AsnGlu 130
   514
   TICTATAATITICCTAATCATCTCCAGTTAAAGIGTATATATATATTATGTATTCATTACAG 334
  454
  335 TTACAGAGTGTTTCAAGTGCCATTCACCTATGTGACAAGAAAAATGGAATTATCTCTG
  ::::::::||| ||| ::: ::: |||||||
---AsnAlalleAlaSerGlyIleLysIleProGluSerLysLys-------
   455 AATAGTGGTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTTTA
  395 AACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCTCAGCTCCATGAA
  -------TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCCT
  151 AspAlaThrAsnAlaArgLysGluLeuAspGluTyrPheArgLysLeuGln-----
   Utata I., Sakamoto S., Imura T., Toh-E A.;
"Yeast plasmids resembling 2 micron DNA: regional similarities and diversities at the molecular level.";
J. Bacteriol. 169:5537-5545(1987)
-:- FUNCTION: PLASMID PARTITION REQUIRE REPI, REP2, AND A CIS-ACTING DNA SEQUENCE (KNOWN AS STB). REP 1 MAY ACT BY INTERCALATING IN THE YEAST NUCLEAR MATRIX AND BINDING STB EITHER DIRECTLY OR VIA
  Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Zygosaccharomyces.
NCBI_TaxID=4954;
   7DF4C06359D4BA35 CRC64;
   357
61
53
100
73
   Length:
Matches:
Conservative:
Mismatches:
   REP2.
SIMILARITY: TO THE P GENE PRODUCT OF PSR1.
   (Rel. 13, Created)
(Rel. 13, Last sequence update)
(Rel. 15, Last annotation update)
  357 AA
  Indels:
  US-09-771-161A-2 (1-1669) x REP1_ZYGBA (1-357)
  Gaps:
  MEDLINE=88058763; PubMed=3680169;
   EMBL, M18274; AAA35283.1; -.
InterPro, IPR008897; Yeast TAF.
Pfam; PF05797; Yeast TAF; I.
Plasmid, Trans-acting factor.
SEQUENCE 357 AA; 40752 WW; 7
   Trans-acting factor B (REP1).
   1.41
94.00
39.72
21.25
3.26%
  Zygosaccharomyces bailii.
   STANDARD;
  SEQUENCE FROM N.A.
   Percent Similarity:
Rest Local Similarity:
  01-AUG-1990 (Rel
   STRAIN=IFO 1047
  Alignment Scores:
   Plasmid pSB2
   01-JAN-1990
01-JAN-1990
   ZYGBA
   115
  515
   Best Local S:
Query Match:
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                 980 TCACCATCTTTAAATTTACTTCAAAATAAAAGCATGTAAGTGACTGTTTTTCAAGAAGAA 1039
   346
   553 GluGluGlnLeuArgArgLeuGlnGluGluArgThrCysLysValCysMetAspArgGlu 572
   493
  230 ATGTATTTT---GTACAAACATATAAAATGTGTTAGAATGTATTTTTACTTCTATAATTTC
   287 CTAATCATCTCCCAGTTAAAGTGTATATATTTATGTATTCATTACAGTTACAGAGTGTT
  Saccharomyces cerevisiae.";
Agric. Biol. Chem. 55:1953-1958(1991).
-!- FUNCTION: Kill sensitive strains of yeast. Optimal pH is 4-4.5
and it is unstable above 30 degrees Celsius.
-!- SUBUNIT: Monomer.
-!- SIMILARITY: TO YEAST YER187W.
  Saccharomycetes;
  MEDLINE=92118315; PubMed=1368726;
Goto K., Fukuda H., Kichise K., Kitano K., Hara S.;
"Cloning and nucleotide sequence of the KHS killer gene of
  01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Killer toxin KHS precursor (Killer of heat sensitive).
KHSI OR KHS OR YER187W-A.
  FB63D9E8C4C27431 CRC64;
   708
35
80
48
   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota; Saccharomycotina, Sacci
Saccharomycetales, Saccharomycetaceae, Saccharomyces
   1040 ATGTGTTTCATA------AAAGGATATTTATATCTCTGT
   Length:
Matches:
Conservative:
Mismatches:
   KILLER TOXIN KHS
   708 AA
  SEQUENCE FROM N.A., AND SEQUENCE OF 37-42.
   Indels:
  US-09-771-161A-2 (1-1669) x KHS1_YEAST (1-708)
   POTENTIAL
   POTENTIAL
  POTENTIAL
  POTENTIAL
   27
36
37
77
97
400
486
79535 MW; L
  EMBL; S77712; AAC60532.1; -. PIR; JQ1148; JQ1148. Germonline; 144546; -. SGD; S0007427; KHS1. Toxin; Signal; Transmembrane.
   3.43
90.00
37.86%
20.87%
3.12%
   STANDARD;
   Percent Similarity:
Best Local Similarity:
  NCBI_TaxID=4932;
   Alignment Scores:
   STRAIN=115;
   YEAST
  TRANSMEM
   TRANSMEM
  TRANSMEN
   SEQUENCE
   Query Match:
DB:
   KHS1 YE
P396<u>9</u>0;
   SIGNAL
  Pred. No.:
  KHS1_YEAST
   CHAIN
   RESULT
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  455 ileargLysAsnargMetAlaLeuPheGlnGinLeurhrHisValLeu-----Prolle 472
   -----AACAAACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGA 979
   513 AlaAlaAlaAsnIlePheLysAsnSerLeuLysGluIleAspSerThrLeuTyrGluAsn 532
   533 LeuPheValGluLysAsnMetLysTyrIleProThrGluAspValSerGlyLeuSerLeu 552
  AAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACACTACTGACATCCAAGGAGAA
  CTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGGACTATGAACTTGTTAGTACC
             -!- SUBCELLULÂR LOCATION: Cytoplasmic (Potential).
-!- TISSUE SPECIFICITY: Expressed in heart, brain, spleen, lung, liver, skeletal muscle, kidney and testis.
-!- SIMILARITY: Belongs to the lamily.
-!- SIMILARITY: Concains 3 BIR repeats.
-!- SIMILARITY: Contains 1 CARD domain.
-!- SIMILARITY: Contains 1 RING-type zinc finger.
inhibit apoptotic suppressor activity (By similarity).
  GAATTTGCCAAAGTTATAGTACAAAAATTGAAAGAT------
  RING-TYPE.
E -> K (IN REF. 2).
E08969D93C6C610D CRC64;
  612
30
25
63
16
  Length:
Matches:
Conservative:
Mismatches:
  Indels:
   SMART; SM00238, BIR; 3.
SMART; SM00134; RARD; 1.
SMART; SM00144; RING; 1.
SMOSITE; PS01282; BIR REPEAT 1; 3.
PROSITE; PS501043; BIR REPEAT 2; 3.
PROSITE; PS00128; PS16209; CARD; 1.
PROSITE; PS00189; ZF RING 1; FALSE NEG.
   US-09-771-161A-2 (1-1669) x BIR2_MOUSE (1-612)
  BIR 1.
BIR 2.
BIR 3.
CARD.
  Apoptosis; Zinc-finger; Repeat.
   MGD; MGI:1197009; Birc3.
InterPro; IPR001370; BIR.
InterPro; IPR001315; CARD.
InterPro; IPR001841; Znf_ring.
  69676 MW;
  EMBL; L49433; AAC42078.1; -. EMBL; U88909; AAC53532.1; -. HSSP; Q13490; 1QBH.
  Pfam; PF00653; BIR; 3.
Pfam; PF00619; CARD; 1.
Pfam; PF00097; zf-C3HC4; 1.
   92.00
41.04%
22.39%
3.19%
  600
380
  Š
  Percent Similarity:
Best Local Similarity:
   Alignment Scores:
  893
  773
  833
  ZN FING
CONFLICT
   SEQUENCE
  Query Match:
DB:
  REPEAT
DOMAIN
   REPEAT
  Pred. No.:
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   Best Local Similarity:
   Percent Similarity:
   Alignment Scores:
   491
  404
   511
   452
  536
  555
  Query Match:
DB:
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   610 SerSerAsnAsnArgPheCysCysLeuLysSerIlePheIleAsnAsnCysLysLysAla 629
  ::: |||||||:::|||| :::
SerArgPheCysAsnHisValValSerTyrTyrProSerGlnAsnAlaThrIleHisLeu 589
  718
  560 CCTGGAAATCACAGTTGGGAT------AGCACCATTTCTGGATCTCAAAGG 604
   -----TrpSerArgValLysGlyValSerCysAsnThrAlaAsnArgLeu 569
  GCTGCATTCTGTGATCACAAGACCACT----CCATGCTCTTCAGCAATAATAAATCCA 658
  -----AGGGAAGACATTGTGAACCAAATGACAGAAGCC 757
  -----AGTGGTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAA 499
   554
  CTCTCAACTGCAGGAAACTCAGAACGTCTGCAGCTGGTATAGCCCAGCAGTGGATCCAG
  GACAATGATTTTTTATCTAGAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGT
                     347 TCAAGTGCCATTCACCTATGTGACAAGAAAATGGAATTATCTCTGAACATACCTGTA
   -----MetMetArgThrHis----
  "The sequence of 29.7 kb from the right arm of chromosome II reveals 13 complete open reading frames, of which ten correspond to new
   STRAIN=S288c;
MEDLINE=94318717; PubMed=8091856;
Becam A.-M. Cullin C., Grzybowska E., Lacroute F., Nasr F.,
Ozier-Kalogeropoulos O., Palucha A., Slonimski P.P., Zagulski M.,
  534 ArgAlaGlyAlaLeuLeuAspĠlyArgValArgThrlleArgPheLeu-----
   MEDINE=99147772; PubMed=8065923; Kato R., Ogawa H.; Anteresential gene, ESR1, is required for mitotic cell growth, D repair and meiotic recombination in Saccharomyces cerevisiae.", Nucleic Acids Res. 22:3104-3112(1994).
  Saccharomycetes;
  genes.";
Yeast 10:S1-S11(1994).
-i- FUNCTION: Required for cell growth, DNA repair and meiotic
   AATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCATGAAAAT
   SEQUENCE FROM N.A.
Weinert T.A., Harlow D.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
  Saccharomyces cerevisiae (Baker's yeast).

Bukaryota, Fungi, Ascomycota, Saccharomycotina, Sacchascomycetales, Saccharomycetaces, Saccharomyces

NCBI_TaxID=4932;
   01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
  2368 AA
  ESRI protein.
ESRI OR MECI OR SAD3 OR YBR136W OR YBR1012.
  PRT;
   630 CysGluSerProSerLeu 635
   TGCCTTAACCAGTCGCTA 775
   AGCAAA-----
  STANDARD;
   SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
   002580;
  YEAST
   758
  629
  290
   719
  605
  570
  407
   514
  200
   550
   555
  458
  ESR1 YEA P38111;
   RESULT 10
ESR1_YEAST
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   523
   511
  535
   554
  -----TGTCCTGGAAATCACAGTTGGGATAGCACCATTTCTGGATCTCAA 601
   403
  510
   451
   ---SergluSerLeuLeuSerglyIleLeuPheSerLeuHisArgIlePheSerHisPhe
  ------ATGGAATTATCTCTGAACATACCT
   ----CTCCAT
   GAAAATAGTGGTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTT
   . S0000340; MEC1.
GO:0005634; C:nucleus; IC.
GO:000076; P:DNA replication checkpoint; IMP.
GO:00007131; P:nucleobase, nucleoside, nucleotide and nucl.
   Pram; PP02259; FAT; 1.

Pram; PP02260; FAT; 1.

Pram; PP02260; FAT; 1.

Pram; PP02260; FAT; 1.

Pram; PP02260; FAT; 1.

Prosite; PS00915; P13 4 KINASE 1; 1.

PROSITE; PS00916; P13 4 KINASE 2; 1.

PROSITE; PS00916; P13 4 KINASE 3; 1.

Meiosis; Transferase; KINASE 3; 1.

Meiosis; Transferase; KINASE 3; 1.

PROSITE; PS0229; P13 4 KINASE 3; 1.

PROSITE; PS0290; P13 4 KINASE 3; 1.

PROSITE; PS0290; P13 4 KINASE 3; 1.

PROSITE; PS0290; P13 4 KINASE 3; 1.

PROSITE; PS0290; P13 4 KINASE 3; 1.

PROSITE; PS0290; P13 4 KINASE 3; 1.

PROSITE; PS0290; P13 4 KINASE 3; 1.

PROSITE; PS0290; P13 4 KINASE 3; 1.

PROSITE; PS0290; P13 4 KINASE 3; 1.

PROSITE; PS0290; P13 4 KINASE 3; 1.

PROSITE; PS0290; P13 4 KINASE 3; 1.

PROSITE; PS0290; P13 4 KINASE 3; 1.

PROSITE; PS020916; P13 4 KINASE 3; 1.

PROSITE; PS020916; P13 4 KINASE 3; 1.

PROSITE; PS020916; P13 4 KINASE 3; 1.

PROSITE; PS020916; P13 4 KINASE 3; 1.

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PROSITE; PS020916; P13 4 KINASE 3; 1.

PROSITE; PS020916; P13 4 KINASE 3; 1.

PROSITE; PS020916; P13 4 KINASE 3; 1.

PROSITE; PS020916; P13 4 KINASE 1.

PROSITE; PS020916; P13 4 KINASE 3; 1.

PROSITE; PS020916; P13 4 KINASE 1.

PROSITE; PS020916; P13 4 KINASE 1.

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PS020916; P13 4 KINASE 1.

PS020916; P13 4 KINASE 1.

PS020916; P13 4 KINASE 1.

PS0
   512 TTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCAC----
                              SIMILARITY: IN THE N-TERMINAL REGIÓN, TO S.POMBE CUT1. SIMILARITY: Belongs to the PI3/PI4-Kinase family.
   GTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAG---
  2368
64
44
126
63
   Conservative:
Mismatches:
Indels:
DEVELOPMENTAL STAGE: Induced during meiosis.
  Length:
Matches:
   US-09-771-161A-2 (1-1669) x ESR1_YEAST (1-2368)
  InterPro; IPR008938; ARM.
InterPro; IPR003151; FAT.
InterPro; IPR003152; PAT.
InterPro; IPR00403; P13 P14 kinase.
InterPro; IPR008941; TPR-like.
  359 CACCTATGTGACAAGAAGAA---
  EMBL; X75891; CAA53494.1; -.
EMBL; U31109; AAA74482.1; -.
EMBL; Z36005; CAA85094.1; -.
EMBL; D11088; BAA01860.1; -.
PIR, S46005; S46005.
GermOnline; 138679; -.
   4.2
89.50
36.36%
21.55%
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"Cloning and characterization of hREV3, the human homolog
  602776;
  Alignment Scores:
   SEQUENCE
   ZN FING
  CONFLICT
  CONFLICT
   VARIANT
  VARIANT
   VARIANT
  VARIANT
   VARIANT
   MIM;
  971 GTTTCTAGATCACCATCTTTAAATTTACTTCAAAATAAAAGCATGTAAGTGACTGTTTTT 1030
  1031 CAA-------GAAGAAATGTGTTTCATAAAAGGATATTTATATCTCTGT 1072
             661
  712
  595 PheAsnIleSerAspSerHisAsnSerGluAspGluHisThrAlaThrLeuIleLysPhe 614
   :::|||||||::::::
LeuGlnSerGlnLysLeuProValValLysGluAsnLeuValIleAlaTrpThrGlnLeu 634
  ||||
ThrLeuThrThrSerAsnAspValPheAspThrLeuLeuLeuLysLeulleAspIlePhe 654
   803 ATGAAAGAGGACTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAA 862
   674
   TTACTAGACACTACTGACATCCAA---GGAGAAGAATTTGCCAAAGTTATAGTACAAAA 919
   694
  920 TIGAAAGAIAAC-----AAACAAAIGGGICTICAGCCTIACCCGGAAAIACTIGIG 970
   715 TyrSerSerLysThrIleLeuAspIlePheGinArgTyrIleIleProTyrAlaIleIle 734
   735 GInTyrLysSerAspValLeuSerGluIleAlaLysIle------MetCys 749
                                   575 LysCysPheMetAsnSerAsnArgTyrLeuArgLeuLeuSerThrArgileIleProLeu 594
  ACAGAAGCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGG-----GACTTGATC 802
   695 LeuGlyLysAsnLeuValGluArgLysValGlyPheGlnAsnLeuIleGluLeuLeuGly 714
  -----TCAACTGCAGGAAACTCAGAACGTCTGCAGCCTGGTATAGCCCAGCAGTGG
            AGGGCTGCATTCTGTGATCACAAGACCACTCCATGCTCTTCAGCAATAATAATCCACTC
   Lin W., Wu X., Wang Z.; Ask Ash Kulling Ask Ash Coll-Length Coll of hash ask full-Length Coll of hash ask full-tength care for damage-induced mutagenesis in humans."; Mutat. Res. 433:89-98(1999).
  Murakumo Y., Rasio D., Roth T., Negrini M., Croce C.M., Fishel R.;
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
   gene, which
   1073 TGCTTTGACTTTTTTTATATAAATCCGTGAGTATTAAAGCTTTATTGAAG 1123
  750 AspGlyAspThrSerLeuileAsnGlnMetLysValAsnLeuLeuLysLys 766
  MEDLINE=98284025; PubMed=9618506;
Gibbs P.B.M., McGregor W.G., Maher V.M., Nisson P., Lawrence
"A human homolog of the Saccharomyces cerevisiae REV3 gene, wi
encodes the catalytic subunit of DNA polymerase zeta.";
Proc. Natl. Acad. Sci. U.S.A. 95:6876-6880(1998).
  DPOZ_HUMAN STANDARD; PRT; 3130 AA.
060673; 043214;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
DNA polymerase zeta catalytic subunit (EC 2.7.7.7) (RREV31.
  TISSUE=Bone marrow, and Leukocyte;
MEDLINE=99202263; PubMed=10102035;
  Homo sapiens (Human)
   TISSUE=Fetal brain;
   [3]
SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
  NCBI_TaxID=9606;
   863
  662
   713
  615
  749
  635
   HUMAN
  RESULT 11
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  MEDLINE=99126315; PubMed=9925914;
Morelli C., Mungall A.J., Negrini M., Barbanti-Brodano G., Croce C.M.;
"Alternative splicing, genomic structure, and fine chromosome
localizative (REV3L.";
Cytogenet. Cell Genet. 83:18-20(1998).
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
  -!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- TISSUE SPECIFICITY: Ubiquitously expressed.
-!- DOMAIN: Its C-terminal part could serve as the catalytic domain during nucleotide polymerization, while its N-terminal part could provide sites for protein-protein interactions with other factors during translesion DNA synthesis.
-!- SIMILARITY: Belongs to the DNA polymerase type-B family.
  PROSITE; PS00116; DNA_POLYMERASE B; 1.
Transferase; DNA-directed DNA polymerase; DNA replication;
DNA-binding; DNA repair; Nuclear protein; Zinc-finger; Polymorphism.
ZN_FING 3042 3057 C4-TYPE (POTENTIAL)
  ъ.
  Fishel
   S -> T.

/FTId=VAR_008519.

V -> I (in dbSNP:3204953).

/FTId=VAR_016147.

E -> Q (IN REF. 4 AND 5).

Y -> C (IN REF. 4 AND 5).

MW, 1C0700900F10BB14 CRC64;
cerevisiae REV3.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
   Roth T., Rasio D., Murakumo Y., Negrini M., Croce C.M., Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases
  GO; GO:0003894; F:zeta DNA polymerase activity; TAS. GO; GO:0006261; P:DNA dependent DNA replication; TAS. InterPro; IPR006172; DNA_pol_B.
InterPro; IPR00613; DNA_pol_B_dom.
InterPro; IPR006133; DNA_pol_B_exo.
InterPro; IPR006138; DNA_pol_B_exo.
   C4-TYPE (POTENTIAL)
   3 -> T.
/FTId=VAR_008517.
  2 -> H.
/FTId=VAR_008516.
   C -> E.
/FTId=VAR_008518.
   Pfam; PF00115; DNA_DO1_B; 1.
Pfam; PF03104; DNA_DO1_B exo; 1.
PRINTS; PR00106; DNAPOLE.
SWART; SW00466; POLEC; 1.
TIGREAMS; TIGR00592; Pol2; 1.
  1156 1156 Y -
3130 AA; 352782 MW;
  EMBL; AF058701; AAC24357.1; --
EMBL; AF071798; AAC24009.1; --
EMBL; AF157476; AAD40184.1; --
EMBL; AF179428; AAG09402.1; --
EMBL; AF179429; AAG09403.1; --
  EMBL; AF035537; AAB88486.1; -. EMBL; AF078695; AAC28460.1; -.
   SEQUENCE OF 79-3130 FROM N.A.
   SEQUENCE OF 79-3130 FROM N.A.
   Genew; HGNC:9968; REV3L.
   1540
  3104
   2607
  3064
  237
   389
   1540
   2607
  3064
   3086
   389
  231
   237
   (DNA) (N)
```

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:::|||||||
1821 IleLeuSerProAspGlyGluLeuValAspValAlaCysGluAspLeuGluLeuTyr 1840
   ::: |||
|802 HisThrArgLysGluMetGlyGlnSerLeuAspSerAla---AsnThrSerPheThrAla 1820
   1841 ValSerArgAsnAsnAspMetLeuThrProThrProAspSerSerProArgSerThrSer 1860
  SerProSerGlnSerLysAsnGlySerPheThrProArgThrAlaAsnIleLeuLys--- 1879
   SerCysTyrSerLeuGluAspSerLeuSerProGluHisAsnTyrAsnPheAspIleAsn 1650
   1651 ThrileGlydinThrGlyPheCysSerPheTyrSerGlySerGlnPheValProAlaAsp 1670
  1671 GlnAsnLeuProGlnLysPheLeuSer---AspAlaValGlnAspLeuPheProGlyGln 1689
   1763 CysValGlnGlnAlaGluAspCysLeuSerGluLysSerArgLeuAsnArgSerSerVal 1782
   1783 SerLysGluValPheLeuSerLeuProGlnProAsn---AsnSerAspTrp11eGlnGly 1801
   781
  CTTCTGTCCAGG-----GACTTG-----ATCATGAAAGAGGACTATGAACTTGTT 826
  869 GACACTACTGACATCCAAGGAGAATTTGCCAAAGTTATAGTACAAAAATTGAAAGAT 928
  350 AGTGCCATTCACCTATGTGACAAGAAAATGGAATTATCTCTGAACATACCTGTAAAT 409
  929 AACAAACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCT 988
  989 ITABATITACTICAAAATAAAAGCATGTAAGTGACTGTTTTTCAAGAAGAAATGTGT 1045
  GluLysSerThrileAspSerAsnGluAsnArgArgHisAsnGlnTrpLysAsnSer---
  -----CAGCCTGGTATAGCCCAGCAGTGGATCCAGAGC
  410 CATGGTCCACAAGAGGAATCATGT------GGATCCTCTCAGCTCCATGAAAAT
  ------AATGATTTTTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTG
  HisHisThrThrAspSerAlaSerTrpIleArgSerGlyThrLeuSerProGluIlePhe
  ---GATAGCACCATTTCTGGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCACTCCA
   ---GAACGTCTG-----
   635 TGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCA---
   AGTGGTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGAC-
3130
68
28
116
87
   CATCACTGTCCTGGAAATCACAGTTGG----------
                                 Conservative:
Mismatches:
  PRT; 1944 AA
                  Matches:
   US-09-771-161A-2 (1-1669) x DPOZ HUMAN (1-3130)
  Indels:
   Gaps:
                                32.11%
22.74%
3.11%
  STANDARD;
 4.29
  ANC1 MOUSE STANDARD P53995; Q8BP33; Q8C772;
                                 Percent Similarity:
Best Local Similarity:
   551
  578
   1709
   1748
   782
   458
   680
   722
  503
  Query Match:
   ANC1_MOUSE
ID ANC1_M
AC P53995
   Pred. No.:
                    Score:
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ARADIANDE-22354683; FUDNGG-12466831; Adachi J., Bono H., Kondo S., Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kiyosawa H., Yankadi Y., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Balarelli K., Hill D.P., Bult C., Hume D.A., Quackenbush J., Achriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., RA Gasterland T., Gariboldi M., Gassi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., RA, Kunochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Naqolott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Naqosima T., Reed J.C., Reed D.J., Reing B.Z., Ringwald M., Sandellin A., Schneider K., Okido T., Pavan W.J., Pertrea G., Pescole G., Sundellin A., Schneider C., Semple C.A., Setcu M., Shimada K., Shimada K., Shimada K., Mahashaw-Boris A., Yanagisawa M., Yang L., Waynshaw-Boris A., Yanagisawa M., Yang L., Waynshaw-Boris A., Yanagisawa M., Yang L., Waynshaw-Boris A., Yanagisawa M., Yang L., Waynshaw H., Kana J., Aizawa K., Arakawa T., Fukuda S., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sakazume W., Imchai K., Ishii X., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Shinayasi of the mouse transcriptome based on functional annotation of G., Thing L., Chanchart C., Handle R., Shinayasa H., Makamura M., Hanalysis of the mouse transcriptome based on functional annotation of C., Finner L., Enging L., Chanchart C., Handle C., Manachart C., Handle C., Carmina M., Chanchart C., Carmina M., Chanchart C., Handle C., Carmina M., Chanchart C., Carmina M., Cha
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  (By
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  -i - FUNCTION: Component of the anaphase promoting complex/cyclosome
  (APC/C), a cell cycle-regulated ubiquitin ligase that controls progression through mitosis and the G1 phase of the cell cycle
  -!- TISSUE SPECIFICITY: Abundantly expressed in proliferating fibroblasts, juvenile testis, adult brain and epididymis.
  STRAIN=CBA; TISSUE=Testis;
MEDLINE=95014147; PubMed=7929068;
Starborg M., Brundell E., Gell K., Hoeoeg C.;
"A novel murine gene encoding a 216-Kba protein is related to a mitotic checkpoint regulator previously identified in Aspergillus
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Anaphase promoting complex subunit 1 (APC1) (Cyclosome subunit 1)
(Protein T9224) (Mitotic checkpoint regulator).
ANAPCI OR TSG24 OR MCPR.
  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
  (By
  SIMILATION .
-!- SUBUNIT: The APC/C is composed of at least 11 subunits
  STRAIN=C57BL/6J; TISSUE=Forelimb, and Lung; MEDLINE=22354683; PubMed=12466851;
   or send an email to license@isb-sib.ch).
   the cell cycle.
-!- SIMILARITY: Contains 4 PC repeats.
  Biol. Chem. 269:24133-24137(1994).
  Mus musculus (Mouse)
  SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
  NCBI_TaxID=10090;
   similarity)
   similarity)
  nidulans."
        HEADER TO COURT OF THE TRANSPORT OF THE
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EMBL; X80169; CAA56450.1; -.

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NCBI_TaxID=9823;
  Sus scrofa (Pig)
  SSUE=Aorta;
   Alignment Scores:
  DOMAIN
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  9/
  Query Match:
DB:
   REPEAT
  No.:
  Pred.
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  326 TCATTACAGTTACAGAGTGTTTCAAGTGCCATT-----CACCTATGTGACAAGAAGAAA 379
  427
  |||
311 GlyGluSerProValAlaSerProPheGlnAsnTyrSerSerIleHisSerGlnSerArg 330
  TCATGTGGATCCTCTCAGCTCCATGAAATAGTGGTTCTCCTGAAACTTCAAGGTCCCTG 487
   341
   601
  |||| ::: ||| ::: ||| 368 ArgPheAsnLeuSerSerHisSerPro 387
   721
  SerGlySerPheAsnAspSerPheLeuAlaPro-----398
  409
  782 CTTCTGTCCAGGGACTTGATCATGAAAGAGGACTATGAACTTGTTAGTACCAAGCCTACA 841
   ------AspHisLeuTrpThrGluThrLeuProAsnIleArgGluLysAsnSer 425
  ----- 353
  354 -----HisSerProAlaLeuGlyValHisSerPhe------SerGlyAlaGln 367
   602 AGGGCTGCATTCTGTGATCACAAGACCACTCCATGCTCTTCAGCAATAATAAATCACCACTC 661
   842 AGGACCTCAAAAGTCAGACAATTACTAGACACTACTGACATCCAAGGAGAAGAATTTGCC 901
  :::|||||||
ThrLeuGlnAsnAlaThrThrSerSerSerLeuThrAlaHisLeuArgSerLeuSerLys
   380 ATGGAATTATCTCTGAACATACCTGTAAATCAT-------GGTCCACACAAGAAA
   548 CTGCATCACTGTCCT-----GGAAATCACAGTTGGGATAGCACCATTTCTGGATCTCAA
   TCAACTGCAGGAAACTCAGAACGTCTGCAGCCTGGTATAGCCCAGCAGTGGATCCAGAGC
   cycle; Cell division; Mitosis; Repeat.
   399 GluThrdluProileval-----ProdluLeucysile-----
  1944
52
25
72
56
  Conservative:
Mismatches:
Indels:
   SerThrSerSerProSerLeuHisSerArgSer----
   US-09-771-161A-2 (1-1669) x ANC1_MOUSE (1-1944)
              PIR; ASS117; ASS117.
MGD; MGI: 103097; Mcpr.
Interpro; IPR012015; APC proteasome.
Pfam; PF01851; PC rep; S.
Ubl conjugation pathway; Cell cycle;
   216086 MW;
EMBL; AK052404; BAC34976.1; -. EMBL; AK077847; BAC37032.1; -.
  conjugation pathway; Cell
  902 AAAGTTATAGTACAA 916
  :::|||:::
CysPheLeuValGlu 447
  4.58
89.00
37.56%
25.37%
3.09%
   1404
1501
1552
112
349
643
   1944 AA;
  Percent Similarity:
Best Local Similarity:
  1366
  Alignment Scores:
   CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
  388
   410
  428
  331
   488
   662
   443
  REPEAT
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REPEAT
   Query Match:
   REPEAT
  RESULT 13
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   Score
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  GATTTCGAGGATGAAGCTCTGAGACACTGAGAGAAGGTAACCAATTAATATGAGCCAGGA 135
   171
  63
   ----ProPheLeuGlyAsnGlnLeuGlnAspSer 77
  Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Suina; Suidae; Sus.
  346 RING-TYPE.
40977 MW; EB2268FA9A6190A4 CRC64;
   358
72
47
1135
1103
   Length:
Matches:
Conservative:
Mismatches:
Indels:
   136 TICAAAGICTGTGGTINCTAAAGITAITTCCCGIIC
  55 AspAlaMetThrGluHisLeuArgHis------
                                     15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
6-OCT-2001 (Rel. 40, Last annotation update)
Putative inhibitor of apoptosis.
358 AA
   SMART; SM00238; BIR; 2.
SMART; SM00114; CARD; 1.
SMART; SM00114; CARD; 1.
SMART; SM00114; RING; 1.
PROSITE; PS01282; BIR_REPEAT_1; 2.
PROSITE; PS0209; CARD; 1.
PROSITE; PS00518; ZF RING 1; FALSE_NEG.
PROSITE; PS00518; ZF RING 2; 1.
Apoptcsis; Zinc-finger; Repeat.
REPEAT
  US-09-771-161A-2 (1-1669) x PIAP_PIG (1-358)
  BIR 1.
BIR 2.
   CARD.
  HSSP, Q13490; 1QBH.
InterPro; IPR001370; BIR.
InterPro; IPR001315; CARD.
InterPro; IPR001315; CARD.
Pfam; PF00653; BIR; 2.
Pfam; PF006519; CARD; 1.
Pfam; PF00097; zf-C3HC4; 1.
  EMBL; U79142; AAC39171.1; -. PIR; JC5964; JC5964.
   64 PheProAsnCys----
   33.33%
20.17%
3.06%
STANDARD;
  Eukaryota; Metazoa;
Mammalia; Eutheria;
   311
358 AA;
   Percent Similarity:
Best Local Similarity:
   EQUENCE FROM N.A.
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  ------SerSerAspGluSerGluThrSerGluAspSerAspIleAspGlyAla 361
  |||||||::
|SerAsnSerSerSerArgGlyAsnSerArgProGlyThrProSerProAspThrGlyAsn 401
   398 ATACCIGIAAAICAIGGICCACAAGAGAAICAIGIGGAICCICICAGCICCAIGAAAAI 457
  290 LeuproGlyLys1leLysProAlaLysGluGluGluGlyProLysGlyLeuAspGluGln 309
   AGGTCCCTGCCAGCTCCTCAAGACAATGATTTTTTTATCTAGAAAAGCTCAAGACTGTTAT
  LysLysAlaProThrProGlnAspAsnLys-----LysLysLysLysGlyAsp-----
   TITATGAAGCTGCATCACTGTCCTGGAAATCACAGTTGGGATAGCACCATTTCTGGATCT
  SerSerSerLeuPheMetGlnLysLysLysThrProProLysLysAspLysLysGlyGly
  ---CCACTCTCAACTGCAGGAAAC
  primary structure of Xenopus and human RAP74.";

Nucleic Acids Res. 20:6736-6736(1992)

-!- FUNCTION: TPILF IS A GENERAL TRANSCRIPTION INITIATION FACTOR BINDS TO RNA POLYMERASE II AND HELPS TO RECRUIT IT TO THE INITIATION COMPLEX IN COLLABORATION WITH TFIIB. IT PROMOTES TRANSCRIPTION ELONGATION.
                             Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
   -!- SUBUNIT: Heterodimer of an alpha and a beta subunit.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: TO OTHER TRANSCRIPTION FACTOR IIF, ALPHA SUBUNIT.
   599 CAAAGGGCTGCATTCTGTGATCACAAGACCACTCCA-------
  MEDLINE-93126122; PubMed-1480494;
Gong D.-W., Haeegawa S., Wada K., Roeder R.G., Nakatani
Horikoshi M.;
   subdomains by
   524
222
90
60
90
   Conservative:
Mismatches:
Indels:
  Pfam; PF05793; TFIIF-alpha; 1.
Transcription regulation; DNA-binding; Nuclear p
SEQUENCE 524 AA; 58699 WW; 8CF3A74A3BF77BB0
   Length:
Matches:
   Elucidation of three putative structural
  US-09-771-161A-2 (1-1669) x T2FA_XENLA (1-524)
  ---TGCTCTTCAGCAATAATAAAT
(Transcription initiation factor RAP74)
   AGTGGTTCTCCTGAAACTTCA----
  IOZI/1; -:
IPRO08851; TFIIF-alpha.
  EMBL; Z17426; CAA78999.1; -.
   5.07
88.00
33.63
23.89
3.06
  Xenopodinae; Xenopus
   835551; 835551.
  SEQUENCE FROM N.A.
   TRANSFAC; T02171;
   Percent Similarity:
Best Local Similarity:
  NCBI_TaxID=8355
  Alignment Scores:
   330
  458
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   362
   nterPro;
   346
  635
  Query Match:
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  TICTAGATCACCATCTTTAAATTTACTTCAAAATAAAAGCATGTAAGTGACTGTTTTCA 1032
   885
   931 CAAACAAATGGGTCTTCAG----------CCTTACCCGGAAATACTTGTGGT 972
  userMetGluGluGlnLeuArgArgLeuGlnGluGluArgThrCysLysValCysMetAs 316
   525
   |||| :::|||
------AsnPro------GluAspGluAsnAlaGluProProAsnAspLe 198
   AGGAGAAGAATTTGCCAAAGTTATAGTACAAAAATTGAAAGAT-------AA 930
  285
  CCTAATCATCTCCAGTTAAAGTGTATATATATTTATGTATTCATTACAGTTACAGAGTGT 345
  TICAAGTGCCATTCACCTATGTGACAAGAAAATGGAATTATCTCTGAACATACCTGT 405
  -ProArg---CysGluTyrLeuIleArgIleLysGlyGlnGluPheIleSerArg---Va 169
   TCAAGACTGTTATTTTATGAAGCTGCATCACTGTCCTGGAAATCACAGTTGGGATAGCAC 585
  CATTICIGGAICTCAAAGGGCTGCATTCTGTGATCACAAGACCACTCCATGCTCTTCAGC 645
   646 AATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAGCCTGGTATAGCCCA 705
  198 uSerLeulleArgLysAsnArgMetAlaLeuPheGlnHisLeuThr-----CysValLe 216
                    -----TACACTGTCTTTTCCTTCAGTTATATGTTATATTCTCAACTCTTTATATTTTCT 225
   PheLysThrPheCys-----His 107
   ArgCysTrpGluSerGlyAspAspProTrpValGluHisAlaLys------TrpPhe 151
  ||| ::: :::||| :::
rlysHisLeuPheValGlnGlnAspIleLysTyrIleProThrGluAsnValSerAspLe
   ProGluGlnLeuAlaSerAlaGlyPheTyrTyrMetGlyHisSerAspAspValLysCys
   TCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTTTTATCTAGAAAAGC
   CCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGGACTATGAACTTGT
   TAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACACTACTGACATCCA
   :||| ::::: ||| ::: sGlyAsnTyrAlaAlaThrIlePheLysAsnSerLeuGlnGluIleAspProMetLeuTy
  TICCATGIATITITGIACAAACATATAAAATGIGITAGATTGIATITITACTICTATAATTT
   406 AAATCATGGTCCACAAAGAGGAATCATGTGGATCCTCTCAGCTCCATGAAAATAGTGGTTC
  01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Transcription initiation factor IIF, alpha subunit (TFIIF-alpha)
  -----AspGlyĠlyLeu------
  1033 AGAAGAAATGTGTTTCATA-----AAAGGATATTTATATCTCTGT
   SerArgTyrThrValSerAsnLeuSerMetGlnThrTyrAlaAla---
   524 AA
  uLeuSerThrSerAsp---
  PheCysCys-----
   STANDARD;
   T2FA XENLA
Q04870;
   904
   316
   78
  108
   346
  128
  135
  152
   526
  169
   586
  180
  973
   226
  94
   286
   466
  RESULT 14
T2FA_XENLA
ID _T2FA_X
AC _004870
DT _01-FEB
DT _01-OCT
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345

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Tracey A., Williams S.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
  MEDLINE=21659781; PubMed=11801724;
   MEDLINE=22158633; PubMed=12168954;
   TISSUE=Brain;
MEDLINE=99087487; PubMed=9872452;
  SEQUENCE OF 6922-8797 FROM N.A.
  SEQUENCE OF 8406-8797 FROM N.A.
  for large proteins in vitro.";
DNA Res. 7:347-355(2000).
  SEQUENCE OF 1-856 FROM N.A.
  TISSUE=Brain;
  TISSUE=Brain;
   TISSUE=Brain;
   TISSUE=Brain;
  REVISIONS
    TCAGAACGTCTGCAGCCTGGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATT 736
  421
   781
  799
  479
   907
  422 SerAsn-----ThrProAlaAlaLysArgLeuLysMetGluAlaGlyProGlnAsnThr 439
  440 SerGlyLysSerThrProGlnProGlnSerGlyLysSerThrProSerSerGlyAspile 459
   800 ATCATGAAAGAGGAC-----TATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAA 853
   Nesprin I (Nuclear envelope spectrin repeat protein 1) (Synaptic nuclear envelope protein 1) (Myne-1) (Myne-1) (Enaptin) (Finaptin) SynE1 OR KIAA0796 OR KIAA1756 OR KIAA1262.
                                 :::
402 ThrSerSerThrLeuArgAlaAlaAlaSerLysLeuGluGlnSerLysArgGlyThrVal
  ---CTTCTGTCCAGGGACTTG
  460 GlnLeuThrGluGluAlaValArgArgTyrLeuThrArgLysProMetThrThrLysAsp
  GTCAGACAATTACTAGACACT-----ACTGACATCCAAGGAGAAGTTTGCCAAAGTT
  "The longest isoform of enaptin/Syne-1, a nuclear envelope associated protein, binds actin cytoskeleton via the alpha-actinin-like actin-
   GTGAACCAAATGACAGAAGCCTGCCTTAACCAGTCGCTAGATGCC-------
   SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), CHARACTERIZATION, AND MUTAGENESIS OF 8758-LEU-CYS-8763.

TISSUE=Heart, Placenta, Skeletal muscle, Spleen, and Testis;

MEDLINE=21652858; PubMed=11792814;

Zhang Q., Skepper J.N., Yang F., Davies J.D., Hegyi L., Roberts R.G., Weissberg D.L., Ellis J.A., Shanahan C.M.;

Weissberg L.L., Ellis J.A., Shanahan C.M.;

Nesprins: a novel family of spectrin-repeat-containing proteins that localize to the nuclear membrane in multiple tissues.";
   [5]
SEQUENCE FROM N.A.
Almeida J., Clark S., Griffiths C., Lloyd D., Parker A., Smith M.,
  Zhang Q., Ragnauth C., Greener M.J., Shanahan C.M., Roberts R.G., "The nesprins are giant actin-binding proteins, orthologous to Drosophila melanogaster muscle protein MSP-300.";
   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
  SNEI TOURING

08NF91; 094990; 08N997; 08TCP1; 08NWW6; 08NWN7; 08WXF6; 096N17;

09C0A7; 09H525; 09H526; 09NS36; 09NU50; 09UJ06; 09UJ07; 09ULF8;

10-OCT-2003 (Rel. 42, Created)

10-OCT-2003 (Rel. 42, Last sequence update)

10-OCT-2003 (Rel. 42, Last annotation update)
  Abraham S., Padmakumar V., Tunggal B., Noegel A.A.,
   SEQUENCE FROM N.A. (ISOFORM 1), AND SUBCELLULAR LOCATION
  Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases
  Zhang Q., Shanahan C.M.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
  SEQUENCE FROM N.A. (ISOFORM 4), AND VARIANT GLY-8323.
   PRT; 8797 AA
   SEQUENCE FROM N.A. (ISOFORMS 8 AND 9).
  TISSUB=Heart, Spleen, and Testis;
MEDLINE=22296983; PubMed=12408964;
Zhang Q., Ragnauth C., Greener M.J.
   Cell Sci. 114:4485-4498(2001).
   908 ATAGTACAAAATTGAAA 925
  Genomics 80:473-481(2002).
  STANDARD;
  Homo sapiens (Human).
  protein, Dince
   NCBI_TaxID=9606;
   Korenbaum E.;
  Braune S.,
  SNE1 HUMAN
  854
   RESULT 15
SNE1 HUMAN
AC 080KP91,
AC 080KP91,
AC 080KP91,
DT 10-OCT-
DT 10-OCT-
DT 10-OCT-
DE Nesprin
DE Nesprin
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Mislow J.M.K., Kim M.S., Davis D.B., McNally B.M.;
"Myne-1, a spectrin repeat transmembrane protein of the myocyte inner nuclear membrane, interacts with lamin A/C.";
J. Cell Sci. 115:61-70(2002).
   Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.; "Construction of expression-ready cDNA clones for KIAA genes: manual curation of 330 KIAA cDNA clones."; DNA Res. 9:99-106(2002).
  TISSUB=Addrenal gland, and Teratocarcinoms;
Ninomiya K., Magatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
Puruya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
Katsuta I., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
Takemoto M., Ota T., Suzuki Y., Sugano S., Nagahari K., Masuho Y.,
"NEDo human cDNA sequencing project.";
  MEDLINE=21082932; PubMed=11214970; Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.; Magase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.; Mara Complete Sequences of unidentified human genes. XIX. The complete sequences of 100 new cDNA clones from brain which code
   "Prediction of the coding sequences of unidentified human genes. XV. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 6:337-345(1999)
   Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Miyajima N.,
Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XI.
The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 5:277-286(1998).
Gough L., Fan J., Lisa G., Chu S., Winnick S., Beck K.A.; "Golgi localization of syne-1."; Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
  Wiemann S.;
   MEDLINE=20039619; PubMed=10574462;
Nagase_T., Ishikawa K.-I., Kikuno R., Hirosawa M., Nomura
   "NEDO human cDNA sequencing project.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
   databases.
   SEQUENCE OF 7631-8797 FROM N.A., AND CHARACTERIZATION
  Ansorge W., Wirkner U., Mewes H.-W., Weil B., Submitted (MAR-2002) to the EMBL/GenBank/DDBJ
   SEQUENCE OF 4219-8797 FROM N.A. (ISOFORM 7).
   SEQUENCE OF 743-8797 FROM N.A. (ISOFORM 6).
  SEQUENCE OF 443-8797 FROM N.A. (ISOFORM 5)
   SEQUENCE OF 28-778 AND 2901-3476 FROM N.A.
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CAB87586.1;

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                               FUNCTION: Involved in the maintenance of nuclear organization and structural integrity. Probable anchoring protein which theters the nucleus to the cytoskeleton. Connects nuclei to the cytoskeleton by interacting with the nuclear envelope and with F-actin in the cytoplasm.
SUBUNIT: Interacts with MUSK, with F-actin via its N-terminal
   prédiction.
CAUTION: Ref.7 (BAB71097) sequence differs from that shown due to
a chimeric CDNA.
   domain, and with LMNA in vitro (By similarity).
SUBCELLULAR LOCATION: Type IV membrane protein (Potential). The largest part of the protein is cytoplasmic, while its C-terminal part is associated with the nuclear envelope, most probably the outer nuclear membrane. In skeletal and smooth muscles, a
  VSP_007139, VSP_007140,
  domain, mediates the nuclear envelope targeting.
SIMILARITY: Belongs to the nesprin family.
SIMILARITY: Contains 1 actin-binding domain.
SIMILARITY: Contains 2 calponin-homology (CH) domains.
SIMILARITY: Contains 12 HAT repeats.
SIMILARITY: Contains 11 HAT repeats.
SIMILARITY: Contains 31 spectrin repeats.
SIMILARITY: Contains 31 spectrin repeats.
SOUTION: Ref. 5 (CAB55865, CAB5866, CAC16281)
sequences differ from that shown due to erroneous gene model
   DOMAIN: The Klarsicht domain, which contains a transmembrane
   CAUTION: Ref.14 sequence differs from that shown due to two frameshifts in positions 8412 and 8784.
             (JAN-1998) to the EMBL/GenBank/DDBJ databases.
   Name=3; Synonyms=Alpha;
IsoId=Q8NF91-3; Sequence=VSP_007132, VSP_007144;
  IsoId=Q8NF91-5; Sequence=VSP_007135; VSP_007136;
Note=No experimental confirmation available;
   IsoId=Q8NF91-6; Sequence=VSP_007137, VSP_007138;
Note=No experimental confirmation available;
   VSP 007142;
   significant amount is found in the sarcomeres. ALTERNATIVE PRODUCTS:
   IsoId=08NF91-7; Sequence=VSP_007141, VSP_007
Note=No experimental confirmation available;
   Event=Alternative splicing; Named isoforms=9;
  IsoId=Q8NF91-4; Sequence=VSP_007134; VSP_007144;
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Isold=Q8NF91-2; Sequence=VSP_007130;
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Ma F.-R.,
Submitted
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   EMBL;
EMBL;
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1848 AspCysPheGlnLeuPheGluGluAlaSerGlnValValGluArgArgGlnLeuAlaLeu 1867
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  633
  694 TGGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAA---ATGAC 750
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   --TCGCTAGATGCCCTTCT
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69
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104
76
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88.00
40.13$
23.08$
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  MEDILINE-90241596; PubMed-9575181; Inchara N., del Peso L., Koseki T., Chen S., Nunez G.; Inchara N., del Peso L., Koseki T., Chen S., Nunez G.; Inchara Experiment a novel protein kinase containing a caspase recruitment domain, interacts with CLARP and regulates CD95-mediated apoptosis."; J. Biol. Chem. 273:12296-12300(1998).
  Erzachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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Last annotation update)
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01-OCT-2002 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
Protein kinase RICK.
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95.5
95.5
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Listing first 45 summaries
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19.39%
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3.66%
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  :::|||||| :::::|||||||| 471 ArgTrpIleAlaAlaArgArgGluGluValValArgGlnMetThrGluAlaCysLeuAsn 490
   826
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   827 AGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACACTACTGACATCCAA 886
   447
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  ------GlyProAlaAla 470
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  448 GinPro-----LeuThrLeuHisProHisProGlnAspPheVal------
  δ
   activity; IEA.
mediates Bc110-independent NF-kappa B activation induced
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J. Biol. Chem., 0:0-0(2002).

G. Biol. Chem., 0:0-0(2002).

G. GO:0005622; C:intracellular; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004713; F:protein.erine/threonine kinase activity; IEA.

GO; GO:0004713; F:protein.erine/threonine kinase activity; IEA.

GO; GO:0006468; P:protein serine/threonine kinase activity; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

R GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

R InterPro; IPR001315; CARD.

R InterPro; IPR001315; For thr pkinase.

R InterPro; IPR002290; Ser_thr_pkinase.

R InterPro; IPR001295; Tyr_pkinase.

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R Pfam; PF00619; CARD; 1.

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  584
28
45
756
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  Length:
Matches:
Conservative:
Mismatches:
Indels:
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  PROSITE, PS50209, CARD, 1.
PROSITE, PS50011, PROTEIN KINASE DOM, 1.
PROSITE: PS00108, PROTEIN KINASE ST; 1.
   US-09-771-161A-2 (1-1669) x Q8JHU4 (1-584)
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ProDom; Proto, Kinase; 1.
SMART; SMO0220; S TKC; 1.
SMART; SMO0219; TYRC; 1.
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52.58%
39.44%
111.63%
  Percent Similarity:
Best Local Similarity:
  Alignment Scores:
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   596 TCTCAAAGGGCTGCATTCTGTGATCACAAGACCACTCCATGCTCTTCAGCAATAATAAAT 655
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Chiang H.C., Hooper L.V., Gordon J.I.;
Agenomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
Science 299:2074-2076(2003).
BMBL; Ag016828; AA075816.1;
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464 ThrAlaAlaThrAsnLeuProAspGluProGluGluProLysLeuAlaPheProLeuIle
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  :::||| :::||| :::
524 HisPheAspAspIleLeuCysLysAlaPheGluHisGluLeuIleSerSerSerTyrLys
  ::: ||||||
484 ProAlaAspIleSerArgAlaGlnLeuIleThrHisLeuIleAsnAsnGlnSerCysSer
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Bacteroidaceae, Bacteroides.
   Hypothetical protein; Complete proteome.
SEQUENCE 791 AA; 88443 MW; 7C72011D0CD93232 CRC64;
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64
44
97
125
14
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  01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
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Matches:
Conservative:
Mismatches:
   383 GAATTATCTCTGAACATACCT------
   Indels:
   791
   Gaps:
  452 TyrThrieuSerLeuGinAlaIle----
  US-09-771-161A-2 (1-1669) x Q8A9V6 (1-791)
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| ,                                     | Alignment Sco<br>Pred. No.:                  | Score:<br>Percent Simil | Best Local S1<br>Query Match:<br>DB:                             | DD:<br>TIS-08-771-161                                          | 921                                                                    |                     | 6                                                                      |            | N                                                            | 98                                                           | 325                                                             | 102                                                                                                                                                                                                                                                                                                                                                                                                                                                           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             |                                             | 169                                                                                                              | 99                                                                                                                                                  | 184                   | 725 | 201 | 785  | 221                                | 816                                                                                                                                                | 241    | 878 | 261                                                                 | 306 | 281                                                                              | 94. |
|---------------------------------------|----------------------------------------------|-------------------------|------------------------------------------------------------------|----------------------------------------------------------------|------------------------------------------------------------------------|---------------------|------------------------------------------------------------------------|------------|--------------------------------------------------------------|--------------------------------------------------------------|-----------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------|---------------------------------------------------------------------|------------------------------------------------------------------|------|-----------------------------------------------------------|-------------------------------------------|------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------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                               | а                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       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| Db 564ThrProSerSerLeuIleLeuPheIle 572 | Qy 656 CCACTCTCAACTGCAGGAAACTCAGAACGTCTG 688 | <br>                    | Qy 689CAGCCTGGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAAC 742 | Db 593 AlaTrpGlnAspValPheAlaGluLysValArgAlaAspAspLeuPheAsn 610 | Qy 743 CAAATGACAGAAGCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGCCAGGGACTTGATC 802 | MetArgPheAlaGlnMetA | Qy 803 ATGAAAGAGGACTATGAACTTGTTAGTACCAAGGCTCAAGGACCTCAAAAGTCAGACAA 862 | Db 622 629 | 863 TTACTAGACACTCGACATCCAAGGAGAAGATTTGCCAAAGTTATAGTACAAAATTG | 630VallysLeuThrAspThrGlnLysLysGluPheAsnArgValPheThrGlnLeuLeu | Qy 923 AAGATACAAAAATGGGTCTTCAGCCTTACCCGGAATACTTGTGGTTTCTAGA 979 | oso nosacommensas memosas as massas costacas activates activates and costacas activates activates and costacas activates activates activates activates activates activates activates activates activates activates activates activates activates activates activates activates activates activates activates activates activates activates activates activates activates activates activates 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713 SerLysleuValSerThrSerVallysSer | 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 1000 Farmer 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ENT. ESC. (NEMETER) 22 CONTROL (NEMETER) 22 CONTROL (NEMETER) 22 CONTROL (NEMETER) | DI 01-MAK-2003 (IIEMBALE1: 23, CICACCO,<br>DT 01-MAK-2003 (TEMBLECE) 23, Last sequence update)<br>DT 01-MAD-2003 (T-EMBLE) 23 Last sequence update) | Hypothetical protein. |     |     | 0, 0 | MEDLINE 22255705; PubMed=12368864; | RA Garoner M.C., Hall N., Fung E., Mnice O., Berriman M., Hyman K.W.,<br>RA Carlson J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., |        |     | RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., |     | RI Laicipalum.;<br>RL Nature 419:498-511(2002).<br>PD PMD: NPOLA033. NNN26447 1. |     |
|                                       |                                              |                         |                                                                  |                                                                |                                                                        |                     |                                                                        |            |                                                              |                                                              |                                                                 |                                                                                                                                                                                                                                                                                                                                                                                              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47 ---CAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAAATTTGAA 1003
  427
  ||||:::|||
nHislieAspAsn----- 137
  :|||
nCysTyrLeullePheGlnGlyValAspGlnAsnlleTyrThrIleLeuLysGlnAsnAg 169
   664
   25 AGGGAAGACATTGTGAACCAAATGACAGAAGCCTGCCTTAACCAGTCGCTAGATGCCCTT 784
   817
   21 GlnGlnAsnAspGluIleAsnGlnGluAspTyrGlnGluArgValMetAsnLeuTyrAsn 240
   18 GAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACACTACT 877
   78 GACATCCAAGGAGAA-----GAATTTGCCAAA 904
   05 GTT------ATAGTACAAAATTGAAA---GATAACAAACAAATGGCTCTT 946
   TCATGTGGATCCTCTCAGCTCCATGAAAATAGTGGTTCTCCTGAAACTTCAAGGTCCCTG 487
  48 CTGCATCACTGTCCTGGAA---ATCACAGTTGGGATAGCACCATTTCTGGATCTCAAAGG 604
   ACTGCAGGAAACTCAGAACGTCTGCAGCCTGGTATAGCCCCAGCAGTGGATCCAGAGCAAA 724
   76 CIGICITITICCTICAGITATATGITATATICICAACICITITATATITICITICC----- 229
  ::::::||| ||| ||| |||:::
| lleLysLeuSerSerTyrSerThrAspHisIleAsnIleCysAspLysIleCysAspAsp 121
  -----yheileAsnLysLeutysLysPheAsnAsnGluAs
  TTACAGTTACAGAGTGTTTCAAGT --- GCCATTCACCTATGTGAC-------
  30 -----TATAAAATGTTTTTGTACAAACA-----TATAAAATGTGTTAGATTGTA
  71 ---AAGAAGAAATGGAATTATCTCTGAACATACCTGTAAATCATGGTCCACAAGAGGAA
   35 GCTGCATTCTGTGATCACAAGACCACTCCATGCTCTTCAGCAATAAATCCACTCTCA
   85 CTGTCCAGGGACTTGATCATGAAGAGGGCTAT------
         Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
  :1A-2 (1-1669) x Q8IJE8 (1-1309)
           0.449
101.50
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   ilarity:
Similarity:
ores:
  62
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| 301 CysAsnThrPhePheLeuLys1leValLysSerPheSerArgHisPheAsnileMetAsn 320 1004 AATAAAAGCATGTAAGTGACTGTTTTCAAGAAAATGTCTTTCATAAAAGGATATTA 1063 1014 | 1064 TATCTCTGTTGCTTTGACTTTTTATATAAAATCCGTGAGTATT 1108<br>                   333 TyrPheTyrIelleSerLeulleTyrAsnLysAspile-LeuThrValAsnPheIleLe 352 | 1109 AAAGCTTTATTGAAGGTTCTTTGGGTAAATATTAGTCTCCCTCC |          |     | 1 392<br>u 392 | <b>4</b> '       | PRELIMINARY; | 01-MAR-2003 (TrEMBLrel. 23, Created) 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel 23, Last sequence update) | protein, conserved. | Frontacium falciparum (isolate 3D7).<br>Plasmodium falciparum (isolate 3D7).<br>Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. | NCBI_TaxID=36329;<br>[1] | P SEQUENCE FROM N.A.<br>X MEDLINE-22255CHO8; PubMed=12368867;<br>A Hall N. Pain A. Berriman M., Churcher C., Harris B., Harris D., | <pre>Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,<br/>Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,</pre> | Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C., Croin A., Davies R., Davie P., Dearfen F., Doggett U., Croin A., Occasional T., Constant Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control of Control o |            | Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,<br>Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N., |                | Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,<br>Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K., | Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J., Sulston J.E., Craig A., Newbold C., Barrell B.G; | "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";<br>Nature 419:527-531(2002). | EMBL, AL034557, CAD49130.1, -<br>GO; GO:0003864, F:catalytic activity, IEA. | ٠.٠   | /34 AA; 83360 MM; /ADBBD463D0603EC | onent Scores: 0.463 Length: | Marches:<br>Conservative: | : 18.18*<br>3.51* | Gaps: | 7-T (T-100A) X (O1177 (T-7.2*) | S AGTITIATACCCAGATATTTTATAGGCTCAATCTCTAGAACCATCCTGCCATGTA 64 |
| 8 & 8                                                                                                                                        | QY.                                                                                                                                             | ç<br>G                                            | ठे व     | 8 8 | g 8            | RESULT<br>Q81121 | A D          | F                                                                                                                                       | 388                 | 800                                                                                                                                          | S S                      | RR                                                                                                                                 | RA<br>RA                                                                                                                                 | <b>88</b> 3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | <b>£ £</b> | R R                                                                                                                                  | & &            | R R                                                                                                                                         | R R                                                                                                        | RL                                                                                           | <u>к</u> к                                                                  | £ ₹ 8 | og i                               | Alig<br>Pred                | Per                       | Se Be             |       | 20                             | ò                                                            |

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569 CACAGTIGGGATAGCACCATTICTGGATCTCAAAGGGCTGCATTCTGTGATCACAAGACC 628
  518
   718
  719 AGCAAAAGGGAAAGACATT-----------GTGAACCAAATGACA 751
  :::|||||||
537 ThrLysArgAsnSerTyrLysValAspLysValProArgIleAsnPheAspAsnMetLys 556
  812 GACTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGAC 871
  573 SerTyrGluLeuIleLysAspGlyValTyrIleLysLysLysIleAsnAsnAsnAsnAsn 592
  ACTACTGACATCCAAGGAGAAGAATTTGCCAAAGTTATAGTACAAAAATTGAAAAGATAAC 931
  ::: | | | | ::: | | | | 313 GlylleGlySerSerThrGluSerSerTyr 342
   335 TTACAGAGTGTTTCAAGTGCCATTCACCTATGTGACAAGAAAAATGGAATTATCTCTG 394
   434 -----GGATCCTCTCAGCTCCAT 451
   419 AsnAsnLysMetAspGlnLysAsnLysAsnHisLysGlyAsnAsnLysSerSerAsnAsn 438
   |||::: :::|||
439 AsnAsnAsnAsnAsnAsnAsnAsnAsnSerCysSerSerSerSerAsnAsnAsnMet 458
  268
  303 AsnAsnLysileProLysileLysLysAspValAsnSerTyrTyrTyrSerSerWetGlu 322
   236 TTTGTA-----CAAACATATAAAATGTGTTAGATT------GTATTTTACTTCTAT 280
  343 AsnSerLeuThr------SerValSerThrIleLeuAlaSerIleGluSerIle 358
   399 TyrTyrThrAsnAsnLysTyrAspAsnLeuTyrSerProAsnLysValThrSerIleAsn 418
65 GGTAATTGTTAGATTTCGAGGATGAAGCTCTGAGACACTGAGAAGGTAACCAATTAAT 124
   -----LysGluLysileGly 282
  125 ATGAGCCAGGATTCAAAGTCTGTGGTTNCTAAAGTTATTTCCCGTTCTACACTGTCTTTT 184
  281 AATTTCCTAATCATCTCCCAGTTAAAGTGTATATATATTTATGTATTCATTACAG----- 334
  185 CCTTCAGTTATATGTTATATT-----CTCAACTCTTTATATTTTCTTTCCATGTAT
   452 GAAAATAGTGGTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTT
  -----TCAGAACGTCTGCAGCCTGGTATAGCCCAGCAGTGGATCCAG
   752 GAAGCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAG
  395 AACATACCTGTAAATCATGGTCCACAAGAG-----GAATCATGT------
   629 ACTCCATGCTCTTCAGCAATAATAAATCCACTCTCA-----ACTGCAGGAAAC-----
   512 ---TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCTGGAAAT
                                    ::: ||||
268 AsnAsnThrGluLysLeuLysAspLysLeu----
   433 -----
   677
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|                                                                 | Oy 487                                              | Oy 488 CCAGCTCCTCAAGACAATGATTTTTATCTAGAAAAGCT 526 |                                                                                                                                          | Qy 554CACTGTCCTGGAAATCACAGTTGGGATAGCACCATTTCTGGAT 596 | Oy 597 CTCAAAGGGTGCATTCTGTGATCACAAGACCACTCCATGCTCTTCAGCAATAATAAATC 656  Db 216 roSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerThrSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSerAlaGlvProSer | 657 CACTCTCAACTGCAGGAAACTCA                                                                                                                                                                                        | Qy 680GAACGTCTGCAGCCTGGTATAGCCCAGCAGTGGATCCAGAGCGAAAAGGG 728                                      | Qy 729 AAGACATTGTGAAATGACAGAAGCCTGCCTTAACCAGTGGCTAGGTGCCCTTCTGT 788 | Qy 789 CCAGGGACTTGATCATGAAGGGCTATGAACTTGTTAGTACCAAGCCTACAAGGACCT 848    1                                                                                                                             | Db 312 lalysMetLysThrAspileGluAsnLeuAsnLysLysAsnAspLeuValLysAspI 332  Oy 909 TAGTACAAAATTGAAAGAAACAAACGGTCTTCAGCCTTACCCGG 959  Db 332 laAlaAsnLeuGlnSerLysLeulanGluAsnGluGlnLeuLysLysSerThrGlnAspG 352 | Qy 960 AAATACTTGTG 970    :::      352 luAsnileVal 355 | SUL                                            | DT 01-MAY-2000 (TrEMBLrel. 13, Created) DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) DT 01-UDN-2003 (TrEMBLrel. 24, Last annotation update) DE Inhibitor of apoptosis protein 2. |                                                                         |                                                                              | "Cloning of cDNA for rat inhibitor of apoptosis protein Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases -!- SIMILARITY: CONPAINS 1 RING-TYPE ZINC FINGER. EMBL; AF190020; AAF04585.1; |
|-----------------------------------------------------------------|-----------------------------------------------------|---------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------|---------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------|------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------|------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| AAACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCTTTA 99 | 992 AATTTACTTCAAAATAAAAGCAIGTAAGTGACTGTTTTCAAGAAGAA | SULT 5                                            | 09J861 PRELIMINARY; PRT; 461 AA.<br>09J861:<br>01-0CT-2000 (TrEMBLrel. 15, Created)<br>01-0CT-2000 (TrEMBLrel. 15, Last sequence update) | ORF76 cg30.<br>Spodoptera e<br>Viruses; dsD           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | RX MEDLINE=20036646; PubMed=10567663;<br>RA TJKel W.F., van Strian E.A., Heldens J.G., Broer R., Zuidema D.,<br>RA Goldbach R.W., Vlak J.M.;<br>RT "Sequence and organization of the spodoptera exigua multicapsid | nucleopolyhedrovirus genome.";<br>J. Gen. Virol. 80:3289-3304(1999).<br>[2]<br>SEQUENCE FROM N.A. |                                                                     | DR EMBL, FAIL98213, AAF13605.1; DR InterPro; IPR001841; Znf_ring. DR Pfam; PF00097; zf-C3HC4; 1. DR SMART; SM00184; RING; 1. DR PROSITE; PS50089; ZF RING; 2; 1. KW Metal-binding; Zinc; Zinc-finger. | SEQUENCE 401 AA; 50820 MW; BCU<br>ignment Scores: 0.484<br>ed. No.: 100.50<br>ore: 36.23\$                                                                                                             | : 20.87% Mismatches:<br>3.49% Indels:<br>12 Gaps:      | US-09-771-161A-2 (1-1669) x Q9U861 (1-461)  QY | TGTAȚT<br>rgAlaI                                                                                                                                                                         | Oy 279 ATAATITCCTAATCATCTCCAGTTAAAGTGTATATATATTTATGTATTCATTACAGTTAC 338 | Qy 339 AGAGTGTTTCAAGTGCATTCACCTATGTGACAAGAAGAAATGGAATTATCTCTGAACA 398 ::: :: | OY 399 TACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTC 443                                                                                                                                      |

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980 TCACCATCTTTAAATTTACTTCAAAATAAAAGCATGTAAGTGACTGTTTTTCAAGAAGAA 1039
  510 LeuPheValGluLysThrMetLysTyrIleProThrGluAspValSerGlyLeuSerLeu 529
   |||::: ||| |||:::
432 IleArgLysAsnArgMetAlaLeuPheGlnGlnLeuThr-----CysVallleProlle
  773 CTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGGACTATGAACTTGTTAGTACC
   833 AAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACACTACTGACATCCAAGGAGAA
   893 GAATTTGCCAAAGTTATAGTACAAAAATTGAAAGAT---------
  929 -----AACAAACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGA
  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
   A CONTROL OF CONTROL O
   1040 ATGTGTTTCATA-----AAAGGATATTTATATCTCTGT 1072
   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
  589
32
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   Last sequence update)
Last annotation update)
                                 -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER
EMBL, AF183431; AAG22971.1; -
   Matches:
Conservative:
Mismatches:
   Ā
   Length:
  Indels:
   Gaps:
   US-09-771-161A-2 (1-1669) x Q9ESE8 (1-589)
   Created)
  01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-0CT-2003 (TrEMBLrel. 25, CG12Z49-PB (LD02989P).
  0.564
100.00
42.54%
23.88%
3.47%
   PRELIMINARY;
  Q13490; 1QBH.
  Percent Similarity:
Best Local Similarity:
  Alignment Scores:
Pred. No.:
  Q81N63;
  Query Match:
   Q8IN63
   RESULT 8
  Q81N63
  Score:
   OC OS GEN DATE OF OCCUPANT OCC
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  980 TCACCATCTTTAAATTTACTTCAAAATAAAGCATGTAAGTGACTGTTTTTCAAGAAGAA 1039
  ||||||| ||||||
|LeuAspAspLeuLeuGluAlaSerValLeuThrLysGluGluHisAspIleIleArgGln 469
   AAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACACTACTGACATCCAAGGAGAA 892
   490 AlaAlaAlaSerValPheLysAsnSerLeuLysGluValAspSerThrLeuTyrGluHis 509
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  530 GluGluGlnLeuArgArgLeuGlnGluGluArgThrCysLysValCysMetAspArgGlu 549
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  CTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGGACTATGAACTTGTTAGTACC
   Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.; "Cloning and Characterization of the Rat Homologs of the Inhibitor of Apoptosis Protein 1, 2, and 3 Genes.";
  Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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GO; GO:0006916; P:anti-apoptosis; IEA.
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InterPro: IPR001841; Znf_ring.
Pfam; PF00613; BIR; 3.
Pfam; PF00619; CARD; 1.
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RAM REDILINES-2196006; PubMed=10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RAM Amanatides P.G., Scherer S.E., Li P.M., Hoskins R.A., Galle R.F.,

RAM Bandtides P.G., Scherer S.E., Iti P.M., Abhubmen M., Henderson S.N.,

Button G.G., Wortman J.R., Yandell M.D., Zhang G., Chen L.X.,

RAM Bandon, C., Baster E.G., Helt G., Nelson C.R., Gabor G.L.,

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RAM Annil J.C., Abbayania A., An H.J., Andrews-Frankoch C., Baldwin D.,

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Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Reriters S., Frise E., Galle R.F., Garg N.S., George R.A.,

Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

Pacleb J., Paragas V., Park S., Puri V., Richards S., Scheeler F.,

A Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,

Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

Sequencing of Drosophila melanogaster genome.",

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
  Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hiradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Clupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., "Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; "Annocation of Drosophila melanogaster genome.", Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Ephydroidea; Drosophilidae; Drosophila.
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George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
S.E., Gibbs R.A., Rubin G.M., Venter C.J.; to the EMBL/GenBank/DDBJ databases.
   64 AlaValArgPheAlaSerSerSerLysGluAlaLysGluPheAlailePro-
   Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., R
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   to the EMBL/GenBank/DDBJ databases
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EMBL; BT004903; AAO47881.1; -.
FlyBase; FBgn0021776; mira.
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GO; GO:00008105; P:asymmetric protein localization; IGI.
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Mismatches:
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3.45%
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   Declares S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
A Banson J., A Manatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
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A Perriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
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A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
A pacleb J., Paragas V., Park S., Patel S., Ffeiffer B.,
A phouanenavong S., Pittman G.S., Patel S., Ffeiffer B.,
Williams S.M., Saveri S., Puri V., Richards S., Scheeler F.,
Killiams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
Sequencing of Drosophila melanogaster genome ";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
   64 AlavalArgPheAlaSerSerSerLysGluAlaLysGluPheAlailePro-----
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   Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
  Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AE003728; AAF55723.2; -. FlyBase; FBGn0021776; mira. GO; GO:00045180; C:basal cortex; NAS. GO:000045180; C:basal cortex; NAS. GO:0000105; P:seymmetric protein localization; IGI. SEQUENCE 829 AA; 93100 MM; BE3AEFD4A454EEAF CRC64;
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Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
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Mismatches:
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|----------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------|---------------------|-------------------------------------------------------------------------|---------------------------------------------------------------------|-----------------------------------------------------------------------------|--------------------------------------------------------------------------------------------|------------------------------|-----|-------------------------------------------------------------------------------------------------------------------------------|----------------------------------------|-------------------------------------------------------------------------------------------------------------------------|----------------------------|----------------------------------------------------------|-----|------------------------------------------------------------------|-------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------|--------|----------------------------------------------------------------------------------------------------------------------------------|-------------------------------------|
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  413 GGTCCACAAGAGGAATCATGTGGATCCTCT-----CAGCTCCATGAAAATAGTGGT
  Oryza sativa (Rice).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeee, Oryza.
   PAC
   STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
Noryaa sativa nipponbare(GA3) genomic DNA, chromosome 1,
clone:P0407B12.";
  Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP002843; BAB17189.1; -.
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869 AA; 97064 MW; E2E59640E0BE63B2 CRC64;
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  1145 CTCCCTCCATGACACTGCAGTATT 1168
   291 GlnAlaArgGluHisCysSerLeu 298
   US-09-771-161A-2 (1-1669) x Q9FTV4 (1-869)
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3.45%
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P0407B12.26.
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  413 GGTCCACAAGAGAATCATGTGGATCCTCTCAGCTCCATGAAAATAGTGGTTCTCCTGAA 472
   ArgleuArgPheArgProThrProSerHisThrAspThrAlaThrGlySerGly----- 117
   GGATCTCAAAAGGGCTGCATTCTGTGATCACAAGACCACTCCATGCTCTTCAGCAATAATA 652
  GlyalaserThrAlaAla-----SerThrProLeuHisSerAlaAlaThr 133
   653 AATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAGCCTGGTATAGCCCCAGCAGTGG 712
  ---ATCCAGAGCAAAAGGGAAGACATTGTGAACCAAATGACAGAAGCC---TGCCTTAAC 766
  CAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGGACTATGAACTTGTT 826
   --- ACCTCAAAAGTCAGACAATTACTAGAC 871
  GCCATTCACCTATGTGACAAGAAAAATGGAATTATCTCTGAACATACCTGTAAATCAT 412
  ---LysGluAspLysLysSerLysGlyLeuArgLeuPheArgThrProSerLeuProGln 99
  |||:::
| AlaValArgPheAlaSerSerLysGluAlaLysGluPheAlaIlePro------
   TGTTATTTTATGAAGCTGCATCACTGTCCTGGAAATCACAGTTGGGATAGCACCATTTCT
   Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
   "Miranda directs Prospero to a daughter cell during Drosophila
  Doe C.Q.,
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GO; GO:0008105; P:asymmetric protein localization; IGI
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IKeelina=Kataoka H., Skeath J.B., Nabeshima Y.,
Matsuzaki F.;
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Nature 390.625-629(1997).
BMBL; AB005661; BAA24111.1; -.
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FlyBase; FBgn0021776; mira.
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| 464TCTCCTGAAACTTCAAGGTCCTGCCAGCTCCTCAAGACAATGATTTTTA 51  357 LeuLeuLeuSerProSerArgSerGlyAsplleGluSerProLysAsplleLeu 37  515 TCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCCTGGAAATCACAGT 57  375 CysGluArgAspAlaGluCys                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | Qy         731 GACATTGTGACCAAATGACAGAAGCCTGCTTAACCAGTGGCTA                                                                                                                                                                                                                                                                                                                                                                                                 | Db 511 AspfrhrAsnSerLeudiudiydiuserLeuAsnLysGluHisGludinLysSerLysGlu 530  Qy 929 AACAAACAAATGGGTCTTCAG 949  :::::                 :::   Db 531 AspGluAsnSerGlyLeuGlu 537  RESULT 13  Q810W9  ID 00810W9  PRELIMINARY; PRT; 949 AA.  AC 0810W9  DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) DT 01-MAR-2003 (TrEMBLrel. 25, Last annotation update) DF Stearcyl-CoA desaturase (Acyl-CoA desaturase), DE Stearcyl-CoA desaturase, faty acid desaturase), DE Stearcyl-CoA desaturase, faty acid desaturase), DE Stearcyl-CoA desaturase, faty acid desaturase, SA DI STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AND STEARCH AN |                                       |

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   AGACAATTACTAGACACTGACATCCAAGGAGAAGAATTTGCCAAAGTTATAGTACAA
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AspLysIleAsnLeuTyrGly-IleTyrValPhePheLeuGlnThrPheTyrIle----
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   256 --AsnPheTrpileAsnAsnMetAsnIleAsnLeuPheLysArgMetIleHisIleLeuA
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Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.,
T "Prediction of the coding sequences of unidentified human genes. XIX.
The complete sequences of 100 new cDNA clones from brain which code
I DNA Res. 7:347-355 (2000).
R EMBL, ABAD1855.1; -.
R InterPro; IPR001611; LRR.
R InterPro; IPR001611; LRR.
R InterPro; IPR002017; Spectrin.
R InterPro; IPR002017; Spectrin.
R Ffam; PF00560; LRR; 4.
R SMARY; SM0446; LRRcap; 1.
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  227 TCCATGTATTTTGTACAAACATATAAAATGTGTTAGATTGTATTTTACTTCTATAATTTC
   39 AspSerThrLeuHisAlaValAsnLeuHisCysAsnAsnIleSerLysIleGluAlaIle
  eGluGlyLeuAsnThrLeuThrLysLeuTyrThrLeuAsnLeuSerCysAsnLeuIle--
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Mismatches:
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   Safieddine S., Ly D., Wang Y.-X., Wang C.-Y., Kachar B., Petralia R., Wenthold R.,
Wenthold R.,
CSCSYN, An ovel syntaxin-interacting protein enriched in the subapical region of inner hair cells.",
Mol. Cell. Neurosci. 0:0-0(2002).
EMBL, AF494296; AAM14616.1;
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   527 CAAGACTGTTATTTT---ATGAAGCTGCATCACTGTCCTGGAAATCACAGTTGGGATAGC
  Syntaxin-interacting protein OCSYN.

Guinea pig).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Mammalia, Eutheria, Robentia, Hystricognathi; Caviidae, Cavia.
  850 AAAAGTCAGACAATTACTAGACACTACTGACATCCAAGGAGAAGAATTTGCC 901
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## 5.1.6 Compugen Ltd. version : GenCore (c) 1993 Copyright

frame\_plus\_n2p model protein search, using nucleic

Run on:

April 12, 2004, 11:14:14 ; Search time 292 Seconds (without alignments) 3.125 Million cell updates/sec

AF027706 4369 score:

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**BLOSUM62** Scoring table:

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

874 segs, 182427 residues Searched: of hits satisfying chosen parameters: Total number

Minimum DB E Maximum DB E

length: 0 length: 2000000000 sed

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 7 summaries

\*pep:

Database

1: /home/sdavid/sdavid-tmp/apr04/swope161/US09925301.pep:\* 2: /home/sdavid/sdavid-tmp/apr04/swope161/6348573.pep:\* 3: /home/sdavid/sdavid-tmp/apr04/swope161/6033855.pep:\*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

27, Appi 1, Appii 1, Appii 3, Appii 4, Appii 5, Appii Sequence 1015, Ap Description Sequence 1 Sequence 3 Sequence 3 Sequence 4 Sequence US-09-925-301-1015 US-09-069-023-27 US-09-069-021-1 US-09-069-023-3 US-09-069-023-3 US-09-069-023-4 US-09-069-023-5 В Query Match Length 544 540 540 531 531 284 64.6 63.6 62.9 57.2 33.8 2849 2827 2821 2778 2778 2501 1475 Result No.

## ALIGNMENTS

|                                |                                                                |                         | and Antibodies                                             |                       |
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| RESULT 1<br>US-09-925-301-1015 | Sequence 1015, Application US/09925301<br>GENERAL INFORMATION: | APPLICANT: Rosen et al. | TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies | FILE REFERENCE: PA106 |
|                                |                                                                |                         |                                                            |                       |

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Mismatches:
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CURRENT FILING DAFE: 2001-08-10
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PRIOR FILING DATE: 2000-03-08
PRIOR PILING DATE: 1909-03-12
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933 CAGATAATGTATAGTGTCACAAGGACATCGACCTGTTATTAATGAAGAAAGTTTGCCA

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Patent No. 6348573
GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohiro
APPLICANT: Arekyoshi
APPLICANT: Koseki, Tarkeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
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CURRENT FILING DATE: 1998-04-27
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Conservative:
Mismatches:
Indels:
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OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
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APPLICATION NUMBER: US/09/019,942
FILING DATE: 06-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
PILING DATE:
   ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/068001
TELECOMMUNICATION INFORMATION:
TELEPAX: 617/542-8906
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SEQUENCE CHARACTERISTICS:
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2821.00
99.81%
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64.57%
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Patent No. 6033855
GENERAL INFORMATION:
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TITLE OF INVENTION: DOMAIN POLYPEPTIDES
NUMBER OF SEQUENCES:
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ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
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COMPUTER READABLE FORM:
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DB:
   TYPE: PRT
ORGANISM: Homo
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  US-09-069-023-1
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   261 HisargalaargmetIleSerLeuIleGluSerGlyTrpalaGlnAsnProAspGluArg 280
   TyrPheMetLysLeuHisHisCysProGlyAsnHisSerTrpAspSerThrIleSerGly 400
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  241 SerValSerGlnGlyHisArgProvalIleAsnGluGluSerLeuProTyrAspIlePro 260
                       884
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CAGAATATCTTATTGGACAATGGATTTCATGTTAAGATTGCAGATTTTGGTTTATCAAAG 731 200 AAAACTGAATATCCTGATGTTGCTTGGCATTGACATTTCGCATCCTGCATGAAATTGCC 611 180 911 371 431 551 791 851 | Sequence 1, Application US/09069023A | Patent No. 6348573 | GENERAL INFORMATION | APPLICANT: Nunez, Gabriel | APPLICANT: Inchara, Nachiro | APPLICANT: Inchara, Nachiro | APPLICANT: Inchara, Nachiro | APPLICANT: Inchara, Nachiro | APPLICANT: Inchara, Nachiro | APPLICANT: Nace | Takeyoshi | TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS | TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS | FILE REPERENCE: UM-03333 | CURRENT APPLICATION NUMBER: US/09/069,023A | CURRENT FILING DATE: 1998-04-27 | NUMBER OF SEQ ID NOS: 38 | SOFTWARE: Patentin Ver. 2.0 | SEQ ID NO 1 | LENGTH: 531 TTACACAAAGCTAGATTTAGTTACATTCTTCCAATTTTGGGAATTTGCAATGAGCCTGAA 491 80 20 9 TTTTTGGGAATAGTTACTGAATACATGCCAAATGGATCATTAAATGAACTCCTACATAGG HislieHisThrProLeuLeuAspSerGluArgLysAspValLeuArgGluAlaGluIle TGGCGCATGATGTCCCTCTCACAGTCACGAAGTAGCAAATCTGCACCAGAAGGAGGACA ATTATCTATATGCCACCTGAAAACTATGAACCTGGACAAAAATCAAGGGCCAGTATCAAG GGCACTGTGTCGTCGCCCGCCACGCAGACTGGCGCGTCCAGGTGGCCGTGAAGCACCTG CACATCCACACTCCGCTGCTCGACAGTGAAAGGAAGGATGTCTTAAGGAAAGCTGAAATT

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TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS FILE REFERENCE: UM-03333
CURRENT APPLICATION NUMBER: US/09/069,023A
CURRENT FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
SEPTWARE: PALENT VEY: 2.0
SEQ ID NO 3
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Matches:
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US-09-069-023-3
; Sequence 3, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Numez, Gabriel
; APPLICANT: Inohara, Nachiro
; APPLICANT: Coseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
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LENGTH: 478
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   CAAATGACAGAAGCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATC 1631
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GAGGAATCATGTGGATCCTCTCAGCTCCATGAAAATAGTGGTTCTCCTGAAACTTCAAGG 1310
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  Sequence 4, Application US/09069023A
; Sequence 4, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
    APPLICANT: Inohara, Nachiro.
    APPLICANT: Inohara, Nachiro.
    APPLICANT: Koseki, Takeyoshi
    TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
    TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
    TITLE OF INVENTION NUMBER: US/09/069,023A
    CURRENT APPLICATION NUMBER: US/09/069,023A
    CURRENT PILING DATE: 1998-04-27
    NUMBER OF SEQ ID NOS: 38
    SOFTWARE: Patentin Ver. 2.0
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US-09-069-023-5

Sequence 5, Application US/09069023A

Sequence 5, Application US/09069023A

Sequence 5, Application US/09069023A

Sequence 5, Application US/09069023A

Sequence 6, Application:

APPLICANT: Nunez, Gabriel

APPLICANT: Nunez, Gabriel

APPLICANT: Koseki, Takeyoshi

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APPLICANT:

TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS

TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS

TITLE OF INVENTION WIMBER: US/09/069,023A

CURRENT APPLICATION NUMBER: US/09/069,023A

CURRENT FILING DATE: 1998-04-27

NUMBER OF SEQ ID NOS: 38

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 5

LENGTH: 284

TYPE: PRT

TYPE: PRT

CREANISM: Homo sapiens

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Matches:
Conservative:
Mismatches:
   Indels:
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1475.00
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(c) 1993 - 2004 Compugen Ltd.
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- nucleic search, using sw model nucleic April 12, 2004, 09:56:56; Search time 154 Seconds (without alignments)
4.025 Million cell updates/sec Run on:

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Perfect score:

1 ggcaccagtctctagaaaag......aaagtcaacagcctgatgtg 2501 Sequence:

Gapop 10.0 , Gapext 0.5 IDENTITY NUC Scoring table:

5 seqs, 123919 residues Searched:

10 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 5 summaries

\*:\*¤ Database

/home/sdavid/sdavid-tmp/apr04/swope161/ai824070.gb\_est1:\*
/home/sdavid/sdavid-tmp/apr04/swope161/aaz48762.genesegn20008:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|        |                    |                               | Human B1 cDNA. Ho |          |          | ACCESSION: AI824070 |  |
|--------|--------------------|-------------------------------|-------------------|----------|----------|---------------------|--|
|        | αı                 | 1 2490.5 99.6 2502 2 AAZ48762 | AAX02558          | AAZ09246 | AC004003 | A1824070            |  |
|        | 80                 | 7                             | m                 | 4        | Ŋ        | П                   |  |
|        | Match Length DB ID | 2502                          | 2098              | 1931     | 116650   | 738                 |  |
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| Result | No.                | -                             | 7                 | m        | 4        | S<br>S              |  |
|        |                    |                               |                   |          |          |                     |  |

## ALIGNMENTS

AAZ48762 standard; cDNA; 2502 BP. Human RICK coding sequence 21-MAR-2000 (first entry) AAZ48762; 

RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC; crapase-8; caspase-10; CD95 signalling; apoptosis signalling pathway; CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation; gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS; aplastic anaemia; ischaemic injury; toxin-induced liver disease; ss.

Homo sapiens

This sequence encodes the human RICK (RIP-like interacting CLARP kinase)

Co Tapoptosis, potentiating apoptosis induced by caspase-8 and caspase-10

during CD95 signalling. The invention provides methods for identifying

during CD95 signalling pathway inhibitors and activators, and methods and

compositions for screening compounds which will modulate the interactions

CC compositions identified: ARC, RICK, and the CIDE family of

activators (GIDE-A, CIDE-B and DREPL). RICK is useful in screening

catalyators (GIDE-A, CIDE-B and DREPL). RICK is useful in screening

compositions identified: ARC, so and the CIDE family of

cativators (GIDE-A, CIDE-B and DREPL). RICK is useful in screening

conflosted with excess cell growth and dysregulation of

disease associated with excess cell growth and dysregulation of

catoptosis. Complexes containing RICK and CLARP can be used in drug

screening assays to identify inhibitor molecules blocking CD95-mediated

conflostification of ARC-like inhibitory compounds may be useful for gene

thrapy treatment of disease with increased cell death in muscle tissue

conflostification of ARC-like inhibitory compounds may be useful for gene

thrapy treatment of disease with increased cell death in muscle tissue

can deadiac disorders. Therapeutic compositions of CIDEs can be used to

treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia,

can be used as resqents for the preparation or affinity chromatography

media, and for diagnostically measuring RICK levels. A specific inhibitor

conf an essential step in the biochemistry of apoptosis is needed. RICK

cinteraction with intracellular factors such as CLARP and PADD appears to

be essential for apoptosis, inhibitors of RICK binding to intracellular

cup propressis factors are potential drug candidates Compositions for identifying apoptosis signaling pathway inhibitors useful for treating diseases. Length 2502; Sequence 2502 BP; 769 A; 535 C; 499 G; 699 T; 0 U; 0 Other; 0; Indels DB 2; 99.6%; Score 2490.5; DB 3 Koseki T; Claim 8; Fig 7b; 93pp; English. 99WO-US009183. 98US-00069023 Matches 2501; Conservative (UNMI ) UNIV MICHIGAN Nunez G, Inohara N, WPI; 2000-072163/06. P-PSDB; AAY59404. Local Similarity W09955134-A2 27-APR-1999; 27-APR-1998; Query Match 

ä 240 180 120 120 180 240 299 9 9 CGCAGCAGGGGCACACCCGGAACCGGCCTGAGCGCCCGGGACCATGAACGGGGAGGCCA GGCACCAGTCTCTAGAAAAGAAGTCAGCTCTGGTTCGGAGAAGCAGCGGCTGGCGTGGGC CATCCGGGGAATGGGCGCCCTCGTGACCTAGTGTTGCGGGGCAAAAAGGGTCTTGCCGGC CATCCGGGGAATGGGCGCCCTCGTGACCTAGTGTTGCGGGGCAAAAAGGGTCTTGCCGGC CTCGCTCGTGCAGGGGCGTATCTGGGCCCCTGAGCGCCGCAGTGGGAGCCTTGGGAGCCGC cecaecaegegeacaccecaegeaccegecereaececcecegeaccareaacegeaegeae GGCACCAGTCTCTAGAAAAGAAGTCAGCTCTGGTTCGGAGAAGCAGCGCCTGGCGTGGGC CTCGCTCGTGCAGGGCGTATCTGGGCGCCTGAGCGCGCAGTGGGAGCCTTGGGAGCCGC TCTGCAGCGCCC-TGCCCACCATTCCCTACCACAAACTCGCCGACCTGCGCTACCTGAGC Gaps 1; 100.0%; Prec. ... 61 121 181 61 121 181 241 g g g ઠે ઠ ð q ò ð

300 CGCGGCGCCTCTGGCACTGTGTCGTCCGCCCACGCAGACTGGCGCGCGTCCAGGTGGCC 359 241 rergeagedeceargeceaectarreceracaeaaeregeegacergegeracergage

|                                                                                                                                         |   | 립 · S      | 1381 CATCACTGTCCTGGAAATCACAGTTGGGATAGCACCATTTCTGGTTCTCAAAGGGCTGCA 1440<br>1440 TTCTGTGATCACAAGACCACTCCATGCTCTTCAGCAATAATAAATCCACTGTGAACTGCA 1499 |
|-----------------------------------------------------------------------------------------------------------------------------------------|---|------------|--------------------------------------------------------------------------------------------------------------------------------------------------|
| GTGAAGCACCTGCACACTCCGCTGCTCGACAGTGAAAAAGATGTCTTAAGA 419<br>                                                                             |   | <b>경</b> 원 | TTCTGTGATCACAAGACCACTCCATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCA 15                                                                                  |
| GAAGCTGAAATTTTACACAAAGCTAGATTTAGTTACATTCTTCCAATTTTGGGAATTTGC 479<br>                                                                    |   | ර් සි ර්   | GGAAACTCAGAACTCTGCAGCCTGGTATACCCCAGCAGCAGTCCAGAGCAAAGGGAA 156 GGAAACTCAGAACGTCTGCAGCCTGGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGGAA 156                   |
| AATGAGCCTGAATTTTTGGGAATAGTTACTGAATACATGCCAAATGGATCATTAAATGAA 539                                                                        |   | e d        | 162                                                                                                                                              |
|                                                                                                                                         |   | දු යු      | 1620 AGGGACTTGATCATGAAAGGGCTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCA 1679                                                                             |
|                                                                                                                                         |   | දු පු      | 1680 AAAGTCAGACAATTACTAGACACTACTGACATCCAAGGAGAAGAATTTGCCAAAGTTATA 1739<br>                                                                       |
| SATTT                                                                                                                                   |   | & a        | 1740 GTACAAAAATTGAAAGATAACAAACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTG 1799<br>                                                                       |
|                                                                                                                                         |   | දු දු      | 1800 GTTTCTAGATCACCATCTTTAAATTTACTTCAAAATAAAAGCATGTAACTGACTG                                                                                     |
| GGTTTATCAAAGTGGGGGTGATGATGTCCCTCTCACAGTCACGAAGTAGCAAATTCTGCACCA 780<br>GAAGGAGGGACAATTATCTATATGCCACCTGAAAACTATGAACCTGGACAAAAATCAAGG 839 |   | දු දු      | 1860 CAAGAAGAAATGTGTTTCATAAAAGGATATTTATATCTCTGTTGCTTTGACTTTTTTAT 1919<br>                                                                        |
|                                                                                                                                         |   | & 4s       | 1920 ATAAAATCCGTGAGTATTAAAGCTTTTATTGAAGGTTCTTTGGGTAAATATTAGTCTCCCT 1979<br>                                                                      |
|                                                                                                                                         |   | S S        | 1980 CCATGACACTGCAGTATTTTTTAATTAATACAAGTAAAAGTTGAATTTGGTTGAATT 2039<br>                                                                          |
| CAAGGA                                                                                                                                  |   | y d        | 2040 IGCTACATAGITCAATITITAAGICTCTITIGITAACAGAAACCACTITIAAAGGAIAGI 2099<br>                                                                       |
| CGTATG 102<br>TTAAAA 107<br>                                                                                                            |   | y<br>D     | 2100 AAITAITCITGITTAIAACAGIGCCITAAGGIAIGAIGIATITICIGAIGGAAGCCAITIT 2159 2101 AAITAITCITGIITAIAACAGIGCCITAAGGIAIGAAGTAITTICIGAAGGAAGCCAITIT 2160  |
|                                                                                                                                         |   | % a        | 2160 CACATICAIGITCITCAIGGAITAITIGITACTIGICTAAGAIGCAAITIGAITITAIGA 2219<br>                                                                       |
| GAAGCT<br>TGTGAC                                                                                                                        |   | 상 점        | 2220 AGTATATACCCTTTACCCACCAGAGACAGTACAGAATCCCTGCCCTAAAATCCCAGGCTT 2279                                                                           |
|                                                                                                                                         |   | \$ g       | 2280 AATTGCCCTACAAAGGGTTATTAATTTAAACTCCATTATTAGATTACATTTTAAAGTT 2339<br>                                                                         |
| GAATCA                                                                                                                                  |   | જ <u>લ</u> | 2340 TTATTTATGAATTCCCTTTAAAAATGATATTTCAAAGGTAAAACAATACAATATAAAGAA 2399<br>                                                                       |
| TGTGGATCCTCTCAGCTCCATGAAAAAGGTTCTCCTGAAACTTCAAGGTCCCTGCCA 1320<br>GCTCCTCAAGACAATGATTTTTTTTTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTG 1379  | - | 상 원        | 2400 AAAAATAAATAATAATAATACGGCTTCCTGTCCCCATTTTTAACCTCAGCCTTCCCTACT 2459 [                                                                         |
| GCTCCTCAAACAATGATTTTTTTTTAAAAAAGCTCAAGACTGTTATTTTATGAAGCTG 1380<br>CATCACTGTCTGGAAATGCGAATAGGAATAGCACCATTTCTGGATTCTCAAAGGGCTGCA 1439    |   | දු දු      | 2460 GTCACCAACAACCAAGCTAAATAAAGTCAACAGCCTGATGTG 2501<br>                                                                                         |
|                                                                                                                                         |   | t<br>i     |                                                                                                                                                  |

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ATCGACCTGTTATTAATGAAGAAAGTTTGCCATATGATATACCTCACCGAGCACGTATGA 1055
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   cczyrcreaca 1235
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  AGAAGAAATGGAATTATCTCTGAACATACCTGTAAATCATGGTCCACAAGAGGAATCAT 1295
  Gregarcerereagerecargaaaragregereereaaacreeaaggreereeag 1355
  CICCICAAGACAAIGAITITITIAICIAGAAAAGCICAAGACIGIIATITIAIGAAGCIGC 1380
   276 TCTGCAGCGCCCTGCCCACCATTCCCTACCACAACTCGCCGACCTGCGCTACCTGAGCC 335
   AACAGCCTTTTGAAGATGTCACCAATCCTTTGCAGATAATGTATAGTGTGTCACACAAGGAC 960
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   CICCTCAAGACAATGATTTTTATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGC
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  New B1 protein regulates cell death and cell survival pathways -
derivatives, DNA and antibodies, also regulate intracellular inflammation
; for treating AIDS, cancer.
   This invention describes the isolation of a novel human B1 protein which can interact with, intracellular mediators or modulators of inflammation, cell death and/or cell survival pathways, directly or indirectly. Cells can be modulated or mediated in inflammation, cell death or cell survival pathways or another intracellular signalling activity using B1. Conditions such as AIDS and cancer can be treated using B1. Antibodies, oligonucleotides and ribozymes can also be used to regulate the above
  275
   300
  120
   155
  180
   215
   240
  95
   B1 protein; intracellular mediator; modulator; inflammation; cell death; cell survival pathway; intracellular signalling; AIDS; cancer; human; ss.
   9
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   CGCAGGAGGGGGCACACCCCGGAACCGGCCTGAGCGCCCGGGAACCATGAACGGGGAGGCCA
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  CATCCGGGGAATGGGCGCCCTCGTGACCTAGTGTTGCGGGGCAAAAAGGGTCTTGCCGGC
   CATCCGGGGAATGGGCGCCCTCGTGACCTAGTGTTGCGGGGCAAAAAGGGTCTTGCCGGC
  CTCGCTCGTGCAGGGGCGTATCTGGGCGCCTGAGCGCGCAGTGGGAGCCTTGGGAGCCGC
   credenteracides de contrator de 
   CGCAGCAGGGGGCACACCCGGAACCGGCCTGAGCGCCCGGGACCATGAACGGGGAGGCCA
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  80.7%; Score 2017.8; DB 3; Length 2098; larity 99.3%; Pred. No. 1.1e-06; Conservative 9; Mismatches 6; Indels 0;
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  Malinin N;
  ВР
   Claim 4; Fig 3B; 90pp; English
  AAX02558 standard; cDNA; 2098
  (YEDA ) YEDA RES & DEV CO LTD
  97IL-00121011.
97IL-00121199.
  98WO-IL000255
   97IL-00121746
   entry)
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   (first
   WPI; 1999-070258/06.
P-PSDB; AAW92795.
   Local Similarity
nes 2016; Conserv
  05-JUN-1997;
30-JUN-1997;
11-SEP-1997;
  Homo sapiens
  W09855507-A2
  01-JUN-1998;
   07-MAY-1999
   10-DEC-1998
   Wallach D,
  Human B1
  36
  61
   96
  121
   156
   181
  216
  241
   AAX02558
  Query Match
  Best Loca
Matches
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   TITCTAGAICACCAICTITAAAITITACTICAAAATAAAAGCAIGTAAGTGACTGTTTTTC 1860
  GGGACTTGATCATGAAAGAGGACTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAA 1680
   1681 AAGTCAGACAATTACTAGACACTACTGACATCCAAGGAGAAGAATTTGCCAAAGTTATAG 1740
   AAGAAGAAATGTGTTTCATAAAAGGATATTTATATCTCTGTTGCTTTGACTTTTTTTATA 1920
  TATTGAAGGTTCTTTGGGTAAATATTAGTCTCCCTC 1980
                   1475
   1500
   1595
   1655
   1656 GGGACTTGATCATGAAGAGGACTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAA 1715
   1476 TCTGTGATCACAAGACCACTCCTTCTTCAGCAATAATAATCCACTCTCAACTGCAG 1535
   GAAACTCAGAACGTCTGCAGCCTGGTATAGCCCCAGCAGTGGATCCAGAGCAAAAGGGAAG 1560
  1620
  1596 ACATTGTGAACCAAATGACAGAAGCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCA
   1741 TACAAAAATTGAAAGATAACAAACAAATGGGTCTTCAGCCTTACCCCGGAAATACTTGTGG
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  TAAAATCCGTGAGTATTAAAGCTT
  CATGACACTGCAGTATTTTTT
   1896
  1921
  1981
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AAZ09246 standard; cDNA; 1931 AAZ09246;

BP

(first entry) 25-OCT-1999

Human CARD-3 cDNA.

CARD-3; caspase recruitment domain; CARD-4; regulation; detection; caspase activation; detection; screening; therapy; diagnosis; disease; apoptotic cell death; Fas/APO-1 receptor complex; ancer; follicular lymphoma; carcinoma; p53 mutation; viral infection; hormone-dependent tumour; autoimmune disorder; Alzheimer's disease; systemic lupus erythematosis; immune-mediated glomerulonephritis; stroke; Parkinson's disease; amyotrophic lateral degeneralis; retinitis pigmentosa; spinal muscular dystrophy; cerebellar degeneration; anaemia; drug; myelodysplastic syndrome; myocardial infarction; cell proliferation; cell differentiation; cell survival; CARD-45; CARD-47; CARD-42; human; ds. 

Homo sapiens

Location/Qualifiers 214. .1836 /\*tag= a

Key

/product= "CARD-3" WO9940102-A1

98US-00019942. 99WO-US002544 05-FEB-1999; 06-FEB-1998;

98US-00099041. 98US-00207359. 08-DEC-1998;

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(MILL-) MILLENNIUM PHARM INC.

Bertin J;

WPI; 1999-494269/41. P-PSDB; AAY31140.

Novel CARD-3 and CARD-4 genes and polypeptides used or treating regulation of cellular proliferation and differentiation and cell survival.

Example 2; Fig 1; 181pp; English.

This invention describes the isolation of novel human caspase recruitment domain, CARD-3 and CARD-4 polynuclectides and proteins and a partial murine CARD-1 protein and genes. The genes and proteins of the invention are involved in the regulation of caspase activation. The caspase crecinitment domain (CARD) polynuclectides, polypeptides, homologues and recruitment domain (CARD) polynuclectides, polypeptides, homologues and antibodies can be used in squeening assays, detection assays, predictive methods may be used to diagnose and treat patients which are suffering from a disorder associated with abnormal level or rate of apportoric cell death, abnormal activity of the TMF receptor complex, abnormal activity of the TMF receptor complex, abnormal activity of the TMF receptor complex, or abnormal activity of the ray be treated fuclude cancer (particularly follicular curvity of the TMF receptor complex, or abnormal activity of the ray be treated fuclude cancer (particularly follicular compendent tumours), autoingmune disorders (e.g. systemic lupus cappendent particular springmune disorders (e.g. systemic lupus cappendent particular dystrophy, cerebellar degeneration, and stroke. CC CARD-3 protein interacts with other cellular proteins, and so can be used for survival. The CARD proteins may also be used to for screen drugs or survival. The CARD proteins may also be used to for screen drugs or compounds which modulate their activity. The CARD-4 specen drugs or compounds which modulate their activity. The CARD-4 specen drugs or cappendent the mann CARD-4 splice variants, CARD-4 and CARD-42. This sequence cappendent the human CARD-4 splice variants, CARD-41 in the method of the invention 

Sequence 1931 BP; 613 A; 429 C; 416 G; 473 T; 0 U; 0 Other;

ö 202 83 GTGACCTAGTGTTGCGGGGCAAAAAGGGTCTTGCCGGCCTCGCTGCTGCAGGGGCGTATC 142 71 TGGGCGCCTGAGCGCGCAGTGGGAGCCTTGGGAGCCGCCGCAGCAGGGGGGCACACCCGGA 12 GTCAGCTCTGGTTCGGAGAAGCAGCGGCTGGCGTGGGCCATCCGGGGATGGGCGCCTC GTCAGCTCTGGTTCGGAGAAGCAGCGGCTGGCGTGGGCCCATCCGGGGAATGGGCGCCTTC ö Query Match
Best Local Similarity 99.7%; Pred. No. 5.3e-06;
Matches 1867; Conservative 0; Mismatches 5; Indels 0 143 72 23 셤 셤 ò ò ਨੇ

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AC004003 116650 bp DNA linear PRI 21-DEC-1999
Homo sapiens BAC clone CTA-437L15 from 8q21, complete sequence.
AC004003
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   1762
  1822
1451
   1511
  1582
  1702
  1691
   USA
  USA
   AGCCTGCCTTAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGGA 1631
   USA
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 11650)
Ozersky, P., Holmes, A. and Broy, M.
The sequence of Homo sapiens BAC clone CTA-437L15
Onpublished
2 (bases 1 to 116650)
Waterston, R.
  Department of Genetics, Washington
Park Avenue, St. Louis, Missouri 63108,
  CTATGAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACAC
   Washington
Missouri 63108,
  TTGGGATAGCACCATTTCTGGTTCTCAAAGGGCTGCATTCTGTGATCACAAGACCACTCC
  TIGGGATAGCACCATITCTGGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCATTCC
  TGGTATAGCCCAGCAGTGGATCCAGAGCCAAAAGGGAAGACATTGTGAAACCAAATGACAGA
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   Department of Genetics,
Park Avenue, St. Louis,
  Direct Submission
Submitted (27-UN-1998) Di
University, 4444 Forest P4
4 (bases 1 to 116650)
Waterston,R.
   Direct Submission
Submitted (15-JAN-1998)
University, 4444 Forest
3 (bases 1 to 116650)
  AC004003.1 GI:2772557
   Homo sapiens (human)
  1894
  1883 AGGATATTATA
  Waterston, R
   Ношо
   1572
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   AAGTTTGCCATATGATATACCTCACCGAGCACGTATGATCTCTCTAATAGAAAGTGGATG 1042
  GGCACACAAATCCCAGATGAAAGACCATCTTTCTTAAAATGTTTAATAGAACTTGAACCAGT 1102
   1032 GGCACAAAATCCAGATGAAAGACCATCTTTCTTAAAATGTTTAATAGAACTTGAACCAGT 1091
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  1343 ATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCCTGGAAATCACAG 1402
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   TAGATTTAGTTACATTCTTCCAATTTTGGGAATTTGCAATGAGCCTGAATTTTTGGGAAT 491
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   682
   671
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  GCCACCTGAAAACTATGAACCTGGACAAAAATCAAGGGCCAGTATCAAGCACGATATATA 862
  852 TAGCTATGCAGTTATCACATGGGAAGTGTTATCCAGAAAACAGCCTTTTGAAGATGTCAC 911
  912 CAATCCTTTGCAGATAATGTATAGTGTGTCACAAGGACATCGACCTGTTATTAATGAAGA 971
                                    311
  GTCCGCCCGCCACACACAGGCGCGTCCAGGTGGCCGTGAAGCACCTGCACATCCACAC 382
  312 Grececececedecadacregecerecederegecereaageaceregeacarecadae 371
  TAGATTTAGTTACATTCTTCCAATTTTGGGAATTTTGCAATGAGCCTGAATTTTTGGGAAT 502
   AGTTACTGAATACATGCCAAATGGATCATTAAATGAACTCCTACATAGGAAAACTGAATA 551
  ATTGGACAATGAATTTCATGTTAAGATTGCAGATTTTTGGTTTATCAAAGTGGCGCATGAT 742
   GTCCCTCTCACAGTCACGAAGTAGCAAATCTGCACCAGAAGGAGGGACAATTATCTATAT 802
  791
   TAGCTATGCAGTTATCACATGGGAAGTGTTATCCAGAAAACAGCCTTTTGAAGATGTCAC 922
  CAATCCTTTGCAGATAATGTATAGTGTGTCACAAGGACATCGACCTGTTATTAATGAAGA 982
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   TTACCTGCACAATATGACTCCTCTTTACTTCATGACTTGAAGACTCAGAATATCTT
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   1103
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  683
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   623
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   Clone CTA-437115 is from a release of the human BAC library CTTB-HS-A. The library contains cloned DNA from human sperm. See: Shizuya et al., proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). The clone is available from Research Genetics, Inc. (http://www.resgen.com).
  NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
   This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
   NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is CTA-237G1. The actual start of
this clone is at base position 1 of CTA-437L15; actual end is at
116650 of CTA-437L15.
   This chromosome 8 clone was provided by Dr. Patrick Concannon (patcon@vmmc.org) at the Virginia Mason Research Institute.
   note="CpG island (%GC=69.1, o/e=0.80, #CpGs=93)"
   This clone contains STS HS275YF1 (NID:g1051703).
Location/Qualifiers
1. .116650
/organism="Homo sapiens"
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
  /872. .40218
/gene="WUGSC:H_RG437L15.1"
  Center project name: H_RG437L15
  5641. ,6075
/rpt_family="Retroviral"
6133. ,6433
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150. 530
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Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Parayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
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www-bio.llnl.gov/bbrp/image/image.html
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Location/Qualifiere

Location/Considerations
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Fatima Bonaldo.

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